

From: Leffers, Gerald
Sent: Thursday, May 01, 2003 3:12 PM
To: STIC-Biotech/ChemLib
Subject: FW: 09/846,456

Thanks for your help. gerry leffers

Gerald G. Leffers Jr., PhD
Examiner, Art Unit 1636
Crystal Mall 1, Room 11A09
703-308-6232

-----Original Message-----

From: Fredman, Jeffrey
Sent: Thursday, May 01, 2003 2:47 PM
T : Leffers, Gerald
Subject: RE: 09/846,456

Gerald,

I don't think you need approval unless it is a rush. You are under the 10,000 nucleotide limit.

Jeff

-----Original Message-----

From: Leffers, Gerald
Sent: Thursday, May 01, 2003 2:00 PM
To: Fredman, Jeffrey
Subject: 09/846,456

Hi Jeff, please approve the following searches for this application. Total nucleic acid length is ~7 kb. SEQ ID NO: 1 (3.2kb), SEQ ID NO: 2 (357 nts), SEQ ID NO: 3 (2.8 kb), SEQ ID NO: 5 (159 nts). Claims drawn to 30 contiguous nucleotides of SEQ ID NOS: 3 & 5; 300 contiguous nucleotides of SEQ ID NO: 1. Other claims to nucleic acids comprising all of SEQ ID NO: 1 or SEQ ID NO: 2. Thanks, Gerry Leffers

Gerald G. Leffers Jr., PhD
Examiner, Art Unit 1636
Crystal Mall 1, Room 11A09
703-308-6232

11E12
MB

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 5/2
Date Completed: 5/12
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version: 5.1.5
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GenCore - nucleic search, using sw model

Run on: May 9, 2003, 11:17:01 : Search time 4647.97 seconds
(without alignments)
9746.207 M.110n cell updates/sec

Title: US-09-846-456-1

Perfect score: 3231
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum db seq length: 0
Maximum db seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: qb_hg:*
- 3: qb_in:*
- 4: qb_om:*
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- 31: em_hg_inv:*
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- 41: em_hg_other:*

Pred. NO. is the number of results predicted by chance to have 1

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	2893	89.5	2893	6	AX351031	Sequence
6	1773	54.9	149034	9	AF275948	Homo sapi
7	1485.4	46.0	1643	6	AX060715	Sequence
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33	347.4	10.8	141762	9	HS198C21	Human DNA
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38	345	10.7	174009	9	AC007842	Homo sapi
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41	342.4	10.6	185153	9	AL162732	Human DNA
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ALIGNMENTS

RESULT 1	AX351029	AX351029	4231 bp	DNA	linear	PAT 06-FEB-2002
LOCUS	Sequence 1 from Patent WO0184746.					
DEFINITION	Sequence 1 from Patent WO0184746.					
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VERSION	AX351029.1	GI:18616385				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
	Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P.,					
	Brewer, B., Duvetier, N., Remaley, A. and Santamarina-Fojo, S.					
TITLE	Regulatory nucleic acid sequences of the abcl gene					

QY	362	AGATGAAGAAACAGCCGGGACAAATGGCTTAATTCCTCAGACAC:TTGGGAGGC	421
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QY	602	TGAGCCATGATGGATCACTCCAGCTCGCTTAGACAGAGCAAGACCGTGTCTGCA	661
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DB	18831	AGTACCTGGGACTCCAGAAATTCCTTGCCTGGTGGCTTCCACATAGCACTTCCAGGCGCTG	18772
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AUTHORS Gu, Y., Cavellier, L., Chiu, S., Yang, X., Rubin, E. and Chandra, J. F.
TITLE Human and mouse ABCA1 comparative sequencing and transgenesis
studies revealing novel regulatory sequences
GENOMICS 73 (1), 66-76 (2001)
MEDLINE 21251004
PubMed 1132567
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AUTHORS Gu, Y., Cavellier, L., Chiu, S., Rubin, E. and Chandra, J. F.
TITLE Direct Submission
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LOCUS Homo sapiens ABCA1 (ABCA1) gene, complete cds.
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ACCESSION AF275948
VERSION AF275948.1 GI:9247085
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 149034)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Cheng J.F., Osorio J., Remaley A., Yang X.P., Haudenschield C.,
Prades C., Chimini G., Blackmon E., Francois T., Duverger M.,
Rubin E.M., Rosier M., Deneffe P., Fredrickson D.S. and Brewer H.B.
Jr.
TITLE Complete genomic sequence of the human ABCA1 gene: analysis of the
human and mouse ATP-binding cassette A promoter
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
MEDLINE 20345099
PUBMED 10884428
REFERENCE 2 (bases 1 to 149034)
AUTHORS Santamarina-Fojo S., Peterson K.M., Knapper C.L., Freeman L.A.,
Remaley A.T., Yang X.-P., Haudenschield C.C., Blackmon E.E.,
Francois T.L. and Brewer H.B. Jr.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Health, Lung and Blood Institute,
Bethesda, MD 20892, USA

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Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, K., Rothman, P., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thornann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., Zimmer, A., and Zody, M.

Direct Submission

Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
(on Jul 13, 2000 this sequence version replaced at: 6765871)

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/km/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2512

Center clone name: L_N_10

* NOTE: This record contains 73 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion in the event that

* the record is updated, the accession number will

* be preserved.

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* 32369 32468: gap of 100 bp

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[illegible]

Quality coverage: 3.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 113579 113678: contig of 6062 bp in length

* 113679 113778: contig of 6062 bp in length

* 113779 113878: contig of 6062 bp in length

* 113879 113978: contig of 6062 bp in length

* 113979 114078: contig of 6062 bp in length

* 114079 114178: contig of 6062 bp in length

* 114179 114278: contig of 6062 bp in length

* 114279 114378: contig of 6062 bp in length

* 114379 114478: contig of 6062 bp in length

* 114479 114578: contig of 6062 bp in length

* 114579 114678: contig of 6062 bp in length

* 114679 114778: contig of 6062 bp in length

* 114779 114878: contig of 6062 bp in length

* 114879 114978: contig of 6062 bp in length

* 114979 115078: contig of 6062 bp in length

* 115079 115178: contig of 6062 bp in length

* 115179 115278: contig of 6062 bp in length

* 115279 115378: contig of 6062 bp in length

* 115379 115478: contig of 6062 bp in length

* 115479 115578: contig of 6062 bp in length

* 115579 115678: contig of 6062 bp in length

* 115679 115778: contig of 6062 bp in length

* 115779 115878: contig of 6062 bp in length

* 115879 115978: contig of 6062 bp in length

* 115979 116078: contig of 6062 bp in length

* 116079 116178: contig of 6062 bp in length

* 116179 116278: contig of 6062 bp in length

* 116279 116378: contig of 6062 bp in length

* 116379 116478: contig of 6062 bp in length

* 116479 116578: contig of 6062 bp in length

<

```
Query Match 17.1%; Score 553.8; DB 2; Length 175064;
Best Local Similarity 84.0%; Pred. No. 1.1e-137;
Matches 569; Conservative 0; Mismatches 107; Indels 1; Gaps 1;

QY 2 CAGGCGATGGTGGCAGGTGCGCTGTATCTCACTTACTCGGAGGTGGAGGTGCAATGAG 61
DB 1678 CCGGGCATGGTGGCAGGTGCGCTGTATCTCACTTACTCGGAGGTGGAGGTGCAATGAG 1619
QY 62 CCCAGATGCGACCATTTGGTGGTGGACCTTCAAAATAGGTAGGAGAGAGAGAGAGAG 121
DB 1618 CCCAGATGCGACCATTTGGTGGTGGACCTTCAAAATAGGTAGGAGAGAGAGAGAGAG 1559
QY 122 AAAAAAAGAAATGATTTTGGTGGTGGACCTTCAAAATAGGTAGGAGAGAGAGAGAGAG 181
DB 1558 AAAAAAAGAAATGATTTTGGTGGTGGACCTTCAAAATAGGTAGGAGAGAGAGAGAGAG 1499
QY 182 GATGAGGTGAGGAGATCAATTAATCTCTTAAATCATCTAGGAGAGATCAATTAAT 241
DB 1498 GATGAGGTGAGGAGATCAATTAATCTCTTAAATCATCTAGGAGAGATCAATTAAT 1439
QY 242 TTAATAACACTCTCTGCTTTTATAACATCATCTGCCAAGGAGCTGAAGCTTCAACAA 301
DB 1438 TTAATAACACTCTCTGCTTTTATAACATCATCTGCCAAGGAGCTGAAGCTTCAACAA 1379
QY 302 AGTTCACTTTCAGAAACCCCTTTGAGGAGACAGAAATATACATCTCTCTTAAATTTAA 361
DB 1378 AGTTCACTTTCAGAAACCCCTTTGAGGAGACAGAAATATACATCTCTCTTAAATTTAA 1319
QY 362 AGATCAAGAAACAGCGCGGACAAATGGCTATGCTGCTGTAATCCGAGCTTGGAGAG 421
DB 1318 AGATCAAGAAACAGCGCGGACAAATGGCTATGCTGCTGTAATCCGAGCTTGGAGAG 1259
QY 422 TGAGCCAGAGATCGCTTGAGCTCCAGAGTTTACAGACAGCTGGAGATTAAGTAAAGAA 481
DB 1258 TGAGCCAGAGATCGCTTGAGCTCCAGAGTTTACAGACAGCTGGAGATTAAGTAAAGAA 1199
QY 482 CCGTGTCTTACAAAAAATACAAAAATAGATGGGTGCTGTGTGATGAGCTGTGCTG 541
DB 1198 CCGTGTCTTACAAAAAATAGGAAATAGATGGGTGCTGTGTGATGAGCTGTGCTG 1139
QY 542 CCAGCTACTTGGAGGCTAAGGTGGAGGATCGCTTGAGCTGAGGAGGAGCTGAGCTAGAC 601
DB 1118 CCAGCTACTTGGAGGCTAAGGTGGAGGATCGCTTGAGCTGAGGAGGAGCTGAGCTAGAC 1080
QY 602 TGAGCCATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 661
DB 1079 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1020
QY 662 AAAAAAGAAATGAAGA 678
DB 1019 NNNNNNNNNNNNNNNNA 1003

RESULT 14
AC021246/c
LOCUS Homo sapiens clone RP11-1N12, LOW-PASS SEQUENCE SAMPLING,
AC021246
AC021246.2 GI:9119882
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Aldrich,N.,
TITLE Homo sapiens chromosome 1 clone RP11-1N12
JOURNAL
PUBLISHED
REFERENCE
AUTHORS Anderson,S., Baldwin,J., Batca,N., Beckert,J., Bickel,A.,
Bohuslavsky,I., Boukhvalter,B., Brown,A., Burkhardt,J., Bustillo,A.,
Choe,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArelano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardner,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howard,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehotsky,J., Levine,R., Liu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rotman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (15-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6705871.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2512
Center clone name: L_N10
-----
* NOTE: This record contains 73 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1 871: contig of 871 bp in length
* 872 971: gap of 100 bp
* 972 1834: contig of 863 bp in length
* 1835 1934: gap of 100 bp
* 1935 2804: contig of 870 bp in length
* 2805 2904: gap of 100 bp
* 2905 3745: contig of 841 bp in length
* 3746 3845: gap of 100 bp
* 3846 4696: contig of 851 bp in length
* 4697 4796: gap of 100 bp
* 4797 5640: contig of 844 bp in length
* 5641 5740: gap of 100 bp
* 5741 6540: contig of 800 bp in length
* 6541 6640: gap of 100 bp
* 6641 7509: contig of 869 bp in length
* 7510 7609: gap of 100 bp
* 7610 8479: contig of 870 bp in length
* 8480 8579: gap of 100 bp
* 8580 9430: contig of 851 bp in length
* 9431 9530: gap of 100 bp
* 9531 10376: contig of 846 bp in length
* 10377 10476: gap of 100 bp
* 10477 11322: contig of 846 bp in length
* 11323 12302: contig of 880 bp in length
* 12303 12402: gap of 100 bp
* 12403 13280: contig of 878 bp in length
* 13281 13480: gap of 100 bp
* 13481 14241: contig of 861 bp in length
* 14242 14441: gap of 100 bp
* 14442 15196: contig of 855 bp in length
* 15197 15296: gap of 100 bp
```

Choe,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArelano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J., Gardner,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howard,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Landers,T., Lehotsky,J., Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McPheters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rotman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

TITLE
JOURNAL

COMMENT

* 15297 16123: contig of 827 bp in length
* 16124 16223: gap of 100 bp
* 16224 17072: contig of 849 bp in length
* 17073 17172: gap of 100 bp
* 17173 18041: contig of 869 bp in length
* 18042 18141: gap of 100 bp
* 18142 19009: contig of 868 bp in length
* 19010 19109: gap of 100 bp
* 19110 19966: contig of 857 bp in length
* 19967 20066: gap of 100 bp
* 20067 20921: contig of 855 bp in length
* 20922 21021: gap of 100 bp
* 21022 21865: contig of 844 bp in length
* 21866 21965: gap of 100 bp
* 21966 22832: contig of 867 bp in length
* 22833 22932: gap of 100 bp
* 22933 23780: contig of 848 bp in length
* 23781 23880: gap of 100 bp
* 23881 24733: contig of 953 bp in length
* 24734 24833: gap of 100 bp
* 24834 25670: contig of 837 bp in length
* 25671 25770: gap of 100 bp
* 25771 26621: contig of 851 bp in length
* 26622 26721: gap of 100 bp
* 26722 27576: contig of 855 bp in length
* 27577 27676: gap of 100 bp
* 27677 28532: contig of 856 bp in length
* 28533 28632: gap of 100 bp
* 28633 29492: contig of 860 bp in length
* 29493 29592: gap of 100 bp
* 29593 30455: contig of 863 bp in length
* 30456 30555: gap of 100 bp
* 30556 31410: contig of 855 bp in length
* 31411 31510: gap of 100 bp
* 31511 32368: contig of 858 bp in length
* 32369 32468: gap of 100 bp
* 32469 33312: contig of 844 bp in length
* 33313 33412: gap of 100 bp
* 33413 34268: contig of 856 bp in length
* 34269 34368: gap of 100 bp
* 34369 35204: contig of 846 bp in length
* 35205 35304: gap of 100 bp
* 35305 36156: contig of 862 bp in length
* 36157 36256: gap of 100 bp
* 36257 37128: contig of 872 bp in length
* 37129 37228: gap of 100 bp
* 37229 38083: contig of 855 bp in length
* 38084 38183: gap of 100 bp
* 38184 39031: contig of 848 bp in length
* 39032 39131: gap of 100 bp
* 39132 40006: contig of 875 bp in length
* 40007 40106: gap of 100 bp
* 40107 40967: contig of 861 bp in length
* 40968 41067: gap of 100 bp
* 41068 41913: contig of 846 bp in length
* 41914 42013: gap of 100 bp
* 42014 42824: contig of 811 bp in length
* 42825 42924: gap of 100 bp
* 42925 43776: contig of 852 bp in length
* 43777 43876: gap of 100 bp
* 43877 44752: contig of 876 bp in length
* 44753 44852: gap of 100 bp
* 44853 45724: contig of 872 bp in length
* 45725 45824: gap of 100 bp
* 45825 46643: contig of 819 bp in length
* 46644 46743: gap of 100 bp
* 46744 47599: contig of 856 bp in length
* 47600 47699: gap of 100 bp
* 47700 48551: contig of 852 bp in length
* 48552 48651: gap of 100 bp
* 48652 49485: contig of 894 bp in length
* 49486 49585: gap of 100 bp
* 49586 50440: contig of 855 bp in length

* 50441 50540: gap of 100 bp
* 50541 51404: contig of 864 bp in length
* 51405 51504: gap of 100 bp
* 51505 52372: contig of 868 bp in length
* 52373 52472: gap of 100 bp
* 52473 53328: contig of 856 bp in length
* 53329 53428: gap of 100 bp
* 53429 54268: contig of 840 bp in length
* 54269 54368: gap of 100 bp
* 54369 55229: contig of 861 bp in length
* 55230 55329: gap of 100 bp
* 55330 56197: contig of 868 bp in length
* 56198 56297: gap of 100 bp
* 56298 57163: contig of 866 bp in length
* 57164 57263: gap of 100 bp
* 57264 58130: contig of 867 bp in length
* 58131 58230: gap of 100 bp
* 58231 59082: contig of 852 bp in length
* 59083 59182: gap of 100 bp
* 59183 60020: contig of 838 bp in length
* 60021 60120: gap of 100 bp
* 60121 60983: contig of 863 bp in length
* 60984 61083: gap of 100 bp
* 61084 61935: contig of 852 bp in length
* 61936 62035: gap of 100 bp
* 62036 62866: contig of 831 bp in length
* 62867 62966: gap of 100 bp
* 62967 63827: contig of 861 bp in length
* 63828 63927: gap of 100 bp
* 63928 64783: contig of 856 bp in length
* 64784 64883: gap of 100 bp
* 64884 65740: contig of 857 bp in length
* 65741 65840: gap of 100 bp
* 65841 66684: contig of 844 bp in length
* 66685 66784: gap of 100 bp
* 66785 67551: contig of 867 bp in length
* 67552 67751: gap of 100 bp

Query Match 15.38; Score 494; DB 2; Length 69570;

Best Local Similarity 92.2%; Pred. No. 1.2e-121;

Matches 518; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 2663 CCCCAGCCGACCCACCTGCCCCCAAGTCCTAGATGTGCTGGGGCGGTGAACGTGCGC 2722

DB 67642 CCCCCNNCCGACACACTCCCCAANTNATAAGATGTGCTGGGGCGGTGAACGTGCGC 67583

QY 2723 CGTTTAAGGGCGGGGCGGGGCHCCAGTGCCTTTCTGCTGAGTGACTGAACATACAAAC 2782

DB 67582 CGTATAAGGGCGGGGCGGGGCTACACGTCTTTGTGCTGAGTGACTGAACATACAC 67523

QY 2783 AGAGGCGTGGCAAGGGGCGGGGAGGAGGAGCAGAGGCTTTGACCGATAGTAACTCT 2842

DB 67522 AGAGCCCGGTAAGGGGCGGGGAGGAGGAGGAGCAGAGGCTTTGACTGATAGTAACTCT 67463

QY 2843 GCCTCGGTGCAACCGCAATCTATAAAGGAAGTATCCCGGCAAAACCCGTAATGCG 2902

DB 67462 GCCTCGGTGCAACCGCAATCTATAAAGGAAGTATCCCGGCAAAACCTGTAATGCG 67403

QY 2903 ACCGAGAGTGAAGTGGGGACCGGACCGCAGAGCCGAGCGACCCCTTCTCTCCCGGCTGC 2962

DB 67402 AGCGAGAGTGAAGTGGGGCGGGGACCGCAGAGCCGAGCGACCCCTTCTCTCCCGGCTGC 67343

QY 2963 GGCAGGCGAGGGGGGAGGCTCGGCGCACACAGAGCGGTTCTCAGGGCGCTTGGCTC 3022

DB 67342 GACAGGACAGGGCGGGGAGGCTCGGCGCACACAGAGCGGTTCTCAGGGCGCTTGGCTC 67283

QY 3023 CTTGTTTTTCCCGGTTCTGTTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGTAGGA 3082

DB 67282 CGTGTTTTTCCCGGTTGTTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGTAGGA 67223

QY 3083 GAAAGAGAGGTAACACAAAGTGGAAAACAGAGTAAAGAGGCTCTCCAGTGACTTATTTGG 3142

DB 67222 GAAAGAGAGGTAACAAAGTGGAAAACAGAGTAAAGAGGCTCTCCAGTGACTTATTTGG 67163

37523 38402: contig of 880 bp in length
 38502: gap of 100 bp
 38503 39380: contig of 878 bp in length
 39381 39480: gap of 100 bp
 39481 40407: contig of 927 bp in length
 40408 40507: gap of 100 bp
 40508 41405: contig of 898 bp in length
 41406 41505: gap of 100 bp
 41506 42399: contig of 894 bp in length
 42400 42499: gap of 100 bp
 42500 43357: contig of 858 bp in length
 43358 43457: gap of 100 bp
 43458 44356: contig of 899 bp in length
 44357 44456: gap of 100 bp
 44457 45325: contig of 869 bp in length
 45326 45425: gap of 100 bp
 45426 46305: contig of 880 bp in length
 46306 46405: gap of 100 bp
 46406 47302: contig of 897 bp in length
 47303 47402: gap of 100 bp
 47403 48293: contig of 891 bp in length
 48294 48393: gap of 100 bp
 48394 49280: contig of 887 bp in length
 49281 49380: gap of 100 bp
 49381 50250: contig of 870 bp in length
 50251 50350: gap of 100 bp
 50351 51209: contig of 859 bp in length
 51210 51309: gap of 100 bp
 51310 52221: contig of 912 bp in length
 52222 52321: gap of 100 bp
 52322 53205: contig of 884 bp in length
 53206 53305: gap of 100 bp
 53306 54225: contig of 920 bp in length
 54226 54325: gap of 100 bp
 54326 55206: contig of 881 bp in length
 55207 55306: gap of 100 bp
 55307 56165: contig of 859 bp in length
 56166 56265: gap of 100 bp
 56266 57124: contig of 859 bp in length
 57125 57224: gap of 100 bp
 57225 58121: contig of 897 bp in length
 58122 58221: gap of 100 bp
 58222 59075: contig of 854 bp in length
 59076 59175: gap of 100 bp
 59176 60058: contig of 894 bp in length
 60059 60158: gap of 100 bp
 60159 61067: contig of 909 bp in length
 61068 61167: gap of 100 bp
 61168 62051: contig of 884 bp in length
 62052 62151: gap of 100 bp
 62152 63022: contig of 871 bp in length
 63023 63122: gap of 100 bp
 63123 64026: contig of 904 bp in length
 64027 64126: gap of 100 bp
 64127 65015: contig of 889 bp in length
 65016 65115: gap of 100 bp
 65116 65975: contig of 863 bp in length
 65976 66075: gap of 100 bp
 66076 66954: contig of 879 bp in length
 66955 67054: gap of 100 bp
 67055 67947: contig of 893 bp in length
 67948 68047: gap of 100 bp
 68048 68934: contig of 887 bp in length
 68935 69034: gap of 100 bp
 69035 69910: contig of 876 bp in length
 69911 70010: gap of 100 bp

Query Match 14.8% Score 478.8; 38 2; Length 90698;
 Best Local Similarity 90.8%; Prod. No. 166-117;
 Matches 543; Conservative 0; Mismatches 49; Indels 5; Gaps 2;
 QY 2 CAGGUCATGGTGGCAGGTGCTTAATCTCAGTACTCGGGAGGTGGAGGTTCATGAG 41
 1 |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 10144 CCGGCATGGTGGCAGGTGCTTAATCTCAGTACTCGGGAGGTGGAGGTTCATGAG 10203
 QY 62 CCCAGATCGCACCATTGCACTCCAGCCTGGGCACACAAAAGGTGAACATCCATCAATTA 121
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 10204 CCCAGATCGCACCATTGCACTCCAGCCTGGGCACACAAAAGGTGAACATCCATCAATTA 10263
 QY 122 AAAAAAAGAAATATTTTGGTGGTGCAGCTTCAATAGTAGGAGAGAGAGAGAGGA 181
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 10264 AAAAAAATATATGATTTTGGTGGTGCAGCTTCAATAGTAGGAGAGAGAGAGAGGA 10323
 QY 182 GATGAGGATCAGGAGATCTAATTAATCTCTTAAATCATCTCTAGGAAAGATAACACCTT 241
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 10324 GATGAGGATCAGGAGATCTAATTAATCTCTTAAATCATCTCTAGGAAAGATAACACCTT 10383
 QY 242 TTAATAAGACTCTCTGCTTTTATAACATCATCTCTGCAAGAGCTCAAGGTTTCAACAA 301
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 10384 TTAATAAGACTCTCTGCTTTTATAACATCATCTCTGCAAGAGCTCAAGGTTTCAACAA 10443
 QY 302 AGTTCACTTTTCAGAAAACCCCTTTTGGAGAGACAGAAATATACATCTTCTCTCCATTTAA 361
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 10444 AGTTCACTTTTCAGAAAACCCCTTTTGGAGAGACAGAAATATACATCTTCTCTCCATTTAA 10502
 QY 362 AGATGAAGAAACAGCCCGGCACAAATGCTTAATGCTGTATCCAGGACATTTGGGAGGC 421
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 10503 AGATGAAGAAACAGCCCGGCACAAATGCTTAATGCTGTATCCAGGACATTTGGGAGGC 10562
 QY 422 TGAGGCACAGGATCGCTTGAGCTCCAGAGTTTGAGACCAGCCTGGATAACATGGCAAAA 481
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 10563 TGAGGCACAGATCGCTTGAGCTCCAGAGTTTGAGACCAGCCTGGATAACATGGCAAAA 10620
 QY 482 CCTCTCTCTACAAAAAAATACAAAAATAGATGGGTGTGTGGATGCGACCTGCTGGTC 541
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 10621 CCTCTCTCTACAAAAAATA---CGAAATTAATGGGGGGGGGGAATGCCCTGTGTGTC 10677
 QY 542 CCAAGCTACTTGGCAGGCTTAAGGTGGGAGGATCGCTTGAGCCCGAGGAGTCAAGTCTAC 599
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 10678 CCAAGCTACTTGGAGGCTAAGGGGGGAGGAGAGCCCTTTACCCCGGGAGACAATCTAC 10735

Search completed: May 9, 2003, 16:18:12
 Job time : 10636 sec

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 16:10:46 : Search time 8408.31 Seconds
(without alignments)
10013.236 Million cell updates/sec

Title: US-09-846-456-3

Perfect score: 2893

Sequence: 1 acaggcatgtgtgcagatg.....ctagtcacgcaaaacccc 2893

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 30

Total number of hits satisfying chosen parameters: 90539

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:

- 1: gb_ba:**
- 2: gb_htg:**
- 3: gb_in:**
- 4: gb_ov:**
- 5: gb_ov:**
- 6: gb_pat:**
- 7: gb_ph:**
- 8: gb_pl:**
- 9: gb_pr:**
- 10: gb_ro:**
- 11: gb_sts:**
- 12: gb_sy:**
- 13: gb_un:**
- 14: gb_vt:**
- 15: em_ba:**
- 16: em_fun:**
- 17: em_in:**
- 18: em_in:**
- 19: em_mu:**
- 20: em_mu:**
- 21: em_or:**
- 22: em_ov:**
- 23: em_pat:**
- 24: em_ph:**
- 25: em_pl:**
- 26: em_ro:**
- 27: em_sts:**
- 28: em_un:**
- 29: em_vt:**
- 30: em_htg_hum:**
- 31: em_htg_inv:**
- 32: em_htg_other:**
- 33: em_htg_mus:**
- 34: em_htg_pln:**
- 35: em_htg_rod:**
- 36: em_htg_man:**
- 37: em_htg_vrt:**
- 38: em_sy:**
- 39: em_htgo_hum:**
- 40: em_htgo_mus:**
- 41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2893	100.0	2893	6	AX351031	Sequence
2	2893	100.0	3231	6	AX351029	Sequence
3	1749	60.5	201144	9	AF287262	Homo sapi
4	1149	39.7	149034	9	AF275948	Homo sapi
5	891	30.8	96717	9	AL359182	Human DNA
6	814	28.1	183999	6	AX092589	Sequence
7	541	18.7	1167	9	AF258623	Homo sapi
8	541	18.7	1167	9	AF258623S1	Homo sapi
9	541	18.7	1643	6	HS252201	Homo sapi
10	541	18.7	1643	6	AX060715	Sequence
11	541	18.7	1643	6	AX060894	Sequence
12	344	11.9	175064	2	AC012230	Homo sapi
13	156	5.4	69570	2	AC012230	Homo sapi
14	152	5.3	90698	2	AC021246	Homo sapi
15	82	2.8	697	9	AC021345	Homo sapi
16	65	2.2	126285	9	AF258627	Homo sapi
17	61	2.1	186889	9	AC004139	Homo sapi
18	61	2.1	206966	2	AL807243	Mus muscu
19	61	2.1	278572	10	AF287263	AF287263 Mus muscu
20	59	2.0	44897	2	AC103824	Homo sapi
21	58	2.0	57662	2	AC107969	Homo sapi
22	58	2.0	81874	9	HS931E15	Human DNA
23	58	2.0	98360	9	HSJ247C2	Human DNA
24	58	2.0	141273	9	AL611933	Human DNA
25	58	2.0	145264	9	AC107939	Homo sapi
26	58	2.0	146312	2	AC015494	Homo sapi
27	58	2.0	155982	2	AC015495	Homo sapi
28	58	2.0	158071	2	AC018988	Homo sapi
29	58	2.0	158450	2	AC068082	Homo sapi
30	58	2.0	162419	2	AC093737	Homo sapi
31	58	2.0	166011	2	AC019307	Homo sapi
32	58	2.0	177533	2	AC069120	Homo sapi
33	58	2.0	188820	2	AC013281	Homo sapi
34	58	2.0	192396	9	AC012668	Homo sapi
35	58	2.0	193314	2	AC087478	Homo sapi
36	58	2.0	194133	9	HSBA425MS	Human DNA
37	58	2.0	195386	2	AL805961	Homo sapi
38	58	2.0	196520	2	AC083830	Homo sapi
39	58	2.0	201197	2	HS424J12	Homo sapien
40	58	2.0	292703	2	AC027176	Homo sapi
41	57	2.0	2532	9	AK094822	Homo sapi
42	57	2.0	4261	9	AB037785	Homo sapi
43	57	2.0	58558	9	AC091813	Homo sapi
44	57	2.0	91907	9	AC131566	Homo sapi
45	57	2.0	104906	9	AC069314	Homo sapi
46	57	2.0	116148	9	AC026423	Homo sapi
47	57	2.0	116650	9	AC004003	Homo sapi
48	57	2.0	117026	9	HS329A5	Human DNA
49	57	2.0	118603	2	AL360017	Homo sapi
50	57	2.0	121600	9	AP003555	Homo sapi
51	57	2.0	125146	9	AL512770	Human DNA
52	57	2.0	134036	9	AC007845	Homo sapi
53	57	2.0	140020	2	AC046162	Homo sapi
54	57	2.0	152558	2	AC013487	Homo sapi
55	57	2.0	154130	9	HS657E11	Human DNA
56	57	2.0	155691	9	AC016868	Homo sapi
57	57	2.0	163437	9	AC092606	Homo sapi
58	57	2.0	174711	9	AC026639	Homo sapi
59	57	2.0	175594	2	AC011134	Homo sapi
60	57	2.0	176212	2	AC084015	Homo sapi
61	57	2.0	177303	2	AC026576	Homo sapi
62	57	2.0	179641	9	AC098591	Homo sapi
63	57	2.0	182427	2	AC061992	Homo sapi
64	57	2.0	184444	9	AL359091	Human DNA
65	57	2.0	185979	9	AC091296	Pan trogl

C 66	57	2.0	187587	9	AC016026	AC016026 Homo sapi	C 139	55	1.9	162746	9	AC006050	AC006050 Homo sapi
C 67	57	2.0	189927	30	AC037439	AC037439 Homo sapi	C 140	55	1.9	163825	2	AC016669	AC016669 Homo sapi
C 68	57	2.0	190428	30	AC017012	AC017012 Homo sapi	C 141	55	1.9	163904	9	AP003070	AP003070 Homo sapi
C 69	57	2.0	196622	9	AC125218	AC125218 Homo sapi	C 142	55	1.9	169418	9	AC104163	AC104163 Homo sapi
C 70	57	2.0	196824	9	AC016543	AC016543 Homo sapi	C 143	55	1.9	169649	9	HS862K6	HS862K6 Homo sapi
C 71	57	2.0	199496	2	AF235096	AF235096 Homo sapi	C 144	55	1.9	171140	9	AC090685	AC090685 Homo sapi
C 72	57	2.0	203003	9	AL731556	AL731556 Human DNA	C 145	55	1.9	171966	2	AC092516	AC092516 Paplo cyn
C 73	57	2.0	206839	2	AC093539	AC093539 Pan trogl	C 146	55	1.9	172949	2	AC124068	AC124068 Homo sapi
C 74	57	2.0	217981	9	AC074051	AC074051 Homo sapi	C 147	55	1.9	173016	2	AC019123	AC019123 Homo sapi
C 75	57	2.0	259685	2	AC063928	AC063928 Homo sapi	C 148	55	1.9	173785	9	AP000355	AP000355 Homo sapi
C 76	57	2.0	280140	2	AC055751	AC055751 Homo sapi	C 149	55	1.9	173864	9	AL365364	AL365364 Human DNA
C 77	57	2.0	303717	2	AC063930	AC063930 Homo sapi	C 150	55	1.9	175986	2	AC023071	AC023071 Homo sapi
C 78	56	1.9	48522	2	AC105112	AC105112 Homo sapi	C 151	55	1.9	175986	2	AC023071	AC023071 Homo sapi
C 79	56	1.9	51815	2	AC068454	AC068454 Homo sapi	C 152	55	1.9	176926	9	AC009078	AC009078 Homo sapi
C 80	56	1.9	139737	9	HS228013	HS228013 Homo sapi	C 153	55	1.9	177402	9	AC007406	AC007406 Homo sapi
C 81	56	1.9	144627	9	AC015710	AC015710 Homo sapi	C 154	55	1.9	179947	2	AC021467	AC021467 Homo sapi
C 82	56	1.9	150812	9	AC004765	AC004765 Homo sapi	C 155	55	1.9	180760	2	AC130435	AC130435 Homo sapi
C 83	56	1.9	155125	9	AC024361	AC024361 Homo sapi	C 156	55	1.9	181683	2	AC021618	AC021618 Homo sapi
C 84	56	1.9	157871	9	AC104365	AC104365 Homo sapi	C 157	55	1.9	182374	2	AP003968	AP003968 Homo sapi
C 85	56	1.9	165036	9	AC100835	AC100835 Homo sapi	C 158	55	1.9	182839	2	AC022619	AC022619 Homo sapi
C 86	56	1.9	166279	9	CNS01DRQ	CNS01DRQ Human chr	C 159	55	1.9	184515	9	AC010653	AC010653 Homo sapi
C 87	56	1.9	171296	9	CNS06C86	AC117694 Human chr	C 160	55	1.9	186010	2	AC073083	AC073083 Homo sapi
C 88	56	1.9	173354	2	AC027554	AC027554 Homo sapi	C 161	55	1.9	186981	9	AC008459	AC008459 Homo sapi
C 89	56	1.9	173692	2	AC025994	AC025994 Homo sapi	C 162	55	1.9	194211	2	AL442633	AL442633 Homo sapi
C 90	56	1.9	176850	2	AC103736	AC103736 Homo sapi	C 163	55	1.9	194955	9	AC084198	AC084198 Homo sapi
C 91	56	1.9	178035	2	AC068680	AC068680 Homo sapi	C 164	55	1.9	203134	9	AC021077	AC021077 Homo sapi
C 92	56	1.9	181637	9	AC117451	AC117451 Homo sapi	C 165	55	1.9	211001	9	AC018695	AC018695 Homo sapi
C 93	56	1.9	183083	9	AC007600	AC007600 Homo sapi	C 166	55	1.9	219017	9	AP000936	AP000936 Homo sapi
C 94	56	1.9	184396	9	AC010853	AC010853 Homo sapi	C 167	55	1.9	246240	6	AR036572	AR036572 Sequence
C 95	56	1.9	194198	2	AC013298	AC013298 Homo sapi	C 168	55	1.9	246240	6	AR036574	AR036574 Sequence
C 96	56	1.9	194627	9	AC096596	AC096596 Homo sapi	C 169	55	1.9	246282	9	HSU91328	HSU91328 Human hered
C 97	56	1.9	195840	9	CNS00006F	AL049869 Human chr	C 170	55	1.9	318488	9	AC005529	AC005529 Homo sapi
C 98	56	1.9	201861	9	AC067796	AC067796 Homo sapi	C 171	55	1.9	328439	2	AL590137	AL590137 Homo sapi
C 99	56	1.9	216902	2	AC018475	AC018475 Homo sapi	C 172	54	1.9	8216	9	AP001617	AP001617 Homo sapi
C 100	56	1.9	227008	2	AP001771	AP001771 Homo sapi	C 173	54	1.9	23599	9	AP001504	AP001504 Homo sapi
C 101	56	1.9	227430	2	AC091590	AC091590 Homo sapi	C 174	54	1.9	43147	9	AP002955	AP002955 Homo sapi
C 102	56	1.9	279308	9	AC091918	AC091918 Homo sapi	C 175	54	1.9	44663	9	AC093518	AC093518 Homo sapi
C 103	55	1.9	13646	9	HUMRBP4	L34219 Homo sapi	C 176	54	1.9	44913	9	AC005786	AC005786 Homo sapi
C 104	55	1.9	39915	2	AC010512	AC010512 Homo sapi	C 177	54	1.9	50334	9	HS995112	HS995112 Human DNA
C 105	55	1.9	51891	2	AC074103	AC074103 Homo sapi	C 178	54	1.9	69537	2	AC107379	AC107379 Homo sapi
C 106	55	1.9	55627	9	AL589951	AL589951 Human DNA	C 179	54	1.9	89738	9	AL513343	AL513343 Human DNA
C 107	55	1.9	64360	2	AC104349	AC104349 Homo sapi	C 180	54	1.9	94343	9	AC005255	AC005255 Homo sapi
C 108	55	1.9	81971	9	AC018753	AC018753 Homo sapi	C 181	54	1.9	95930	9	AC106033	AC106033 Homo sapi
C 109	55	1.9	84841	9	AL391813	AL391813 Human DNA	C 182	54	1.9	96075	9	AL590639	AL590639 Human DNA
C 110	55	1.9	85500	9	HS199H16	AL022320 Human DNA	C 183	54	1.9	102349	9	AL161671	AL161671 Human DNA
C 111	55	1.9	87925	9	AC005318	AC005318 Homo sapi	C 184	54	1.9	142116	9	AC034215	AC034215 Homo sapi
C 112	55	1.9	88238	9	AL353780	AL353780 Human DNA	C 185	54	1.9	145833	2	AC125837	AC125837 Rattus no
C 113	55	1.9	94882	2	AC002317	AC002317 Homo sapi	C 186	54	1.9	147345	9	AL158824	AL158824 Human DNA
C 114	55	1.9	110000	2	AC135900_1	Continuation (2 of	C 187	54	1.9	152867	9	AC027671	AC027671 Homo sapi
C 115	55	1.9	119082	9	AP000903	AP000903 Homo sapi	C 188	54	1.9	153716	9	AL590631	AL590631 Human DNA
C 116	55	1.9	125686	9	HS503G16	754020 Human DNA	C 189	54	1.9	155699	9	AL360176	AL360176 Human DNA
C 117	55	1.9	127145	9	HS1119A7	AL122313 Human DNA	C 190	54	1.9	157381	9	AC007606	AC007606 Homo sapi
C 118	55	1.9	127286	2	AC025246	AC025246 Homo sapi	C 191	54	1.9	160069	2	AC064867	AC064867 Homo sapi
C 119	55	1.9	135405	9	AC000025	AC000025 Homo sapi	C 192	54	1.9	163739	2	AC012406	AC012406 Homo sapi
C 120	55	1.9	136098	9	AC006970	AC006970 Homo sapi	C 193	54	1.9	165375	2	AC073357	AC073357 Homo sapi
C 121	55	1.9	136646	2	AL138726	AL138726 Human DNA	C 194	54	1.9	166297	2	AC011271	AC011271 Homo sapi
C 122	55	1.9	138532	2	AL139222	AL139222 Homo sapi	C 195	54	1.9	166500	9	AC007785	AC007785 Homo sapi
C 123	55	1.9	140834	2	AC007460	AC007460 Homo sapi	C 196	54	1.9	168230	2	AC010624	AC010624 Homo sapi
C 124	55	1.9	141456	9	AL355300	AL355300 Human DNA	C 197	54	1.9	170517	9	AC010545	AC010545 Homo sapi
C 125	55	1.9	143583	9	HS467016	AL009031 Human DNA	C 198	54	1.9	170919	9	CNS01DXJ	AL139353 Human chr
C 126	55	1.9	145373	9	AC005599	AC005599 Homo sapi	C 199	54	1.9	170970	9	AL354707	AL354707 Human DNA
C 127	55	1.9	147594	9	AC013829	AC013829 Homo sapi	C 200	54	1.9	172462	2	AC091147	AC091147 Homo sapi
C 128	55	1.9	1489750	9	AC002426	AC002426 Genomic s	C 201	54	1.9	173389	2	AC048385	AC048385 Homo sapi
C 129	55	1.9	148975	2	AC012145	AC012145 Homo sapi	C 202	54	1.9	173484	2	AC021145	AC021145 Homo sapi
C 130	55	1.9	149308	9	AC005527	AC005527 Homo sapi	C 203	54	1.9	174230	9	AC024073	AC024073 Homo sapi
C 131	55	1.9	154772	9	AL138764	AL138764 Human DNA	C 204	54	1.9	175618	2	AC046167	AC046167 Homo sapi
C 132	55	1.9	155138	9	AL139260	AL139260 Human DNA	C 205	54	1.9	175831	2	AC015720	AC015720 Homo sapi
C 133	55	1.9	156619	2	AC013361	AC013361 Homo sapi	C 206	54	1.9	175999	2	AC021154	AC021154 Homo sapi
C 134	55	1.9	157566	9	AC022517	AC022517 Homo sapi	C 207	54	1.9	176092	2	AC068222	AC068222 Homo sapi
C 135	55	1.9	158193	2	AC010828	AC010828 Homo sapi	C 208	54	1.9	182659	9	AC023830	AC023830 Homo sapi
C 136	55	1.9	160450	9	AC087388	AC087388 Homo sapi	C 209	54	1.9	185145	9	AC087433	AC087433 Homo sapi
C 137	55	1.9	161054	9	AC104444	AC104444 Homo sapi	C 210	54	1.9	188769	2	AP002809	AP002809 Homo sapi
C 138	55	1.9	161355	2	AC011154	AC011154 Homo sapi	C 211	54	1.9	189757	9	AC023593	AC023593 Homo sapi

C 212	54	1.9 190776	2	AC064813	AC064813 Homo sapi	C 285	53	1.8 174711	2	AC025515	AC025515 Homo sapi
C 213	54	1.9 193020	9	AL138759	AL138759 Human DNA	C 286	53	1.8 174903	2	AC124039	AC124039 Macaca mu
C 214	54	1.9 203228	9	AC092718	AC092718 Homo sapi	C 287	53	1.8 177045	2	AC015970	AC015970 Homo sapi
C 215	54	1.9 203773	9	AC097369	AC097369 Homo sapi	C 288	53	1.8 179220	9	AC114493	AC114493 Homo sapi
C 216	54	1.9 207961	2	AC014282	AC014282 Homo sapi	C 289	53	1.8 180133	9	AL138885	AL138885 Human DNA
C 217	54	1.9 211422	9	AC073493	AC073493 Homo sapi	C 290	53	1.8 183487	2	AC106828	AC106828 Homo sapi
C 218	54	1.9 219256	9	AP001743	AP001743 Homo sapi	C 291	53	1.8 184118	9	AC016580	AC016580 Homo sapi
C 219	54	1.9 219635	2	AL390207	AL390207 Homo sapi	C 292	53	1.8 184313	9	AL445584	AL445584 Human DNA
C 220	53	1.8 2638	9	AK026796	AK026796 Homo sapi	C 293	53	1.8 185351	9	AC015801	AC015801 Homo sapi
C 221	53	1.8 4452	9	AK074112	AK074112 Homo sapi	C 294	53	1.8 186052	9	AC104187	AC104187 Homo sapi
C 222	53	1.8 4734	9	HSPD4CG7	AL157415 Homo sapi	C 295	53	1.8 187274	2	AL391096	AL391096 Homo sapi
C 223	53	1.8 34688	9	AC005759	AC005759 Homo sapi	C 296	53	1.8 188065	2	AC018689	AC018689 Homo sapi
C 224	53	1.8 36284	9	HSATJ9610	AL1003610 Homo sapi	C 297	53	1.8 189048	2	AC090739	AC090739 Homo sapi
C 225	53	1.8 36852	9	AC106891	AC106891 Homo sapi	C 298	53	1.8 189148	2	AC068262	AC068262 Homo sapi
C 226	53	1.8 42133	9	AP001060	AP001060 Homo sapi	C 299	53	1.8 192307	9	AC005971	AC005971 Homo sapi
C 227	53	1.8 44296	9	AC004471	AC004471 Homo sapi	C 300	53	1.8 193076	2	AC090617	AC090617 Homo sapi
C 228	53	1.8 63930	2	AC106017	AL106017 Homo sapi	C 301	53	1.8 193690	2	AC118559	AC118559 Homo sapi
C 229	53	1.8 66254	9	AL137791	AL137791 Human DNA	C 302	53	1.8 197676	2	AC022344	AC022344 Homo sapi
C 230	53	1.8 73516	2	AC041001	AC041001 Homo sapi	C 303	53	1.8 197748	2	AC026283	AC026283 Homo sapi
C 231	53	1.8 74509	2	AF260012	AF260012 Homo sapi	C 304	53	1.8 198557	2	AC025250	AC025250 Homo sapi
C 232	53	1.8 74999	9	AC008960	AC008960 Homo sapi	C 305	53	1.8 199579	9	AC093536	AC093536 Homo sapi
C 233	53	1.8 75148	9	AC091545	AC091545 Homo sapi	C 306	53	1.8 200458	2	AC019237	AC019237 Homo sapi
C 234	53	1.8 81514	9	HSATJ9616	AL109616 Homo sapi	C 307	53	1.8 200542	2	CNS018G3	CNS018G3 Homo sapi
C 235	53	1.8 83306	9	AC062021	AC062021 Homo sapi	C 308	53	1.8 206537	9	AC099777	AC099777 Homo sapi
C 236	53	1.8 83690	9	AC106864	AC106864 Homo sapi	C 309	53	1.8 218047	30	AC068624	AC068624 Homo sapi
C 237	53	1.8 90434	2	AC007952	AC007952 Homo sapi	C 310	53	1.8 221909	2	AC021705	AC021705 Homo sapi
C 238	53	1.8 91938	2	AL129838	AL129838 Pan trogl	C 311	53	1.8 340000	9	AP001712	AP001712 Homo sapi
C 239	53	1.8 94074	9	HSBC17A95	AL450224 Homo sapi	C 312	53	1.8 340000	9	AP001753	AP001753 Homo sapi
C 240	53	1.8 96975	9	AC004975	AC004975 Homo sapi	C 313	52	1.8 475	6	AX390668	AX390668 Sequence
C 241	53	1.8 96995	9	AC008149	AC008149 Homo sapi	C 314	52	1.8 2544	9	AK094363	AK094363 Homo sapi
C 242	53	1.8 101098	9	AC002427	AC002427 Homo sapi	C 315	52	1.8 3527	9	AK090951	AK090951 Homo sapi
C 243	53	1.8 103476	9	AC123912	AC123912 Homo sapi	C 316	52	1.8 5072	9	AK090406	AK090406 Homo sapi
C 244	53	1.8 108400	9	HUMDGCRCN	127570 Homo sapi	C 317	52	1.8 5987	11	HS50024T	HS50024T H. sapiens
C 245	53	1.8 110000	2	AC003656	AC003656 Homo sapi	C 318	52	1.8 14475	9	AC007078	AC007078 Homo sapi
C 246	53	1.8 113148	9	AC093241	AC093241 Homo sapi	C 319	52	1.8 48103	9	AL356282	AL356282 Human DNA
C 247	53	1.8 115710	2	AL139015	AL139015 Homo sapi	C 320	52	1.8 54405	2	AC111158	AC111158 Homo sapi
C 248	53	1.8 115928	9	AC037475	AC037475 Homo sapi	C 321	52	1.8 56415	9	HSJ994024	HSJ994024 Human DNA
C 249	53	1.8 116103	9	AL606465	AL606465 Human DNA	C 322	52	1.8 63578	9	AC109356	AC109356 Homo sapi
C 250	53	1.8 117946	9	AC023513	AC023513 Homo sapi	C 323	52	1.8 64214	9	AL512408	AL512408 Human DNA
C 251	53	1.8 119580	9	AP000466	AP000466 Homo sapi	C 324	52	1.8 66008	9	AC024582	AC024582 Homo sapi
C 252	53	1.8 120825	9	HSJ739M16	AL109627 Human DNA	C 325	52	1.8 66887	9	AF411057	AF411057 Homo sapi
C 253	53	1.8 133284	2	AC104231	AC104231 Homo sapi	C 326	52	1.8 66954	2	AL591214	AL591214 Human DNA
C 254	53	1.8 136589	2	AC090319	AC090319 Homo sapi	C 327	52	1.8 67412	2	AC131573	AC131573 Homo sapi
C 255	53	1.8 143456	9	AL513465	AL513465 Human DNA	C 328	52	1.8 71166	2	AC099819	AC099819 Homo sapi
C 256	53	1.8 146463	9	AC114971	AC114971 Homo sapi	C 329	52	1.8 72159	9	AL160161	AL160161 Homo sapi
C 257	53	1.8 146878	2	AC011174	AC011174 Homo sapi	C 330	52	1.8 80527	9	AC092290	AC092290 Homo sapi
C 258	53	1.8 150013	2	AC010780	AC010780 Homo sapi	C 331	52	1.8 93403	9	AC073261	AC073261 Homo sapi
C 259	53	1.8 150684	9	AL442445	AL442445 Human DNA	C 332	52	1.8 94718	9	AC026770	AC026770 Homo sapi
C 260	53	1.8 154918	9	AL138781	AL138781 Human DNA	C 333	52	1.8 98647	2	AC025777	AC025777 Homo sapi
C 261	53	1.8 155025	9	AC034246	AC034246 Homo sapi	C 334	52	1.8 99716	9	AL512454	AL512454 Human DNA
C 262	53	1.8 155125	9	AC024561	AC024561 Homo sapi	C 335	52	1.8 104140	9	AC008122	AC008122 Homo sapi
C 263	53	1.8 157193	9	AL355315	AL355315 Human DNA	C 336	52	1.8 106539	9	AF225839	AF225839 Homo sapi
C 264	53	1.8 157672	9	AC113114	AC113114 Homo sapi	C 337	52	1.8 108625	9	AL356773	AL356773 Homo sapi
C 265	53	1.8 157929	9	AL593844	AL593844 Homo sapi	C 338	52	1.8 108907	9	AL135911	AL135911 Human DNA
C 266	53	1.8 158838	9	CNS05TDN	AC156825 Human chr	C 339	52	1.8 110000	2	AC112773	AC112773 Homo sapi
C 267	53	1.8 158840	9	AC091577	AC091577 Homo sapi	C 340	52	1.8 111998	9	AC011509	AC011509 Homo sapi
C 268	53	1.8 160569	9	AC015878	AC015878 Homo sapi	C 341	52	1.8 112748	9	AC007242	AC007242 Homo sapi
C 269	53	1.8 160957	9	AC114487	AC114487 Homo sapi	C 342	52	1.8 123004	9	AC073846	AC073846 Homo sapi
C 270	53	1.8 162820	9	AL138765	AL138765 Human DNA	C 343	52	1.8 126368	9	HS104363	HS104363 Homo sapi
C 271	53	1.8 162921	2	AC093367	AC093367 Homo sapi	C 344	52	1.8 126543	2	AC026156	AC026156 Homo sapi
C 272	53	1.8 162976	9	AC114301	AC114301 Homo sapi	C 345	52	1.8 129435	9	AL391314	AL391314 Human DNA
C 273	53	1.8 164473	2	AP001108	AP001108 Homo sapi	C 346	52	1.8 131345	9	AC069023	AC069023 Homo sapi
C 274	53	1.8 166309	9	AC011944	AC011944 Homo sapi	C 347	52	1.8 133246	2	AC091026	AC091026 Homo sapi
C 275	53	1.8 166717	2	AC125612	AC125612 Homo sapi	C 348	52	1.8 133258	9	AC004944	AC004944 Homo sapi
C 276	53	1.8 167390	9	AC067263	AC067263 Homo sapi	C 349	52	1.8 133614	2	AC025433	AC025433 Homo sapi
C 277	53	1.8 168080	2	AC009047	AC009047 Homo sapi	C 350	52	1.8 133690	9	AL158074	AL158074 Human DNA
C 278	53	1.8 169646	9	AL160269	AL160269 Human DNA	C 351	52	1.8 134308	9	AC011488	AC011488 Homo sapi
C 279	53	1.8 169758	2	AL356139	AL356139 Homo sapi	C 352	52	1.8 135964	9	AC005914	AC005914 Homo sapi
C 280	53	1.8 170245	9	AC092814	AC092814 Homo sapi	C 353	52	1.8 137473	2	AC015944	AC015944 Homo sapi
C 281	53	1.8 170783	2	AC024943	AC024943 Homo sapi	C 354	52	1.8 137718	9	AL137066	AL137066 Human DNA
C 282	53	1.8 171274	2	AC026476	AC026476 Homo sapi	C 355	52	1.8 137945	2	AL133508	AL133508 Homo sapi
C 283	53	1.8 172200	2	AC022626	AC022626 Homo sapi	C 356	52	1.8 138063	9	AC092473	AC092473 Homo sapi
C 284	53	1.8 172657	9	AC015963	AC015963 Homo sapi	C 357	52	1.8 138839	9	HUAC002400	HUAC002400 Human chr

C 356	52	1.8 140179	2	AC084688	AC084688 Homo sapi	C 431	52	1.8 183619	9	AC007339	AC007339 Homo sapi
C 357	52	1.8 140919	9	AC110747	AC110747 Homo sapi	C 432	52	1.8 185316	9	AP002797	AP002797 Homo sapi
C 358	52	1.8 143423	9	AC116192	AC116192 Human DNA	C 433	52	1.8 185367	2	AC092977	AC092977 Homo sapi
C 359	52	1.8 144620	9	AC023787	AC023787 Homo sapi	C 434	52	1.8 186109	2	AP001890	AP001890 Homo sapi
C 360	52	1.8 145242	9	AC008610	AC008610 Homo sapi	C 435	52	1.8 186524	2	AC024465	AC024465 Homo sapi
C 361	52	1.8 145579	2	AC015737	AC015737 Homo sapi	C 436	52	1.8 186920	9	AP000824	AP000824 Homo sapi
C 362	52	1.8 145616	9	HS108K11	285986 Human DNA S	C 437	52	1.8 189174	9	AC092687	AC092687 Homo sapi
C 363	52	1.8 147461	9	AC027348	AC027348 Homo sapi	C 438	52	1.8 189219	9	AC092982	AC092982 Homo sapi
C 364	52	1.8 147565	2	AC080145	AC080145 Homo sapi	C 439	52	1.8 189355	2	AC053339	AC053339 Homo sapi
C 365	52	1.8 148278	9	AC006101	AC006101 c11b_3p_	C 440	52	1.8 190253	2	AC090500	AC090500 Homo sapi
C 366	52	1.8 148507	9	AC008784	AC008784 Homo sapi	C 441	52	1.8 191717	2	AC104115	AC104115 Homo sapi
C 367	52	1.8 148656	9	AC005482	AC005482 Homo sapi	C 442	52	1.8 192420	2	AC129804	AC129804 Homo sapi
C 368	52	1.8 149401	2	AC074032	AC074032 Homo sapi	C 443	52	1.8 194486	2	AC016771	AC016771 Homo sapi
C 369	52	1.8 149563	9	AC116348	AC116348 Homo sapi	C 444	52	1.8 195723	2	AC087732	AC087732 Homo sapi
C 370	52	1.8 150377	2	AC102797	AC102797 Homo sapi	C 445	52	1.8 195782	9	AC074389	AC074389 Homo sapi
C 371	52	1.8 150573	9	AC097473	AC097473 Homo sapi	C 446	52	1.8 196263	2	AC131385	AC131385 Homo sapi
C 372	52	1.8 150573	9	AC097473	AC097473 Homo sapi	C 447	52	1.8 196852	9	AC084866	AC084866 Homo sapi
C 373	52	1.8 150573	9	AC097473	AC097473 Homo sapi	C 448	52	1.8 198567	9	AL157877	AL157877 Human DNA
C 374	52	1.8 151008	2	AC035146	AC035146 Homo sapi	C 449	52	1.8 200861	2	AC116566	AC116566 Homo sapi
C 375	52	1.8 152555	9	AL354830	AL354830 Human DNA	C 450	52	1.8 201764	2	AL359818	AL359818 Homo sapi
C 376	52	1.8 152555	9	AL354830	AL354830 Human DNA	C 451	52	1.8 202768	2	AC092345	AC092345 Homo sapi
C 377	52	1.8 152786	9	AL135778	AL135778 Human DNA	C 452	52	1.8 204504	2	AC022487	AC022487 Homo sapi
C 378	52	1.8 153951	2	AC019027	AC019027 Homo sapi	C 453	52	1.8 204504	2	AC091043	AC091043 Homo sapi
C 379	52	1.8 155837	9	AL445495	AL445495 Human DNA	C 454	52	1.8 209410	9	AC106885	AC106885 Homo sapi
C 380	52	1.8 156043	2	AC013631	AC013631 Homo sapi	C 455	52	1.8 209907	2	AC078778	AC078778 Homo sapi
C 381	52	1.8 157288	2	AC116561	AC116561 Homo sapi	C 456	52	1.8 209907	2	AC034201	AC034201 Homo sapi
C 382	52	1.8 157288	2	AC116561	AC116561 Homo sapi	C 457	52	1.8 212753	9	HS21242	295114 Human DNA S
C 383	52	1.8 157435	9	HS50024	AL034850 Human DNA	C 458	52	1.8 213613	2	AC013405	AC013405 Homo sapi
C 384	52	1.8 158482	2	AC025346	AC025346 Homo sapi	C 459	52	1.8 217929	9	AL133395	AL133395 Human DNA
C 385	52	1.8 159365	9	AL392111	AL392111 Human DNA	C 460	52	1.8 220581	2	AC015918	AC015918 Homo sapi
C 386	52	1.8 159562	9	AC034205	AC034205 Homo sapi	C 461	52	1.8 223735	9	AC096677	AC096677 Homo sapi
C 387	52	1.8 159637	2	AC007990	AC007990 Homo sapi	C 462	52	1.8 240379	9	AC005077	AC005077 Homo sapi
C 388	52	1.8 159713	9	AC087190	AC087190 Homo sapi	C 463	52	1.8 260967	2	AC068769	AC068769 Homo sapi
C 389	52	1.8 160301	2	AC130417	AC130417 Homo sapi	C 464	52	1.8 260967	2	AC098584	AC098584 Homo sapi
C 390	52	1.8 160915	2	AC011084	AC011084 Homo sapi	C 465	51	1.8 269301	2	AC098584	AC098584 Homo sapi
C 391	52	1.8 161179	2	AC083954	AC083954 Homo sapi	C 466	51	1.8 269301	2	HS038671	U38671 Human Alu r
C 392	52	1.8 161538	9	AL139188	AL139188 Human DNA	C 467	51	1.8 1025	9	HS342941	AL342941 Human DNA
C 393	52	1.8 162805	2	AC020565	AC020565 Homo sapi	C 468	51	1.8 1159	9	F272846S06	AF272826 Homo sapi
C 394	52	1.8 162901	9	AL512656	AL512656 Human DNA	C 469	51	1.8 1479	9	AK098617	F4098617 Homo sapi
C 395	52	1.8 163689	9	AL451065	AL451065 Homo sapi	C 470	51	1.8 3407	9	HS01791	AF136270 Homo sapi
C 396	52	1.8 163731	9	AC008949	AC008949 Homo sapi	C 471	51	1.8 3423	9	HS0591P1	AF135120 Homo sapi
C 397	52	1.8 164302	9	AC122457	AC122457 Homo sapi	C 472	51	1.8 3926	9	HS103F2	Y0998 H.sapiens T
C 398	52	1.8 165554	2	AC025114	AC025114 Homo sapi	C 473	51	1.8 3994	9	AL358173	AL358173 Human DNA
C 399	52	1.8 165596	2	AC091588	AC091588 Homo sapi	C 474	51	1.8 4360	9	AR018045	AB018045 Homo sapi
C 400	52	1.8 165749	2	AC011502	AC011502 Homo sapi	C 475	51	1.8 5190	9	HS1ADNAG	X76775 H.sapiens H
C 401	52	1.8 165749	2	AC020685	AC020685 Homo sapi	C 476	51	1.8 13996	9	AC112722	AC112722 Homo sapi
C 402	52	1.8 166606	2	AC020685	AC020685 Homo sapi	C 477	51	1.8 14699	9	AF351720	AF351720 Homo sapi
C 403	52	1.8 166839	2	AL359391	AL359391 Homo sapi	C 478	51	1.8 26303	9	HS0536	X54156 Human p53 g
C 404	52	1.8 167656	9	AC079468	AC079468 Homo sapi	C 479	51	1.8 26303	9	HS0536	U94789 Human p53 g
C 405	52	1.8 167985	2	AC022576	AC022576 Homo sapi	C 480	51	1.8 24119	9	HS447E6	AL031724 Human DNA
C 406	52	1.8 168513	2	AC031982	AC031982 Homo sapi	C 481	51	1.8 24813	9	AL357532	AL357532 Human DNA
C 407	52	1.8 169454	9	AP001592	AP001592 Homo sapi	C 482	51	1.8 28409	9	AL354930	AL354930 Human DNA
C 408	52	1.8 169612	2	AC027493	AC027493 Homo sapi	C 483	51	1.8 36452	9	AC004753	AC004753 Homo sapi
C 409	52	1.8 169825	9	AC012454	AC012454 Homo sapi	C 484	51	1.8 48491	9	AC006049	AC006049 Homo sapi
C 410	52	1.8 170761	9	CNS05TER	AC059405 Human chr	C 485	51	1.8 48598	9	AC013531	AC013531 Homo sapi
C 411	52	1.8 171541	2	AC048482	AC048482 Homo sapi	C 486	51	1.8 38629	9	AC114267	AC114267 Homo sapi
C 412	52	1.8 171978	2	AC009649	AC009649 Homo sapi	C 487	51	1.8 38902	9	HS027	296104 Human DNA S
C 413	52	1.8 172853	9	AC084495	AC084495 Homo sapi	C 488	51	1.8 39004	9	AC004510	AC004510 Homo sapi
C 414	52	1.8 172964	9	AC069413	AC069413 Homo sapi	C 489	51	1.8 39236	9	AC000387	AC000387 Gemic s
C 415	52	1.8 173117	2	AL357885	AL357885 Homo sapi	C 490	51	1.8 39261	9	AC000084	AC000084 Homo sapi
C 416	52	1.8 173677	9	AC084768	AC084768 Homo sapi	C 491	51	1.8 39569	9	AC003048	AC003048 Homo sapi
C 417	52	1.8 173728	9	AC018507	AC018507 Homo sapi	C 492	51	1.8 42304	9	AC002491	AC002491 Homo sapi
C 418	52	1.8 174144	2	AC091765	AC091765 Homo sapi	C 493	51	1.8 42616	9	AC005566	AC005566 Homo sapi
C 419	52	1.8 174311	2	AL365319	AL365319 Homo sapi	C 494	51	1.8 4316	9	AP000041	AP000041 Homo sapi
C 420	52	1.8 174527	2	AC092859	AC092859 Homo sapi	C 495	51	1.8 4316	9	AC092298	AC092298 Homo sapi
C 421	52	1.8 174741	9	AC040977	AC040977 Homo sapi	C 496	51	1.8 43715	9	AB015355	AB015355 Homo sapi
C 422	52	1.8 175162	9	AL590103	AL590103 Human DNA	C 497	51	1.8 44090	9	AC000080	AC000080 Homo sapi
C 423	52	1.8 176153	9	AC006287	AC006287 Homo sapi	C 498	51	1.8 45416	9	AC000090	AC000090 Homo sapi
C 424	52	1.8 176967	2	AC022742	AC022742 Homo sapi	C 499	51	1.8 46465	2	AC006183	AC006183 Homo sapi
C 425	52	1.8 178494	9	AC009819	AC009819 Homo sapi	C 500	51	1.8 47480	9	AL356354	AL356354 Human DNA
C 426	52	1.8 178710	2	AC106766	AC106766 Homo sapi	C 501	51	1.8 51146	2	AC090342	AC090342 Homo sapi
C 427	52	1.8 179655	9	AC018740	AC018740 Homo sapi	C 502	51	1.8 51480	9	AP000261	AP000261 Homo sapi
C 428	52	1.8 179969	9	AC016643	AC016643 Homo sapi	C 503	51	1.8 51923	9	AL356983	AL356983 Human DNA
C 429	52	1.8 180531	9	AC008745	AC008745 Homo sapi						
C 430	52	1.8 180533	2	AC119427	AC119427 Homo sapi						
	52	1.8 181636	2	AC025138	AC025138 Homo sapi						

504	1.8	53157	9	AL136302	AC136452 Human DNA	577	51	1.8	112484	9	AP002336	AP002336 Homo sapi
505	1.8	54982	2	AL100814	AL100814 Homo sapi	578	51	1.8	112898	2	AC008552	AC008552 Homo sapi
506	1.8	56570	2	AL153194	AL153194 Human DNA	579	51	1.8	114231	2	HS390C10	HS390C10 Homo sapi
507	1.8	56737	2	AC025208	AC025208 Homo sapi	580	51	1.8	114584	2	AF252827	AF252827 Homo sapi
508	1.8	56940	2	AC105427	AC105427 Homo sapi	581	51	1.8	115278	9	AL119819	AL119819 Human DNA
509	1.8	59012	9	HSABLOC2	U75F2 Human ARB. f	582	51	1.8	115583	9	HS1751K20	HS1751K20 Human DNA
510	1.8	63945	9	AC091979	AC091979 Homo sapi	583	51	1.8	117264	2	AC127024	AC127024 Homo sapi
511	1.8	64470	2	AC103400	AC103400 Mus muscu	584	51	1.8	117431	2	HS850H21	HS850H21 Human DNA
512	1.8	66686	2	AC087659	AC087659 Homo sapi	585	51	1.8	117493	9	HSJ654H19	HSJ654H19 Human DNA
513	1.8	67188	2	AC104364	AC104364 Homo sapi	586	51	1.8	117893	9	HS109M1	HS109M1 Human DNA
514	1.8	67289	2	AC040394	AC040394 Homo sapi	587	51	1.8	117952	9	AL133541	AL133541 Human DNA
515	1.8	67445	9	AL159146	AL159146 Human DNA	588	51	1.8	117962	9	AF312032	AF312032 Homo sapi
516	1.8	68037	9	AY046055	AY046055 Homo sapi	589	51	1.8	118819	9	AP000647	AP000647 Homo sapi
517	1.8	68662	9	AL133293	AL133293 Human DNA	590	51	1.8	118875	2	AL108051	AL108051 Homo sapi
518	1.8	69570	2	AC021246	AC021246 Homo sapi	591	51	1.8	120015	2	AL354860	AL354860 Homo sapi
519	1.8	69912	2	AC010322	AC116322 Homo sapi	592	51	1.8	120030	9	AC002075	AC002075 Homo sapi
520	1.8	71627	9	AC004851	AC004851 Homo sapi	593	51	1.8	121739	9	AC006084	AC006084 Homo sapi
521	1.8	73686	9	AP000280	AP000280 Homo sapi	594	51	1.8	121739	9	AC006084	AC006084 Homo sapi
522	1.8	76702	9	HS756074	AL135072 Human DNA	595	51	1.8	121856	2	AC022575	AC022575 Homo sapi
523	1.8	76850	9	AC003109	AL135072 Human DNA	596	51	1.8	122186	6	AX051112	AX051112 Sequence
524	1.8	77888	9	AL1590611	AL1590611 Human DNA	597	51	1.8	122591	9	AL157786	AL157786 Human DNA
525	1.8	79611	9	AC002486	AC002486 Human DNA	598	51	1.8	122591	9	AL157786	AL157786 Human DNA
526	1.8	79914	9	AC005159	AC005159 Homo sapi	599	51	1.8	122717	2	AP001186	AP001186 Homo sapi
527	1.8	80914	9	AC007959	AC007959 Homo sapi	600	51	1.8	122889	9	HSDA204F4	HSDA204F4 Human DNA
528	1.8	81768	9	AL662825	AL662825 Human DNA	601	51	1.8	123004	9	AC087892	AC087892 Homo sapi
529	1.8	81826	9	HS078645	U75F45 Human colla	602	51	1.8	123554	9	AB023049	AB023049 Homo sapi
530	1.8	82976	9	AC005031	AC005031 Homo sapi	603	51	1.8	124001	9	HS886K2	HS886K2 Human DNA
531	1.8	83332	9	AL138651	AL138651 Homo sapi	604	51	1.8	125549	9	AL645941	AL645941 Human DNA
532	1.8	84686	9	AL138651	AL138651 Homo sapi	605	51	1.8	125878	2	AC108924	AC108924 Homo sapi
533	1.8	85538	9	HS751022	AL138651 Homo sapi	606	51	1.8	126045	9	HS1010E17	HS1010E17 Human DNA
534	1.8	86130	9	AC005165	AC005165 Homo sapi	607	51	1.8	126290	2	AC099483	AC099483 Homo sapi
535	1.8	86299	9	AL359158	AL359158 Homo sapi	608	51	1.8	126380	2	AP000714	AP000714 Homo sapi
536	1.8	86719	9	HSJ906P16	AL359158 Homo sapi	609	51	1.8	126503	9	AC008114	AC008114 Homo sapi
537	1.8	87424	9	AC006377	AC006377 Homo sapi	610	51	1.8	126956	2	HS88B1	HS88B1 Human DNA
538	1.8	89874	30	AL356483	AL356483 Human DNA	611	51	1.8	127335	2	AC068083	AC068083 Homo sapi
539	1.8	90476	9	AC015910	AC015910 Homo sapi	612	51	1.8	128473	9	AC004241	AC004241 Homo sapi
540	1.8	91202	2	AC006186	AC006186 Homo sapi	613	51	1.8	129643	9	AC011507	AC011507 Homo sapi
541	1.8	92118	9	AC074484	AC074484 Homo sapi	614	51	1.8	130278	9	AC005664	AC005664 Homo sapi
542	1.8	94224	9	HS651120	AL136659 Human DNA	615	51	1.8	131078	9	HSU80017	HSU80017 Homo sapien
543	1.8	94535	2	HS1141E20	AL136659 Human DNA	616	51	1.8	131602	2	AC034263	AC034263 Homo sapi
544	1.8	95218	9	AC019066	AC019066 Homo sapi	617	51	1.8	131602	2	AC034263	AC034263 Homo sapi
545	1.8	95782	9	AC025775	AC025775 Homo sapi	618	51	1.8	131673	9	HS336H9	HS336H9 Human DNA
546	1.8	96202	9	AL138654	AL138654 Human DNA	619	51	1.8	132433	9	HS0321081	HS0321081 Human DNA
547	1.8	96963	9	AC015855	AC015855 Homo sapi	620	51	1.8	132755	9	AC008670	AC008670 Homo sapi
548	1.8	96978	9	AC024075	AC024075 Homo sapi	621	51	1.8	133516	9	AL591409	AL591409 Human DNA
549	1.8	97128	9	AL662845	AL662845 Human DNA	622	51	1.8	133801	9	AC092540	AC092540 Homo sapi
550	1.8	98309	2	AL671924	AL671924 Homo sapi	623	51	1.8	134245	9	HS1052M9	HS1052M9 Human DNA
551	1.8	100000	9	AP000035	AP000035 Homo sapi	624	51	1.8	135305	9	HSJ1112D6	HSJ1112D6 Homo sapi
552	1.8	100000	9	AP000039	AP000039 Homo sapi	625	51	1.8	135618	2	AL359965	AL359965 Homo sapi
553	1.8	100000	9	AP000109	AP000109 Homo sapi	626	51	1.8	135996	2	AL356007	AL356007 Homo sapi
554	1.8	100000	9	AP000197	AP000197 Homo sapi	627	51	1.8	137217	2	HS0211L10	HS0211L10 Homo sapi
555	1.8	100000	9	AP000197	AP000197 Homo sapi	628	51	1.8	137343	9	AP000945	AP000945 Homo sapi
556	1.8	100000	9	AP000197	AP000197 Homo sapi	629	51	1.8	138093	9	AL606467	AL606467 Homo sapi
557	1.8	100000	9	AP000197	AP000197 Homo sapi	630	51	1.8	138879	9	AL606467	AL606467 Homo sapi
558	1.8	102151	9	HS979N1	AL076659 Human DNA	631	51	1.8	138928	9	AC124210	AC124210 Homo sapi
559	1.8	103122	9	AC005663	AC005663 Homo sapi	632	51	1.8	139035	9	AL356102	AL356102 Human DNA
560	1.8	103146	9	HS187N21	HS03036 Human DNA	633	51	1.8	139173	9	AC009140	AC009140 Homo sapi
561	1.8	103179	9	AP000619	AP000619 Homo sapi	634	51	1.8	139776	9	AL160165	AL160165 Human DNA
562	1.8	103186	9	AL158218	AL158218 Human DNA	635	51	1.8	139966	9	AC004820	AC004820 Homo sapi
563	1.8	103370	9	AL161656	AL161656 Human DNA	636	51	1.8	140476	9	AC104465	AC104465 Homo sapi
564	1.8	103930	9	AL358214	AL358214 Human DNA	637	51	1.8	141073	9	AC100827	AC100827 Homo sapi
565	1.8	104429	9	AP003787	AP003787 Homo sapi	638	51	1.8	141848	2	AC107980	AC107980 Homo sapi
566	1.8	104892	9	AL589664	AL589664 Human DNA	639	51	1.8	141991	2	HS0382109	HS0382109 Human DNA
567	1.8	106658	9	AL606468	AL606468 Human DNA	640	51	1.8	142273	2	AL391994	AL391994 Human DNA
568	1.8	107381	2	AC115093	AC115093 Homo sapi	641	51	1.8	142634	2	AC018778	AC018778 Homo sapi
569	1.8	108836	9	AC059147	AC059147 Homo sapi	642	51	1.8	142830	9	AC007097	AC007097 Homo sapi
570	1.8	109018	9	HSJ1129A6	AL069673 Human DNA	643	51	1.8	143409	2	AP001787	AP001787 Homo sapi
571	1.8	109378	9	AC022143	AC022143 Homo sapi	644	51	1.8	143618	9	AL137856	AL137856 Human DNA
572	1.8	109891	9	HS112K5	HS05987 Human DNA	645	51	1.8	144098	9	AC104967	AC104967 Homo sapi
573	1.8	109902	9	HS0346C2	AL132275 Human DNA	646	51	1.8	144588	2	AC012239	AC012239 Homo sapi
574	1.8	110816	9	AC002404	AC002404 Human Chir	647	51	1.8	145063	2	AC027069	AC027069 Homo sapi
575	1.8	111293	9	HS156L9	AL213222 Homo sapi	648	51	1.8	145066	2	AP002418	AP002418 Homo sapi
576	1.8	111344	9	AL139403	AL139403 Human DNA	649	51	1.8	145131	2	AC013822	AC013822 Homo sapi
								1.6	145206	9	AC026170	AC026170 Homo sapi

c 650	51	1.8 145442	9	AC004859	AC004859 Homo sapi	c 723	51	1.8 164057	9	AL590138	AL590138 Human DNA
c 651	51	1.8 146083	9	AC099480	AC099480 Homo sapi	c 724	51	1.8 164519	9	AL138712	AL138712 Human DNA
c 652	51	1.8 146250	2	AC074240	AC074240 Homo sapi	c 725	51	1.8 164587	9	AC023001	AC023001 Homo sapi
c 653	51	1.8 147244	9	AC005969	AC005969 Homo sapi	c 726	51	1.8 164604	9	AL138682	AL138682 Human DNA
c 654	51	1.8 147767	2	AC105030	AC105030 Homo sapi	c 727	51	1.8 165077	2	AC024493	AC024493 Homo sapi
c 655	51	1.8 148068	9	CNS01RHN	AL161873 Human chr	c 728	51	1.8 165483	2	AL591362	AL591362 Homo sapi
c 656	51	1.8 148271	9	AL392046	AL392046 Human DNA	c 729	51	1.8 165868	2	AC021719	AC021719 Homo sapi
c 657	51	1.8 149188	9	AC114781	AC114781 Homo sapi	c 730	51	1.8 166124	9	AF238375	AF238375 Homo sapi
c 658	51	1.8 149244	9	AL683842	AL683842 Human DNA	c 731	51	1.8 166181	9	HS37E16	HS37E16 Homo sapi
c 659	51	1.8 149324	2	AL157822	AL157822 Homo sapi	c 732	51	1.8 166206	2	AC009668	AC009668 Homo sapi
c 660	51	1.8 149710	2	AC022563	AC022563 Homo sapi	c 733	51	1.8 166254	9	AL359983	AL359983 Human DNA
c 661	51	1.8 150397	2	CNS05TD2	AL355423 Homo sapi	c 734	51	1.8 166765	9	AC112496	AC112496 Homo sapi
c 662	51	1.8 151031	9	AC112222	AC112222 Homo sapi	c 735	51	1.8 166837	2	AC087895	AC087895 Homo sapi
c 663	51	1.8 151228	9	AL662800	AL662800 Human DNA	c 736	51	1.8 166941	2	AC008049	AC008049 Homo sapi
c 664	51	1.8 151302	9	AC073617	AC073617 Homo sapi	c 737	51	1.8 166989	2	AC013554	AC013554 Homo sapi
c 665	51	1.8 151712	9	AC008385	AC008385 Homo sapi	c 738	51	1.8 167185	9	AC093132	AC093132 Papio cyn
c 666	51	1.8 151976	9	AC024588	AC024588 Homo sapi	c 739	51	1.8 167390	9	AC007263	AC007263 Homo sapi
c 667	51	1.8 153702	9	AL645730	AL645730 Human DNA	c 740	51	1.8 167479	9	AL445235	AL445235 Human DNA
c 668	51	1.8 154066	9	HS24018	AL621808 Human DNA	c 741	51	1.8 167594	2	AC100791	AC100791 Homo sapi
c 669	51	1.8 154068	9	AL356292	AL356292 Human DNA	c 742	51	1.8 167631	2	AC016032	AC016032 Homo sapi
c 670	51	1.8 154405	9	AC009275	AC009275 Homo sapi	c 743	51	1.8 167633	9	AL513534	AL513534 Human DNA
c 671	51	1.8 154604	2	AC104974	AC104974 Homo sapi	c 744	51	1.8 167671	2	AC090081	AC090081 Homo sapi
c 672	51	1.8 154935	2	AL356781	AL356781 Homo sapi	c 745	51	1.8 167749	2	AC016416	AC016416 Homo sapi
c 673	51	1.8 154994	9	AC099755	AC099755 Homo sapi	c 746	51	1.8 167831	2	AC027723	AC027723 Homo sapi
c 674	51	1.8 155085	9	AC010412	AC010412 Homo sapi	c 747	51	1.8 168063	2	AC090699	AC090699 Homo sapi
c 675	51	1.8 155308	2	AC109487	AC109487 Homo sapi	c 748	51	1.8 168481	2	AC025094	AC025094 Homo sapi
c 676	51	1.8 155439	9	AC008626	AC008626 Homo sapi	c 749	51	1.8 168613	9	AC091133	AC091133 Homo sapi
c 677	51	1.8 155521	9	AC069335	AC069335 Homo sapi	c 750	51	1.8 168872	2	AC019036	AC019036 Homo sapi
c 678	51	1.8 156089	2	AC013750	AC013750 Homo sapi	c 751	51	1.8 168900	2	AC024418	AC024418 Homo sapi
c 679	51	1.8 156399	9	AC002456	AC002456 Homo sapi	c 752	51	1.8 168981	2	AC126347	AC126347 Homo sapi
c 680	51	1.8 156503	9	AC011511	AC011511 Homo sapi	c 753	51	1.8 169007	9	AC034193	AC034193 Homo sapi
c 681	51	1.8 156580	9	AP003493	AP003493 Homo sapi	c 754	51	1.8 169347	9	AC007327	AC007327 Homo sapi
c 682	51	1.8 156633	2	AC113431	AC113431 Homo sapi	c 755	51	1.8 170048	2	AC025240	AC025240 Homo sapi
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c 684	51	1.8 157289	9	AC069421	AC069421 Homo sapi	c 757	51	1.8 170336	2	AC011244	AC011244 Homo sapi
c 685	51	1.8 157299	2	AC083932	AC083932 Homo sapi	c 758	51	1.8 170392	9	AC060765	AC060765 Homo sapi
c 686	51	1.8 157358	9	AC016745	AC016745 Homo sapi	c 759	51	1.8 170722	2	AC087847	AC087847 Homo sapi
c 687	51	1.8 157545	2	AL163535	AL163535 Homo sapi	c 760	51	1.8 170772	2	AC016454	AC016454 Homo sapi
c 688	51	1.8 158405	9	AC009753	AC009753 Homo sapi	c 761	51	1.8 170823	2	AC092294	AC092294 Homo sapi
c 689	51	1.8 158424	9	CNS01R13	AL162632 Human chr	c 762	51	1.8 171068	9	AL356241	AL356241 Human DNA
c 690	51	1.8 158817	9	AP005353	AP005353 Homo sapi	c 763	51	1.8 171073	2	AL590609	AL590609 Homo sapi
c 691	51	1.8 158838	9	CNS05TDN	AL356605 Human chr	c 764	51	1.8 171099	9	AC092544	AC092544 Homo sapi
c 692	51	1.8 159098	2	AC016484	AC016484 Homo sapi	c 765	51	1.8 171381	9	AL162730	AL162730 Human DNA
c 693	51	1.8 159122	2	AC025556	AC025556 Homo sapi	c 766	51	1.8 171550	9	AC079322	AC079322 Homo sapi
c 694	51	1.8 159263	9	AC092544	AC092544 Homo sapi	c 767	51	1.8 171606	2	AL591118	AL591118 Homo sapi
c 695	51	1.8 159351	2	AC018783	AC018783 Homo sapi	c 768	51	1.8 171739	9	AC093294	AC093294 Homo sapi
c 696	51	1.8 159597	9	AC008747	AC008747 Homo sapi	c 769	51	1.8 171902	2	AP000846	AP000846 Homo sapi
c 697	51	1.8 159692	9	AC016727	AC016727 Homo sapi	c 770	51	1.8 172217	2	AC068391	AC068391 Homo sapi
c 698	51	1.8 159787	2	AC016285	AC016285 Homo sapi	c 771	51	1.8 172358	9	AC011895	AC011895 Homo sapi
c 699	51	1.8 160525	2	AC027074	AC027074 Homo sapi	c 772	51	1.8 172393	2	AC025740	AC025740 Homo sapi
c 700	51	1.8 160545	9	AC036214	AC036214 Homo sapi	c 773	51	1.8 172403	2	AC017061	AC017061 Homo sapi
c 701	51	1.8 160656	2	AL592072	AL592072 Homo sapi	c 774	51	1.8 172543	9	AP004287	AP004287 Homo sapi
c 702	51	1.8 160658	9	AC024258	AC024258 Homo sapi	c 775	51	1.8 172577	2	AL365174	AL365174 Homo sapi
c 703	51	1.8 160754	9	AC007613	AC007613 Homo sapi	c 776	51	1.8 172588	2	AC007430	AC007430 Homo sapi
c 704	51	1.8 160994	9	AC044800	AC044800 Homo sapi	c 777	51	1.8 172880	9	AC027419	AC027419 Homo sapi
c 705	51	1.8 161109	2	AC034594	AC034594 Homo sapi	c 778	51	1.8 173083	2	AC034272	AC034272 Homo sapi
c 706	51	1.8 161179	2	AC066601	AC066601 Homo sapi	c 779	51	1.8 173087	9	AC010809	AC010809 Homo sapi
c 707	51	1.8 161199	2	AC066601	AC066601 Homo sapi	c 780	51	1.8 173184	9	AC112515	AC112515 Homo sapi
c 708	51	1.8 161499	2	AC015488	AC015488 Homo sapi	c 781	51	1.8 173317	9	AC016637	AC016637 Homo sapi
c 709	51	1.8 161505	9	AP001888	AP001888 Homo sapi	c 782	51	1.8 173359	2	AP000922	AP000922 Homo sapi
c 710	51	1.8 161540	9	AC076972	AC076972 Homo sapi	c 783	51	1.8 173456	9	AC055758	AC055758 Homo sapi
c 711	51	1.8 161788	2	AC025619	AC025619 Homo sapi	c 784	51	1.8 173463	9	AL359092	AL359092 Human DNA
c 712	51	1.8 161976	2	AC012415	AC012415 Homo sapi	c 785	51	1.8 174018	2	AL445311	AL445311 Homo sapi
c 713	51	1.8 161987	9	AC079848	AC079848 Homo sapi	c 786	51	1.8 174074	9	AC018891	AC018891 Homo sapi
c 714	51	1.8 162107	2	AP002423	AP002423 Homo sapi	c 787	51	1.8 174283	2	AC013723	AC013723 Homo sapi
c 715	51	1.8 162314	9	AC061965	AC061965 Homo sapi	c 788	51	1.8 174346	9	AC108173	AC108173 Homo sapi
c 716	51	1.8 162450	6	AK211792	AK211792 Sequence	c 789	51	1.8 174400	9	AC011603	AC011603 Homo sapi
c 717	51	1.8 163338	9	AL162426	AL162426 Human DNA	c 790	51	1.8 175028	9	AC066692	AC066692 Homo sapi
c 718	51	1.8 163390	9	AL137058	AL137058 Human DNA	c 791	51	1.8 175053	2	AC023226	AC023226 Homo sapi
c 719	51	1.8 163541	9	AC068954	AC068954 Homo sapi	c 792	51	1.8 175127	2	AC016048	AC016048 Homo sapi
c 720	51	1.8 163891	9	AC092647	AC092647 Homo sapi	c 793	51	1.8 175129	2	AC021490	AC021490 Homo sapi
c 721	51	1.8 163924	2	AL162592	AL162592 Homo sapi	c 794	51	1.8 175265	2	AC063964	AC063964 Homo sapi
c 722	51	1.8 163958	2	AC019303	AC019303 Homo sapi	c 795	51	1.8 175345	9	AC073065	AC073065 Homo sapi

796	51	1.8 175582	9	AC023590	AC023590 Homo sapi	869	51	1.8 190430	2	AC118987	AC118987 Pan trogl
797	51	1.8 175940	9	AL133551	AL133551 Human DNA	C 870	51	1.8 190580	9	AC010184	AC010184 Homo sapi
798	51	1.8 175970	9	AC097488	AC097488 Homo sapi	C 871	51	1.8 190870	2	AC126614	AC126614 Homo sapi
799	51	1.8 175998	9	AC087238	AC087238 Homo sapi	C 872	51	1.8 190871	9	AC044797	AC044797 Homo sapi
800	51	1.8 176286	2	AL391234	AL391234 Homo sapi	C 873	51	1.8 191111	9	AC007458	AC007458 Homo sapi
801	51	1.8 176437	2	AC022037	AC022037 Homo sapi	C 874	51	1.8 191594	9	AL160282	AL160282 Human DNA
802	51	1.8 176602	9	AC116665	AC116665 Papio cyn	C 875	51	1.8 191652	9	AL354668	AL354668 Human DNA
803	51	1.8 176806	9	AC090438	AC090438 Homo sapi	C 876	51	1.8 191665	9	AC027627	AC027627 Homo sapi
804	51	1.8 177080	9	AC027288	AC027288 Homo sapi	C 877	51	1.8 191830	2	AC026332	AC026332 Homo sapi
805	51	1.8 177675	9	AC008266	AC008266 Homo sapi	C 878	51	1.8 193118	2	AC067728	AC067728 Homo sapi
806	51	1.8 177806	9	AC093106	AC093106 Homo sapi	C 879	51	1.8 193214	9	AC069461	AC069461 Homo sapi
807	51	1.8 177993	9	AC093334	AC093334 Homo sapi	C 880	51	1.8 193387	2	AC009368	AC009368 Homo sapi
808	51	1.8 178338	2	AC125633	AC125633 Homo sapi	C 881	51	1.8 193366	9	AC093420	AC093420 Homo sapi
809	51	1.8 178377	9	AC007685	AC007685 Homo sapi	C 882	51	1.8 194109	2	AC121338	AC121338 Homo sapi
810	51	1.8 178494	2	AC124884	AC124884 Papio cyn	C 883	51	1.8 194395	2	AC084370	AC084370 Homo sapi
811	51	1.8 178515	2	AC015551	AC015551 Homo sapi	C 884	51	1.8 194681	2	AC084057	AC084057 Homo sapi
812	51	1.8 178872	9	AL162718	AL162718 Human DNA	C 885	51	1.8 194976	9	AL513165	AL513165 Human DNA
C 813	51	1.8 179155	9	AL353748	AL353748 Human DNA	C 886	51	1.8 195496	2	AC021809	AC021809 Homo sapi
C 814	51	1.8 179308	9	AC114402	AC114402 Homo sapi	C 887	51	1.8 195621	2	AC021714	AC021714 Homo sapi
C 815	51	1.8 179462	2	AC021102	AC021102 Homo sapi	C 888	51	1.8 196518	9	AC116154	AC116154 Homo sapi
C 816	51	1.8 179470	2	AL162211	AL162211 Homo sapi	C 889	51	1.8 196710	2	AC126470	AC126470 Homo sapi
C 817	51	1.8 179599	2	AC013278	AC013278 Homo sapi	C 890	51	1.8 196720	2	AC116941	AC116941 Pan trogl
C 818	51	1.8 179597	9	AC006960	AC006960 Homo sapi	C 891	51	1.8 197215	9	AP002954	AP002954 Homo sapi
C 819	51	1.8 179757	2	AC067879	AC067879 Homo sapi	C 892	51	1.8 197456	2	AC005054	AC005054 Homo sapi
C 820	51	1.8 179779	2	AC026012	AC026012 Homo sapi	C 893	51	1.8 198285	6	AX411170	AX411170 Sequence
C 821	51	1.8 180268	2	AC023648	AC023648 Homo sapi	C 894	51	1.8 198285	9	HSEVMHC	HSEVMHC
C 822	51	1.8 180399	2	AF001144	AF001144 Homo sapi	C 895	51	1.8 198456	2	AC069337	AC069337 Homo sapi
C 823	51	1.8 180535	9	AC018952	AC018952 Homo sapi	C 896	51	1.8 199421	9	AP000941	AP000941 Homo sapi
C 824	51	1.8 180537	2	AC023266	AC023266 Homo sapi	C 897	51	1.8 199458	2	AC099570	AC099570 Homo sapi
C 825	51	1.8 180707	2	AC024460	AC024460 Homo sapi	C 898	51	1.8 199437	2	AC091575	AC091575 Homo sapi
C 826	51	1.8 180726	2	AC090343	AC090343 Homo sapi	C 899	51	1.8 199832	2	AC087884	AC087884 Homo sapi
C 827	51	1.8 180890	2	AC018402	AC018402 Homo sapi	C 900	51	1.8 200368	9	AC096341	AC096341 Homo sapi
C 828	51	1.8 180995	9	AC117500	AC117500 Homo sapi	C 901	51	1.8 200536	9	AL356093	AL356093 Human DNA
C 829	51	1.8 181041	2	AC087677	AC087677 Homo sapi	C 902	51	1.8 200542	2	CNS01RG3	CNS01RG3 Homo sapi
C 830	51	1.8 181228	2	AC011086	AC011086 Homo sapi	C 903	51	1.8 200822	9	AL591806	AL591806 Human DNA
C 831	51	1.8 181324	9	AL160032	AL160032 Human DNA	C 904	51	1.8 200897	9	AC092058	AC092058 Homo sapi
C 832	51	1.8 181470	9	AC016659	AC016659 Homo sapi	C 905	51	1.8 201823	9	HSG120K12	HSG120K12
C 833	51	1.8 182009	2	AC074288	AC074288 Homo sapi	C 906	51	1.8 201886	9	AC092700	AC092700 Homo sapi
C 834	51	1.8 182231	9	AL137020	AL137020 Human DNA	C 907	51	1.8 202383	9	AC009973	AC009973 Homo sapi
C 835	51	1.8 182340	9	AC024417	AC024417 Homo sapi	C 908	51	1.8 202983	2	AC024249	AC024249 Homo sapi
C 836	51	1.8 182378	9	AC012400	AC012400 Homo sapi	C 909	51	1.8 203262	9	HSBA416N2	HSBA416N2
C 837	51	1.8 182810	9	AC022491	AC022491 Homo sapi	C 910	51	1.8 204153	9	AC074091	AC074091 Homo sapi
C 838	51	1.8 183100	9	AC021074	AC021074 Homo sapi	C 911	51	1.8 204590	2	AC093130	AC093130 Papio cyn
C 839	51	1.8 183216	2	AL161726	AL161726 Homo sapi	C 912	51	1.8 204927	2	AF254982	AF254982 Homo sapi
C 840	51	1.8 183378	2	AC011004	AC011004 Homo sapi	C 913	51	1.8 205590	2	AC067917	AC067917 Homo sapi
C 841	51	1.8 184280	9	AP003557	AP003557 Homo sapi	C 914	51	1.8 206578	2	AC026529	AC026529 Homo sapi
C 842	51	1.8 184361	2	AC012481	AC012481 Homo sapi	C 915	51	1.8 206590	9	AC026991	AC026991 Homo sapi
C 843	51	1.8 184535	2	CNS05TCJ	CNS05TCJ Homo sapi	C 916	51	1.8 206854	9	AC003974	AC003974 Homo sapi
C 844	51	1.8 184947	2	AC096849	AC096849 Pan trogl	C 917	51	1.8 207017	2	AC023373	AC023373 Homo sapi
C 845	51	1.8 184989	2	AC113392	AC113392 Homo sapi	C 918	51	1.8 207062	9	AF295017	AF295017 Homo sapi
C 846	51	1.8 185207	2	AC084350	AC084350 Homo sapi	C 919	51	1.8 207069	9	AC090922	AC090922 Homo sapi
C 847	51	1.8 185255	9	AC090666	AC090666 Homo sapi	C 920	51	1.8 207698	9	AC018808	AC018808 Homo sapi
C 848	51	1.8 185407	9	AC073288	AC073288 Homo sapi	C 921	51	1.8 208656	2	AC023778	AC023778 Homo sapi
C 849	51	1.8 185446	9	AC090517	AC090517 Homo sapi	C 922	51	1.8 208953	9	CNS01RH3	CNS01RH3 Human chr
C 850	51	1.8 186321	9	AC006511	AC006511 Homo sapi	C 923	51	1.8 209756	9	AC040165	AC040165 Homo sapi
C 851	51	1.8 186535	2	AL589793	AL589793 Homo sapi	C 924	51	1.8 209861	2	AC021196	AC021196 Homo sapi
C 852	51	1.8 186643	2	AC117273	AC117273 Papio cyn	C 925	51	1.8 210852	2	AC034102	AC034102 Homo sapi
C 853	51	1.8 186838	2	AC092947	AC092947 Homo sapi	C 926	51	1.8 210852	2	AC034102	AC034102 Homo sapi
C 854	51	1.8 187080	2	AC010308	AC010308 Homo sapi	C 927	51	1.8 210891	2	AC116025	AC116025 Homo sapi
C 855	51	1.8 187157	9	AL139384	AL139384 Human DNA	C 928	51	1.8 210933	2	AC027394	AC027394 Homo sapi
C 856	51	1.8 187615	2	AC020724	AC020724 Homo sapi	C 929	51	1.8 211542	2	AC073206	AC073206 Homo sapi
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Pullinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C.,
Aouizerat,B.E., Fielding,C.J. and Kane,J.P.
Analysis of hABCI gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms
Biochem. Biophys. Res. Commun. 271 (2000) In press
2 (bases 224 to 1167)
Pullinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C.,
Aouizerat,B.E., Fielding,C.J. and Kane,J.P.
Direct Submission
Submitted (20-APR-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
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Direct Submission
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COMMENT
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ORIGIN
Query Match      18.7%   Score 541;   DB 9;   Length 1167;
Best local similarity 100.0%;   Pred. No. 2.6e-293;
Matches 541;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  2130  TTGTGTTGTTCTTTTGTGTTTGTGTCGCTCTCTCTCAATTTCACGAGAACGA 2189
      |||||||
DB   168  TTGTGTTGTTCTTTTGTGTTTGTGTCGCTCTCTCTCAATTTCACGAGAACGA 227
      |||||||

QY  2190  TAAGATGTTCTCTCGGTCCTCTGAGGAGACCTCGGAGCTCAGGCTGGCAATCTCCAA 2249
      |||||||

```

	Query Match	18.7%	Score 541	DB 9	Length 1167
	Best Local Similarity	100.0%	Pred. No. 2.6e-293		
	Matches 541	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	2130	TTTGTGTGTTCTTTTGTGTTTGTGGCTCTCTCTCAATTTATCAAGAAGCA	2189		
Db	168	TTTGTGTGTTCTTTTGTGTTTGTGGCTCTCTCTCAATTTATCAAGAAGCA	227		
Qy	2190	GTAAGATGTCTCTCGGCTCTCTGAGGAGACCTGGGAGCTCAGGCTGGAAATCTCCAA	2249		

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W.-J., Zimmer, A. and Zody, M.

TITLE JOURNAL

Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Apr 22, 2000 this sequence version replaced gl:6454333.

All repeats were identified using RepeatMasker.

Smit, A.F.A. & Green, P. (1998-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBK

Web site: <http://www.seq.wi.mit.edu>

Contact: sequence-submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2510

Center clone name: L_M10

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960741

Consensus quality: 117571 bases at least Q40

Consensus quality: 145749 bases at least Q35

Consensus quality: 160940 bases at least Q20

Insert size: 185000; agarose-fp

Insert size: 171264; sum-of-contigs

Quality coverage: 2.9 in Q20 bases; agarose-fp

Quality coverage: 3.2 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently

consists of 39 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 1003: contig of 1093 bp in length

1004 1103: gap of 100 bp

1104 2634: contig of 1531 bp in length

2635 2734: gap of 100 bp

2735 4415: contig of 1681 bp in length

4416 4515: gap of 100 bp

4516 5785: contig of 1270 bp in length

5786 5885: gap of 100 bp

5886 7879: contig of 1994 bp in length

7880 9686: contig of 1707 bp in length

9687 9786: gap of 100 bp

9787 12253: contig of 2467 bp in length

12254 12353: gap of 100 bp

12354 15228: contig of 2875 bp in length

15229 15328: gap of 100 bp

15329 17200: contig of 1872 bp in length

17201 17300: gap of 100 bp

17301 20131: contig of 2831 bp in length

20132 20231: gap of 100 bp

20232 20587: contig of 2466 bp in length

20588 22687: gap of 100 bp

22688 25707: contig of 3020 bp in length

25708 25807: gap of 100 bp

25808 28184: contig of 2377 bp in length

28185 28284: gap of 100 bp

28285 31338: contig of 3054 bp in length

31339 31438: gap of 100 bp

31439 34299: contig of 2861 bp in length

34300 34399: gap of 100 bp

34400 38318: contig of 4319 bp in length

38319 38418: gap of 100 bp

38419 42835: contig of 4417 bp in length

42836 42935: gap of 100 bp

42936 45448: contig of 2513 bp in length

45449 45548: gap of 100 bp

45549 48116: contig of 2568 bp in length

48117 48216: gap of 100 bp

48217 52618: contig of 4402 bp in length

52619 52718: gap of 100 bp

52719 56592: contig of 3874 bp in length

56593 56692: gap of 100 bp

56693 59635: contig of 2943 bp in length

59636 59735: gap of 100 bp

59736 63661: contig of 3926 bp in length

63662 63761: gap of 100 bp

63762 68437: contig of 4676 bp in length

68438 68537: gap of 100 bp

68538 71458: contig of 2921 bp in length

71459 71558: gap of 100 bp

71559 76888: contig of 5330 bp in length

76889 76988: gap of 100 bp

76989 82113: contig of 5125 bp in length

82114 82213: gap of 100 bp

82214 88220: contig of 6007 bp in length

88221 88320: gap of 100 bp

88321 93499: contig of 5179 bp in length

93500 93599: gap of 100 bp

93600 97901: contig of 4302 bp in length

97902 98001: gap of 100 bp

98002 103016: contig of 5015 bp in length

103017 103116: gap of 100 bp

103117 109178: contig of 6062 bp in length

109179 109278: gap of 100 bp

109279 117307: contig of 8029 bp in length

117308 117407: gap of 100 bp

117408 124079: contig of 6672 bp in length

124080 124179: gap of 100 bp

124180 131281: contig of 7102 bp in length

131282 131381: gap of 100 bp

131382 138059: contig of 6678 bp in length

138060 138159: gap of 100 bp

138160 145491: contig of 7332 bp in length

145492 145591: gap of 100 bp

145592 157391: contig of 11800 bp in length

157392 157491: gap of 100 bp

157492 175064: contig of 17573 bp in length.

FEATURES

SOURCE

1. 175064
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/db_xref="taxon:9606"
/clone="RP11-1M10"
/clone_lib="RPC1-11 Human Male BAC"

misc_feature

1. 1603

/note="assembly_fragment"

1. 34. 2634

/note="assembly_fragment"

2745. 4415

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/note="assembly_fragment"

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25808. 28184

/note="assembly_fragment"

28185. 31338

/note="assembly_fragment"

31439. 34299

/note="assembly_fragment"

34300. 38318

/note="assembly_fragment"

38319. 42835

/note="assembly_fragment"

42836. 42935

/note="assembly_fragment"

42936. 45448

/note="assembly_fragment"


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1465 AAATCATGCTAGGAAGATACACACCTTTTAAATACACTCTCTGCTTTTATAAATCATC 1406
CY 275 TGCCAGGAGCTCAAGAGTTTCAACAAAGTTTCACTTTCAGAAATGCTTTTCAGAGAGAC 334
1405 TGCCAGGAGCTCAAGAGTTTCAACAAAGTTTCACTTTCAGAAATGCTTTTCAGAGAGAC 1346
CY 335 AGAATATACATCTCTCTCTCATTTTAAAGATCAAGAAATAGGCTGGGCAATAGCTAA 344
1445 AGAATATACATCTCTCTCTCATTTTAAAGATCAAGAAATAGGCTGGGCAATAGCTAA 1286
CY 395 GCTGTGAATCCAGCACTTTGGAGGCTGAGGCCA 429
1285 GCTGTGAATCCAGCACTTTGGAGGCTGAGGCCA 1251

RESULT 13
AC021246
TAXUS
DEFINITION Homo sapiens clone RP11-IN10. LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC021246
VERSION AC021246.2 GI:9119882
KEYWORDS HTG; HTGS, PHASE0.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69570)
Birken,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RP11-IN10
Unpublished
2 (bases 1 to 69570)
Birken,B., Linton,L., Nusbaum,C., Lander,E., Altham,H., Allen,N.,
Anderson,S., Balgwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Chowpei,Y., Collangelo,M., Collins,S., Collamore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Feneator,J.,
Foreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Liu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrum,J., Meneses,L., Morton,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donne,J.P., Oliver,I.M., Peterson,K.,
Pierre,N., Pisani,C., Poilara,V., Raymond,C., Riley,R., Richmond,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thumann,J.,
Stojanovic,N., Subramanian,A., Talanas,J., Testaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vogt,A., Wexler,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced nt:6705971.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/km/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WBIR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 12512
Center clone name: 1_N_10
-----
* NOTE: This record contains 73 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.

```

* However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 871: contig of 871 bp in length
 872 971: gap of 100 bp
 972 1834: contig of 863 bp in length
 1835 1934: gap of 100 bp
 1935 2804: contig of 870 bp in length
 2805 2904: gap of 100 bp
 2905 3745: contig of 841 bp in length
 3746 3845: gap of 100 bp
 3846 4696: contig of 851 bp in length
 4697 4796: gap of 100 bp
 4797 5640: contig of 844 bp in length
 5641 5740: gap of 100 bp
 5741 6540: contig of 800 bp in length
 6541 6640: gap of 100 bp
 6641 7509: contig of 869 bp in length
 7510 7609: gap of 100 bp
 7610 8479: contig of 870 bp in length
 8480 8579: gap of 100 bp
 8580 9430: contig of 851 bp in length
 9431 9530: gap of 100 bp
 9531 10376: contig of 846 bp in length
 10377 10476: gap of 100 bp
 10477 11322: contig of 846 bp in length
 11323 11422: gap of 100 bp
 11423 12302: contig of 880 bp in length
 12303 12402: gap of 100 bp
 12403 13280: contig of 878 bp in length
 13281 13380: gap of 100 bp
 13381 14241: contig of 861 bp in length
 14242 14341: gap of 100 bp
 14342 15196: contig of 855 bp in length
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 15297 16123: contig of 827 bp in length
 16124 16223: gap of 100 bp
 16224 17072: contig of 849 bp in length
 17073 17172: gap of 100 bp
 17173 18041: contig of 869 bp in length
 18042 18141: gap of 100 bp
 18142 19009: contig of 868 bp in length
 19010 19109: gap of 100 bp
 19110 19966: contig of 857 bp in length
 19967 20066: gap of 100 bp
 20067 20921: contig of 855 bp in length
 20922 21021: gap of 100 bp
 21022 21865: contig of 844 bp in length
 21866 21965: gap of 100 bp
 21966 22832: contig of 867 bp in length
 22833 22932: gap of 100 bp
 22933 23780: contig of 848 bp in length
 23781 23880: gap of 100 bp
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 24734 24833: gap of 100 bp
 24834 25670: contig of 837 bp in length
 25671 25770: gap of 100 bp
 25771 26621: contig of 851 bp in length
 26622 26721: gap of 100 bp
 26722 27576: contig of 855 bp in length
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 27677 28532: contig of 856 bp in length
 28533 28632: gap of 100 bp
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 31511 32368: contig of 858 bp in length
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* 35305 36156: contig of 852 bp in length
* 36157 36256: gap of 100 bp
* 36257 37128: contig of 872 bp in length
* 37129 37228: gap of 100 bp
* 37229 38083: contig of 855 bp in length
* 38084 38183: gap of 100 bp
* 38184 39031: contig of 848 bp in length
* 39032 39131: gap of 100 bp
* 39132 40006: contig of 875 bp in length
* 40007 40106: gap of 100 bp
* 40107 40967: contig of 861 bp in length
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* 54369 55229: contig of 861 bp in length
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* 56298 57163: contig of 866 bp in length
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* 57264 58130: contig of 867 bp in length
* 58131 58230: gap of 100 bp
* 58231 59082: contig of 852 bp in length
* 59083 59182: gap of 100 bp
* 59183 60020: contig of 838 bp in length
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* 60121 60983: contig of 863 bp in length
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* 61936 62035: gap of 100 bp
* 62036 62866: contig of 841 bp in length
* 62867 62966: gap of 100 bp
* 62967 63827: contig of 861 bp in length
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* 63928 64783: contig of 856 bp in length
* 64784 64883: gap of 100 bp
* 64884 65740: contig of 857 bp in length
* 65741 66684: contig of 844 bp in length
* 66685 66784: gap of 100 bp
* 66785 67651: contig of 867 bp in length
* 67652 67751: gap of 100 bp

Query Match 5.4% Score 156; DB 2; Length 69570;
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Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2464 GGAAGAAAAATTCGGAAAGCAGGATTAGAGGAAGCAAAATTCACCTGGTGCCTTTGGC 2523
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Db 41199 TGCCGGGAATGTGACCTAGAGAGTCTCGGGCGAGCCGAGCCGAGCGGTTCCTCCGCGC 41258
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QY 2584 TCTTAGGCGGGCGCCCGCGGGGGAAGGAGCGAGCCGAGCGGTTCCTCCGCGC 2643
|||||
Db 41259 TCTTAGGCGGGCGCCCGCGGGGGAAGGAGCGAGCCGAGCGGTTCCTCCGCGC 41318
|||||

QY 2644 GCTGTACCTCCACCCACCCACCCACCC 2670
|||||
Db 41319 GCTGTACCTCCACCCACCCACCCACCC 41345
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RESULT 14
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DEFINITION AC021345
ACCESSION AC021345
VERSION AC021345.2 GI:9130845
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Grantiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90698)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-24J9
Unpublished
2 (bases 1 to 90698)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavsky,L., Bouckhalter,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Feneator,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,P., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Tschmann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6705761.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L483
Center clone name: 24_J_9

* NOTE: This record contains 92 individual
* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 910: contig of 910 bp in length.
* 1011 1010: gap of 100 bp.
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* 1874 1973: contig of 861 bp in length.
* 1974 2824: contig of 851 bp in length.
* 2825 2924: gap of 100 bp.
* 2925 3802: contig of 878 bp in length.
* 3803 3902: gap of 100 bp.
* 3903 4816: contig of 914 bp in length.
* 4817 4916: gap of 100 bp.
* 4917 5759: contig of 843 bp in length.
* 5760 5859: gap of 100 bp.
* 5860 6764: contig of 905 bp in length.
* 6765 6864: gap of 100 bp.
* 6865 7747: contig of 883 bp in length.
* 7748 7847: gap of 100 bp.
* 7848 8755: contig of 908 bp in length.
* 8756 8855: gap of 100 bp.
* 8856 9753: contig of 898 bp in length.
* 9754 9853: gap of 100 bp.
* 9854 10757: contig of 904 bp in length.
* 10758 10857: gap of 100 bp.
* 10858 11732: contig of 875 bp in length.
* 11733 11832: gap of 100 bp.
* 11833 12739: contig of 907 bp in length.
* 12740 12839: gap of 100 bp.
* 12840 13710: contig of 871 bp in length.
* 13711 13810: gap of 100 bp.
* 13811 14684: contig of 874 bp in length.
* 14685 14784: gap of 100 bp.
* 14785 15662: contig of 878 bp in length.
* 15663 15762: gap of 100 bp.
* 15763 16677: contig of 915 bp in length.
* 16678 16777: gap of 100 bp.
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* 17679 17778: gap of 100 bp.
* 17779 18679: contig of 901 bp in length.
* 18680 18779: gap of 100 bp.
* 18780 19632: contig of 854 bp in length.
* 19633 19732: gap of 100 bp.
* 19733 20634: contig of 922 bp in length.
* 20635 20734: gap of 100 bp.
* 20735 21620: contig of 881 bp in length.
* 21621 21720: gap of 100 bp.
* 21721 22579: contig of 859 bp in length.
* 22580 22679: gap of 100 bp.
* 22680 23568: contig of 889 bp in length.
* 23569 23668: gap of 100 bp.
* 23669 24554: contig of 886 bp in length.
* 24555 24654: gap of 100 bp.
* 24655 25521: contig of 867 bp in length.
* 25522 25621: gap of 100 bp.
* 25622 26487: contig of 866 bp in length.
* 26488 26587: gap of 100 bp.
* 26588 27464: contig of 877 bp in length.
* 27465 27564: gap of 100 bp.
* 27565 28466: contig of 902 bp in length.
* 28467 28566: gap of 100 bp.
* 28567 29464: contig of 898 bp in length.
* 29465 29564: gap of 100 bp.
* 29565 30447: contig of 893 bp in length.
* 30448 30547: gap of 100 bp.
* 30548 31453: contig of 906 bp in length.
* 31454 31553: gap of 100 bp.

* 31554 32452: contig of 899 bp in length.
* 32453 32552: gap of 100 bp.
* 32553 33447: contig of 895 bp in length.
* 33448 33547: gap of 100 bp.
* 33548 34435: contig of 888 bp in length.
* 34436 34535: gap of 100 bp.
* 34536 35433: contig of 898 bp in length.
* 35434 35533: gap of 100 bp.
* 35534 36440: contig of 907 bp in length.
* 36441 36540: gap of 100 bp.
* 36541 37442: contig of 882 bp in length.
* 37443 37522: gap of 100 bp.
* 37523 38402: contig of 880 bp in length.
* 38403 38502: gap of 100 bp.
* 38503 39380: contig of 878 bp in length.
* 39381 39480: gap of 100 bp.
* 39481 40407: contig of 927 bp in length.
* 40408 40507: gap of 100 bp.
* 40508 41405: contig of 898 bp in length.
* 41406 41505: gap of 100 bp.
* 41506 42399: contig of 894 bp in length.
* 42400 42499: gap of 100 bp.
* 42500 43357: contig of 858 bp in length.
* 43358 43457: gap of 100 bp.
* 43458 44356: contig of 899 bp in length.
* 44357 44456: gap of 100 bp.
* 44457 45325: contig of 869 bp in length.
* 45326 45425: gap of 100 bp.
* 45426 46305: contig of 880 bp in length.
* 46306 46405: gap of 100 bp.
* 46406 47302: contig of 897 bp in length.
* 47303 47402: gap of 100 bp.
* 47403 48293: contig of 891 bp in length.
* 48294 48393: gap of 100 bp.
* 48394 49280: contig of 887 bp in length.
* 49281 49380: gap of 100 bp.
* 49381 50250: contig of 870 bp in length.
* 50251 50350: gap of 100 bp.
* 50351 51209: contig of 859 bp in length.
* 51210 51309: gap of 100 bp.
* 51310 52221: contig of 912 bp in length.
* 52222 52321: gap of 100 bp.
* 52322 53205: contig of 884 bp in length.
* 53206 53305: gap of 100 bp.
* 53306 54225: contig of 920 bp in length.
* 54226 54325: gap of 100 bp.
* 54326 55206: contig of 881 bp in length.
* 55207 55306: gap of 100 bp.
* 55307 56165: contig of 859 bp in length.
* 56166 56265: gap of 100 bp.
* 56266 57124: contig of 859 bp in length.
* 57125 57224: gap of 100 bp.
* 57225 58121: contig of 897 bp in length.
* 58122 58221: gap of 100 bp.
* 58222 59075: contig of 854 bp in length.
* 59076 59175: gap of 100 bp.
* 59176 60058: contig of 883 bp in length.
* 60059 60158: gap of 100 bp.
* 60159 61067: contig of 909 bp in length.
* 61068 61167: gap of 100 bp.
* 61168 62051: contig of 884 bp in length.
* 62052 62151: gap of 100 bp.
* 62152 63022: contig of 871 bp in length.
* 63023 63122: gap of 100 bp.
* 63124 64026: contig of 904 bp in length.
* 64027 64126: gap of 100 bp.
* 64127 65015: contig of 889 bp in length.
* 65016 65115: gap of 100 bp.
* 65116 65975: contig of 860 bp in length.
* 65976 66075: gap of 100 bp.
* 66076 66954: contig of 879 bp in length.
* 66955 67094: gap of 100 bp.
* 67095 67947: contig of 893 bp in length.

Green, P. (1996-1997);
http://ftp.genome.washington.edu/RM/RepeatMasker.html.
FEATURES
Location/Qualifiers
1..126295
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="HRC84389"
/clone_lib="Peter de Jong/ human PAC library"
repeat_region
complement(2..193)
/rpt_family="AluSx"
repeat_region
complement(235..410)
/rpt_family="MER5A"
repeat_region
complement(479..640)
/rpt_family="MIR"
repeat_region
complement(714..1012)
/rpt_family="AluSc"
repeat_region
1140..1269
/rpt_family="L2"
repeat_region
complement(2503..2646)
/rpt_family="MER5B"
repeat_region
complement(2647..2954)
/rpt_family="AluJb"
repeat_region
complement(2955..2998)
/rpt_family="MER5B"
repeat_region
3758..4544
/rpt_family="L2"
repeat_region
4743..4873
/rpt_family="FLAM_C"
repeat_region
complement(5068..5364)
/rpt_family="AluJb"
repeat_region
complement(6403..6675)
/rpt_family="AluSx"
repeat_region
6782..6950
/rpt_family="MIR"
repeat_region
complement(7379..7734)
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repeat_region
complement(7735..7840)
/rpt_family="(GGGA)n"
repeat_region
complement(7841..7876)
/rpt_family="purine-rich"
repeat_region
complement(7883..7988)
/rpt_family="Tigger1"
repeat_region
complement(7989..8597)
/rpt_family="Tigger1"
repeat_region
complement(8604..8741)
/rpt_family="FLAM_C"
repeat_region
complement(8759..9456)
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repeat_region
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repeat_region
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repeat_region
10754..11095
/rpt_family="MER47A"
repeat_region
complement(11106..11949)
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repeat_region
12033..12147
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repeat_region
12148..12235
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repeat_region
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repeat_region
13224..13251
/rpt_family="MIR"
repeat_region
13252..13544
/rpt_family="AluSx"
repeat_region
13545..13769
/rpt_family="MIR"
repeat_region
14208..14364
/rpt_family="MER5A"
repeat_region
complement(14835..15195)

repeat_region
complement(15353..15497)
/rpt_family="L2"
repeat_region
complement(15662..15828)
/rpt_family="MLTIG"
repeat_region
complement(16301..16607)
/rpt_family="AluY"
repeat_region
17500..17802
/rpt_family="AluSx"
repeat_region
complement(18474..18774)
/rpt_family="AluSg"
repeat_region
18825..18902
/rpt_family="MIR"
repeat_region
complement(19656..19771)
/rpt_family="MER20"
repeat_region
19834..20129
/rpt_family="AluSp"
repeat_region
complement(20145..20168)
/rpt_family="(CAAAA)n"
repeat_region
complement(20169..20451)
/rpt_family="AluSx"
repeat_region
complement(20456..20765)
/rpt_family="AluSx"
repeat_region
complement(21023..21343)
/rpt_family="LIM4"
repeat_region
21344..21630
/rpt_family="AluSx"
repeat_region
complement(21631..21700)
/rpt_family="LIM4"
repeat_region
22291..22526
/rpt_family="MIR"
repeat_region
23606..23899
/rpt_family="AluJo"
repeat_region
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/rpt_family="L2"
repeat_region
complement(25816..25978)
/rpt_family="LIMD"
repeat_region
26161..26465
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repeat_region
complement(26630..26725)
/rpt_family="MIR"
repeat_region
complement(26902..26958)
/rpt_family="(CA)n"
repeat_region
complement(26959..27179)
/rpt_family="AluJb"
repeat_region
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repeat_region
27712..28009
/rpt_family="AluSx"
repeat_region
complement(28773..29080)
/rpt_family="AluSx"
repeat_region
29132..29580
/rpt_family="LMC5"
repeat_region
29962..30097
/rpt_family="L2"
repeat_region
30275..30566
/rpt_family="AluSx"
repeat_region
complement(31041..31353)
/rpt_family="AluSg"
repeat_region
complement(32362..32571)
/rpt_family="AluSg/x"
repeat_region
complement(33470..33781)
/rpt_family="AluJb8"
repeat_region
complement(35504..35774)
/rpt_family="LMC3A"
repeat_region
35830..35906
/rpt_family="AluJo"
repeat_region
35907..36194
/rpt_family="AluY"
repeat_region
36204..36516
/rpt_family="AluSg"
repeat_region
36517..36682
/rpt_family="AluJo"

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repeat_region complement(36689..37629)

Query Match
Best local Similarity 100.0%; Score 65; DB 9; Length 126295;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 GAATCGACTACTGAACCTGCTCCGGGTCAAGCGATTCTCTGGGTAAGCTGC 1076
|||||
DB 4115 GATCGACTACTGAACCTGCTCCGGGTCAAGCGATTCTCTGGGTAAGCTGC 41174

QY 1077 CTGAG 1081
|||||
DB 31175 CTGAG 31179

RESULT 17
AL807243/c
LOCUS      186889 bp      DNA      linear      HTG 30-JUN-2002
DEFINITION Mus musculus chromosome 4 clone RP23-25D17, *** SEQUENCING IN
PROGRESS ***, 24 unordered pieces.
ACCESSION AL807243
VERSION    2.1
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Mus.
            Mclay,K.
            (bases 1 to 186889)

Direct Submission
Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail: enquiries@
humquerry@sanger.ac.uk
humquerry@sanger.ac.uk
on Jul 2, 2002 This sequence version replaced gi:21268136.

----- Genome Center
Center: Wellcome Trust Sanger Institute
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Project name: BM25D17
----- Summary Statistics
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 175959 bases at least Q40
Consensus quality: 179463 bases at least Q30
Consensus quality: 182069 bases at least Q20
Insert size: 184589; sum-of contigs
Insert size: 189466; 5.5% error; adaptor-seq
Quality coverage: 4.72x in 920 bases; sum-of contigs Quality
coverage: 4.82x in 920 bases; adaptor-seq
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 4849: contig of 4849 bp in length
* 4850 4949: gap of 100 bp
* 4950 22620: contig of 17671 bp in length
* 22621 22720: gap of 100 bp
* 22721 29963: contig of 7243 bp in length
* 29964 30063: gap of 100 bp
* 30064 40087: contig of 10024 bp in length
* 40088 40187: gap of 100 bp
* 40188 44438: contig of 4251 bp in length
* 44439 44538: gap of 100 bp
* 44539 48960: contig of 4422 bp in length
* 48961 49060: gap of 100 bp
* 49061 56007: contig of 6947 bp in length
*
* 56008 56107: gap of 100 bp
* 56108 58284: contig of 2177 bp in length
* 58285 58384: gap of 100 bp
* 58385 60786: contig of 2402 bp in length
* 60787 60886: gap of 100 bp
* 60887 66707: contig of 5821 bp in length
* 66708 66807: gap of 100 bp
* 66808 92102: contig of 25295 bp in length
* 92103 92202: gap of 100 bp
* 92203 99909: contig of 7707 bp in length
* 99910 100009: gap of 100 bp
* 100010 103760: contig of 3751 bp in length
* 103761 103860: gap of 100 bp
* 103861 110765: contig of 6905 bp in length
* 110766 110865: gap of 100 bp
* 110866 114685: contig of 3820 bp in length
* 114686 114785: gap of 100 bp
* 114786 125959: contig of 11174 bp in length
* 125960 126059: gap of 100 bp
* 126060 128749: contig of 2690 bp in length
* 128750 128849: gap of 100 bp
* 128850 132373: contig of 3524 bp in length
* 132374 132473: gap of 100 bp
* 132474 134930: contig of 2457 bp in length
* 134931 135030: gap of 100 bp
* 135031 139301: contig of 4271 bp in length
* 139302 139401: gap of 100 bp
* 139402 144448: contig of 5047 bp in length
* 144449 144548: gap of 100 bp
* 144549 147074: contig of 2526 bp in length
* 147075 147174: gap of 100 bp
* 147175 156317: contig of 9143 bp in length
* 156318 156417: gap of 100 bp
* 156418 186889: contig of 30472 bp in length.

FEATURES
Source
1..186889
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
/clone "RP23-25D17"
/clone_lib="RPC1-23"
1..4849
/feature="assembly_fragment:01920
fragment_chain:1"
4950..22620
/feature="assembly_fragment:01761
fragment_chain:1"
22721..29963
/feature="assembly_fragment:00140
fragment_chain:1"
30064..40087
/feature="assembly_fragment:00335
fragment_chain:1"
40188..44438
/feature="assembly_fragment:00241
fragment_chain:1"
44539..48960
/feature="assembly_fragment:01430
fragment_chain:1"
49061..56007
/feature="assembly_fragment:01667
fragment_chain:1"
56108..58284
/feature="assembly_fragment:00965
fragment_chain:2"
58385..60786
/feature="assembly_fragment:01660
fragment_chain:2"
60887..66707
/feature="assembly_fragment:00374
fragment_chain:2"
66808..92102
/feature="assembly_fragment:01792

```

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misc_feature      fragment_chain:2"
92203...99909
/note="assembly_fragment:01082
fragment_chain:2"
100010...103760
/note="assembly_fragment:00358
fragment_chain:2"
103861...110765
/note="assembly_fragment:01182
fragment_chain:3"
110866...114685
/note="assembly_fragment:01582
fragment_chain:3"
114786...125959
/note="assembly_fragment:00043
fragment_chain:3"
126060...128749
/note="assembly_fragment:00352
fragment_chain:3"
128850...132373
/note="assembly_fragment:00217
fragment_chain:4"
132474...134930
/note="assembly_fragment:01737
fragment_chain:4"
135031...139301
/note="assembly_fragment:00487"
139402...144448
/note="assembly_fragment:00557"
144549...147074
/note="assembly_fragment:01442"
147175...156317
/note="assembly_fragment:01564.0"
156418...186889
/note="assembly_fragment:01773"
BASE COUNT      52900 a 39593 c 40710 q 51348 t 2348 others
ORIGIN

Query Match      2.18; Score 61; DB 2; Length 195889;
Best Local Similarity 100.0%; Pred. No. 3,5e-22;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2744 CTCACGTCCTTCCTGCTGACTGACTACATACAGAGCGGGGAGAGGGGGCGG 2803
|||||
DB 9251 CTCACGTCCTTCCTGCTGACTGACTACATACAGAGCGGGGAGAGGGGGCGG 99192

QY 2804 G 2804
I
DB 99191 G 99191

RESULT 18
AC021850/c
LOCUS          AC021850      206966 bp      DNA      linear      PRI 09-MAY-2001
DEFINITION     Homo sapiens BAC clone RP11-389E17 from 4, complete sequence.
ACCESSION      AC021850
VERSION        AC021850.8 GI:12863232
KEYWORDS       HTC.
SOURCE         Homo sapiens.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 206966)
Suiston,J.E. and Waterston,R.
TITLE          Toward a complete human genome sequence
JOURNAL        Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE        99063792
PUBMED         9847074
REFERENCE      2 (bases 1 to 206966)
AUTHORS        Kang,K., Maupin,R. and Ureta-M.
TITLE          The sequence of Homo sapiens BAC clone RP11-389E17
JOURNAL        Unpublished
REFERENCE      3 (bases 1 to 206966)

```

AUTHORS TITLE JOURNAL:

REFERENCE
AUTHORS
TITLE
JOURNAL:

REFERENCE
AUTHORS
TITLE
JOURNAL:

COMMENT

Waterston,R.H.
Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 206966)
Waterston,R.H.
Direct Submission
Submitted (16-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 206966)
Waterston,R.
Direct Submission
Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 16, 2001 this sequence version replaced gi:11761497.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
----- Summary Statistics

Center project name: H_NH0389E17

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e. phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPC1-11 human BAC library was made from the blood of one male
donor, as described by Osogawa,K., Moon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-62B4. Actual start of this
clone is at base position 1 of RP11-389E17. Actual end is at base
position 206966 of RP11-389E17.

FEATURES

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source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-389E17"
/clone_lib="RPC1-11"
3..256
/rpt_family="L1"
389..509
/rpt_family="L1"
523..1023
/rpt_family="L1"
repeat_region
repeat_region
repeat_region

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repeat_region 1088. .1319 /rpt_family-"L1"
repeat_region 1775. .1908 /rpt_family-"MIR"
repeat_region 1930. .1950 /rpt_family-"MIR"
repeat_region 2531. .2753 /rpt_family-"AT_rich"
repeat_region 2772. .2792 /rpt_family-"Alu"
repeat_region 2987. .3022 /rpt_family-"AT_rich"
repeat_region 3223. .3260 /rpt_family-"AT_rich"
repeat_region 3386. .3523 /rpt_family-"AT_rich"
repeat_region 3775. .4559 /rpt_family-"MIR"
repeat_region 4595. .4763 /rpt_family-"ERV1"
repeat_region 5163. .5193 /rpt_family-"ERV1"
repeat_region 5276. .5297 /rpt_family-"(CA)n"
repeat_region 7864. .8032 /rpt_family-"AT_rich"
repeat_region 8397. .8660 /rpt_family-"MIR"
repeat_region 8877. .8991 /rpt_family-"ERV1"
repeat_region 9049. .9235 /rpt_family-"GA_rich"
repeat_region 9284. .9364 /rpt_family-"L2"
repeat_region 9388. .9734 /rpt_family-"L1"
repeat_region 11490. .11628 /rpt_family-"L1"
repeat_region 12620. .12715 /rpt_family-"L2"
repeat_region 12726. .12923 /rpt_family-"MER2_type"
repeat_region 12950. .13462 /rpt_family-"MER2_type"
repeat_region 17273. .17508 /rpt_family-"MER2_type"
repeat_region 18160. .18215 /rpt_family-"Alu"
repeat_region 18689. .18810 /rpt_family-"L2"
repeat_region 19217. .19324 /rpt_family-"MIR"
repeat_region 20012. .20292 /rpt_family-"L1"
repeat_region 20476. .20830 /rpt_family-"L1"
repeat_region 23028. .23085 /rpt_family-"MER2_type"
repeat_region 23483. .23612 /rpt_family-"AT_rich"
repeat_region 23878. .23976 /rpt_family-"Achoho"
repeat_region 24263. .24404 /rpt_family-"AT_rich"
repeat_region 24706. .24903 /rpt_family-"MIR"
repeat_region 26677. .27207 /rpt_family-"MIR"
repeat_region 27597. .27619 /rpt_family-"MER1_type"
repeat_region 28709. .28781 /rpt_family-"AT_rich"
repeat_region 29420. .29635 /rpt_family-"AT_rich"

repeat_region 29865. .29898 /rpt_family-"Alu"
repeat_region 29979. .30116 /rpt_family-"MIR"
repeat_region 30773. .31036 /rpt_family-"L2"
repeat_region 41039. .41722 /rpt_family-"L2"
repeat_region 52160. .52333 /rpt_family-"CR1"
repeat_region 31594. .34090 /rpt_family-"L1"
repeat_region 34248. .34275 /rpt_family-"AT_rich"
repeat_region 34635. .34825 /rpt_family-"L1"
repeat_region 35013. .35078 /rpt_family-"AT_rich"
repeat_region 35645. .35691 /rpt_family-"(CA)n"
repeat_region 36784. .37028 /rpt_family-"L1"
repeat_region 37100. .37171 /rpt_family-"L1"
repeat_region 37381. .37431 /rpt_family-"AT_rich"
repeat_region 37582. .38445 /rpt_family-"ERV1"
repeat_region 39128. .39148 /rpt_family-"AT_rich"
repeat_region 40735. .40755 /rpt_family-"AT_rich"
repeat_region 40826. .41030 /rpt_family-"AT_rich"

Query Match 2.1% Score 61; DB 9; Length 206966;
Best Local Similarity 100.0%; Pred. No. 3.5e-22;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 GATCTGACATCAGTAACTCTGCTCCGGGTTCAAGCGATTCTCTGCTGCTCAGCCTC 1076
|||||
DB 45729 GATCTGACATCAGTAACTCTGCTCCGGGTTCAAGCGATTCTCTGCTGCTCAGCCTC 45670

QY 1077 C 1077
DB 45664 C 45669

RESULT 14

AF287263 AF287263 278572 bp DNA linear ROD 23-APR-2001
LOCUS Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1)
DEFINITION gene, complete cds.

AF287263 AF287263.1 GI:11611824

VERSION AF287263.1

KEYWORDS Mus musculus.

SOURCE Mus musculus.

ORGANISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 278572)

AUTHORS Qiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F.

TITLE Human and mouse ABCA1 comparative sequencing and transgenesis

studies revealing novel regulatory sequences

JOURNAL Genomics 73 (1), 66-76 (2001)

MEDLINE 21251004

PUBMED 11352567

REFERENCE 2 (bases 1 to 278572)

AUTHORS Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.F.

TITLE Direct Submission

JOURNAL Submitted (14-JUL-2000) Genome Science Department, Lawrence

Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,

CA 94720, USA

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
 Barna, N., Bastien, V., Bloom, T., Boquslavsky, L., Boukhalter, B.,
 Canarata, J., Chang, J., Chazaro, B., Choquet, Y., Collymore, A.,
 Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Fodae, S.,
 Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
 Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A.,
 Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
 McCarthy, M., Meldrum, J., Mencus, L., Mihova, T., Muegg, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Phunkhang, P., Pierre, N., Raymond, C., Rella, R., Rose, C., Rodoy, P.,
 Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Stange-Thumann, N., Stojanovic, N., Talamas, J.,
 Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zalcoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jul 30, 2002 this sequence version replaced gi:17149709.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L21813

Center clone name: 2319_0_14

NOTE: This record contains 54 individual

sequencing reads that have not been assembled into
 contigs. Runs of N are used to separate the reads
 and the order in which they appear is completely
 arbitrary. Low-pass sequence sampling is useful for
 identifying clones that may be gene-rich and allows
 overlap relationships among clones to be detected.
 However, it should not be assumed that this clone
 will be sequenced to completion. In the event that
 the record is updated, the accession number will
 be preserved.

1 734: contig of 74 bp in length
 735 834: gap of 100 bp
 835 1552: contig of 718 bp in length
 1553 1652: gap of 100 bp
 1653 2405: contig of 754 bp in length
 2406 2505: gap of 100 bp
 2506 3239: contig of 734 bp in length
 3240 3339: gap of 100 bp
 3340 4094: contig of 755 bp in length
 4095 4194: gap of 100 bp
 4195 4930: contig of 736 bp in length
 4931 5030: gap of 100 bp
 5031 5753: contig of 723 bp in length
 5754 5853: gap of 100 bp
 5854 6627: contig of 774 bp in length
 6628 6727: gap of 100 bp
 6728 7449: contig of 722 bp in length
 7450 7549: gap of 100 bp
 7550 8322: contig of 773 bp in length
 8323 8422: gap of 100 bp
 8423 9126: contig of 704 bp in length
 9127 9226: gap of 100 bp
 9227 9973: contig of 747 bp in length
 9974 10073: gap of 100 bp
 10074 10811: contig of 748 bp in length
 10812 10911: gap of 100 bp
 10912 11635: contig of 724 bp in length
 11636 11735: gap of 100 bp
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 12490 12589: gap of 100 bp
 12590 13349: contig of 760 bp in length
 13350 13449: gap of 100 bp
 13450 14174: contig of 725 bp in length
 14175 14274: gap of 100 bp
 14275 15022: contig of 748 bp in length
 15023 15122: gap of 100 bp
 15123 15716: contig of 594 bp in length
 15717 15816: gap of 100 bp
 15817 16563: contig of 747 bp in length
 16564 16663: gap of 100 bp
 16664 17387: contig of 724 bp in length
 17388 17487: gap of 100 bp
 17488 18227: contig of 740 bp in length
 18228 18327: gap of 100 bp
 18328 19058: contig of 731 bp in length
 19059 19158: gap of 100 bp
 19159 19883: contig of 725 bp in length
 19884 19983: gap of 100 bp
 19984 20734: contig of 751 bp in length
 20735 20834: gap of 100 bp
 20835 21541: contig of 707 bp in length
 21542 21641: gap of 100 bp
 21642 22399: contig of 758 bp in length
 22400 22499: gap of 100 bp
 22500 23236: contig of 737 bp in length
 23237 23336: gap of 100 bp
 23337 24091: contig of 755 bp in length
 24092 24191: gap of 100 bp
 24192 24926: contig of 735 bp in length
 24927 25026: gap of 100 bp
 25027 25760: contig of 734 bp in length
 25761 25860: gap of 100 bp
 25861 26603: contig of 743 bp in length
 26604 26703: gap of 100 bp
 26704 27396: contig of 693 bp in length
 27397 27496: gap of 100 bp
 27497 28246: contig of 750 bp in length
 28247 28346: gap of 100 bp
 28347 29074: contig of 728 bp in length
 29075 29174: gap of 100 bp
 29175 29914: contig of 740 bp in length
 29915 30014: gap of 100 bp
 30015 30732: contig of 718 bp in length
 30733 30832: gap of 100 bp
 30833 31591: contig of 759 bp in length
 31592 31691: gap of 100 bp
 31692 32298: contig of 607 bp in length
 32299 32398: gap of 100 bp
 32399 33145: contig of 747 bp in length
 33146 33245: gap of 100 bp
 33246 33978: contig of 733 bp in length
 33979 34078: gap of 100 bp
 34079 34825: contig of 747 bp in length
 34826 34925: gap of 100 bp
 34926 35664: contig of 739 bp in length
 35665 35764: gap of 100 bp
 35765 36499: contig of 735 bp in length
 36500 36599: gap of 100 bp
 36600 37348: contig of 749 bp in length
 37349 37448: gap of 100 bp
 37449 38206: contig of 758 bp in length
 38207 38306: gap of 100 bp
 38307 39038: contig of 732 bp in length
 39039 39138: gap of 100 bp
 39139 39880: contig of 742 bp in length
 39881 39980: gap of 100 bp
 39981 40732: contig of 752 bp in length
 40733 40832: gap of 100 bp
 40833 41538: contig of 706 bp in length
 41539 41638: gap of 100 bp
 41639 42396: contig of 758 bp in length

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* 42397 42496: gap of 100 bp
* 42497 43236: contig of 740 bp in length
* 43237 43336: gap of 100 bp
* 43337 44060: contig of 724 bp in length
* 44061 44160: gap of 100 bp
* 44161 44897: contig of 737 bp in length.
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  /db_xref="taxon:9606"
  /chromosome="8"
  /map="8"
  /clone="CTD-2319014"

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FEATURES

source

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Query Match      2.0%  Score 59;  Db 2;  Length 44897;
Best Local Similarity 100.0%;  Pred. No. 4,26-21;
Matches 59;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
OY 1189 GCCACCTGGCTGCCAAAGTGGTGGATACAGCATGACGACACTGGATACAGTCA 1247
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Db 7019 GCCACCTGGCTGCCAAAGTGGTGGATACAGCATGACGACACTGGATACAGTCA 7077

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RESULTS 21
AC107969/c
LOCUS      AC107969      57662 bp    DNA    linear    HTG 24-JAN-2002
DEFINITION Homo sapiens chromosome 11 clone CTD-2028015 map 11, LOW PASS
SEQUENCE INFORMATION
AC107969
VERSION      AC107969.1  GI:18308697
KEYWORDS     HTG; HTGS_PHASE0.
SOURCE      Homo sapiens.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 57662)
AUTHORS     Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE       Homo sapiens chromosome 11, clone CTD-2028015
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 57662)
AUTHORS     Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
Brown,A., Barna,N., Hastien,V., Boguslavsky,L., Hookgaiter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faru,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardy,J.,
Ginde,S., Gord,S., Goyette,M., Graham,E., Grand-Pierre,N.,
Hanus,H., Horton,L., Hulme,W., Iliev,I., Johnson,K., Jones,C.,
Kamat,A., Karatas,A., Kelis,C., Labèque,K., Lander,E.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., Marletta,C.,
Maddonald,P., Major,J., Marquis,N., Matthews,G., McCarthy,M.,
McEwan,P., McKernan,K., Meldrum,J., Menes,L., Mihov,I.,
Minca,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,K., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phukhang,P., Pierre,N., Pollara,V., Raymond,C.,
Reita,R., Ribback,M., Riley,R., Rise,C., Rovey,P., Ryan,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stefanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testa,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triggilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W., Young,G.,
Zainoun,J., Zemek,L., Zimmer,A. and Zody,X.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu

```

```

----- Project Information
Center project name: L24518
Center clone name: 2028_0.15
NOTE: This record contains 73 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.

```

```

1 717: contig of 717 bp in length
718 817: gap of 100 bp
818 1525: contig of 708 bp in length
1526 1625: gap of 100 bp
1626 2265: contig of 640 bp in length
2266 2365: gap of 100 bp
2366 3050: contig of 685 bp in length
3051 3150: gap of 100 bp
3151 3845: contig of 695 bp in length
3846 3945: gap of 100 bp
3946 4577: contig of 632 bp in length
4578 4677: gap of 100 bp
4678 5369: contig of 692 bp in length
5370 5469: gap of 100 bp
5470 6151: contig of 682 bp in length
6152 6251: gap of 100 bp
6252 6955: contig of 704 bp in length
6956 7055: gap of 100 bp
7056 7804: contig of 749 bp in length
7805 7904: gap of 100 bp
7905 8603: contig of 699 bp in length
8604 8703: gap of 100 bp
8704 9392: contig of 689 bp in length
9393 9492: gap of 100 bp
9493 10155: contig of 663 bp in length
10156 10255: gap of 100 bp
10256 10948: contig of 693 bp in length
10949 11048: gap of 100 bp
11049 11603: contig of 555 bp in length
11604 11703: gap of 100 bp
11704 12386: contig of 683 bp in length
12387 12486: gap of 100 bp
12487 13187: contig of 701 bp in length
13188 13287: gap of 100 bp
13288 13988: contig of 701 bp in length
13989 14088: gap of 100 bp
14089 14795: contig of 707 bp in length
14796 14895: gap of 100 bp
14896 15532: contig of 637 bp in length
15533 15632: gap of 100 bp
15633 16347: contig of 715 bp in length
16348 16447: gap of 100 bp
16448 17155: contig of 708 bp in length
17156 17255: gap of 100 bp
17256 17961: contig of 706 bp in length
17962 18061: gap of 100 bp
18062 18723: contig of 662 bp in length
18724 18823: gap of 100 bp
18824 19476: contig of 653 bp in length
19477 19576: gap of 100 bp
19577 20274: contig of 698 bp in length
20275 20374: gap of 100 bp
20375 21074: contig of 700 bp in length
21075 21174: gap of 100 bp
21175 21867: contig of 693 bp in length
21868 21967: gap of 100 bp
21968 22680: contig of 713 bp in length
22681 22780: gap of 100 bp

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```
* 22781 23495: contig of 715 bp in length
* 23496 23595: gap of 100 bp
* 23596 24227: contig of 632 bp in length
* 24228 24327: gap of 100 bp
* 24328 25032: contig of 705 bp in length
* 25033 25132: gap of 100 bp
* 25133 25838: contig of 706 bp in length
* 25839 25938: gap of 100 bp
* 25939 26651: contig of 713 bp in length
* 26652 26751: gap of 100 bp
* 26752 27431: contig of 680 bp in length
* 27432 27531: gap of 100 bp
* 27532 28232: contig of 701 bp in length
* 28233 28332: gap of 100 bp
* 28333 29032: contig of 700 bp in length
* 29033 29132: gap of 100 bp
* 29133 29838: contig of 706 bp in length
* 29839 29938: gap of 100 bp
* 29939 30653: contig of 715 bp in length
* 30654 30753: gap of 100 bp
* 30754 31466: contig of 713 bp in length
* 31467 31566: gap of 100 bp
* 31567 32272: contig of 706 bp in length
* 32273 32372: gap of 100 bp
* 32373 33009: contig of 637 bp in length
* 33010 33109: gap of 100 bp
* 33110 33827: contig of 718 bp in length
* 33828 33927: gap of 100 bp
* 33928 34646: contig of 719 bp in length
* 34647 34746: gap of 100 bp
* 34747 35451: contig of 705 bp in length
* 35452 35551: gap of 100 bp
* 35552 36244: contig of 693 bp in length
* 36245 36344: gap of 100 bp
* 36345 36993: contig of 649 bp in length
* 36994 37093: gap of 100 bp
* 37094 37777: contig of 684 bp in length
* 37778 37877: gap of 100 bp
* 37878 38587: contig of 710 bp in length
* 38588 38687: gap of 100 bp
* 38688 39375: contig of 688 bp in length
* 39376 39475: gap of 100 bp
* 39476 40179: contig of 704 bp in length
* 40180 40279: gap of 100 bp
* 40280 40986: contig of 707 bp in length
* 40987 41086: gap of 100 bp
* 41087 41749: contig of 563 bp in length
* 41750 41849: gap of 100 bp
* 41850 42551: contig of 762 bp in length
* 42552 42651: gap of 100 bp
* 42652 43363: contig of 712 bp in length
* 43364 43463: gap of 100 bp
* 43464 44144: contig of 681 bp in length
* 44145 44244: gap of 100 bp
* 44245 44939: contig of 695 bp in length
* 44940 45039: gap of 100 bp
* 45040 45740: contig of 701 bp in length
* 45741 45840: gap of 100 bp
* 45841 46513: contig of 673 bp in length
* 46514 46613: gap of 100 bp
* 46614 47307: contig of 694 bp in length
* 47308 47407: gap of 100 bp
* 47408 48097: contig of 690 bp in length
* 48098 48197: gap of 100 bp
* 48198 48884: contig of 687 bp in length
* 48885 48984: gap of 100 bp
* 48985 49700: contig of 716 bp in length
* 49701 49800: gap of 100 bp
* 49801 50484: contig of 684 bp in length
* 50485 50584: gap of 100 bp
* 50585 51288: contig of 704 bp in length
* 51289 51388: gap of 100 bp
* 51389 52107: contig of 719 bp in length
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```
* 52108 52207: gap of 100 bp
* 52208 52909: contig of 702 bp in length
* 52910 53009: gap of 100 bp
* 53010 53665: contig of 656 bp in length
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* 53766 54444: contig of 679 bp in length

Query Match      2.0%   Score 58;   DB 2;   Length 57662;
Best Local Similarity 100.0%;   Pred. No. 1.6e-20;
Matches 58;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGGCATGAGCCACTGCGCCAGC 1244
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Db 39017 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGGCATGAGCCACTGCGCCAGC 38960

RESULT 22
HS931E15/c
LOCUS
DEFINITION
  Human DNA sequence from clone 931E15 on chromosome Xq25. Contains
  SIFS, GSSs and genomic marker DXS8098, complete sequence.
ACCESSION
  AL023575
VERSION
  AL023575.1 GI:3618163
KEYWORDS
  HTG; DXS8098.
SOURCE
  Homo sapiens.
ORGANISM
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 81874)
  Pavitt,K.
  Direct Submission
  Submitted (24-SEP-1998) Sanger Centre, Hinxton, Cambridgeshire,
  CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
  requests: clonerequests@sanger.ac.uk
  On Sep 18, 1998 this sequence version replaced gi:3550203.
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  corresponding to the overlapping clone, as we submit sequences with
  only a small overlap as described above.
  This sequence has been finished according to sequence map criteria
  as follows. An attempt is made to resolve all sequencing problems,
  such as compressions and repeats, but not necessarily within known
  annotated human repeat sequence elements (e.g. Alu). Where the
  sequence is ambiguous, there is an annotation using the 'unsure'
  feature key.
  This sequence was generated from part of bacterial clone contigs of
  human chromosome X, constructed by the Sanger Centre Chromosome X
  Mapping Group. Further information can be found at
  http://www.sanger.ac.uk/HGP/ChrX
  931E15 is from the library RPC15 constructed at the Roswell Park
  Cancer Institute by the group of Pieter de Jong. For further
  details see http://bacpac.med.buffalo.edu/VECTOR:pcypac2
  IMPORTANT: This sequence is not the entire insert of clone 931E15.
  It may be shorter because we only sequence overlapping sections
  once, or longer because we arrange for a small overlap between
  neighbouring submissions.
  The true left end of 424J12 (282207) is at 36643 in this sequence.
  The true right end of 506G2 (282213) is at 37431.

FEATURES
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      1..81874
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      /db_xref="taxon:9606"
      /map="q25"
      /clone="Rp5-931E15"
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      569..687
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repeat_region complement(1365. .1664)
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repeat_region 2767. .3067
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repeat_region complement(4220. .4537)
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repeat_region 5644. .5948
repeat_region /note="AluY repeat: matches 1. .301 of consensus"
repeat_region 5950. .6115
repeat_region /note="AluSg repeat: matches 133. .290 of consensus"
repeat_region 6156. .6393
repeat_region /note="L1 repeat: matches 4377. .4731 of consensus"
repeat_region 6629. .6979
repeat_region /note="MER2 repeat: matches 1. .95 of consensus"
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repeat_region /note="L1 repeat: matches 4728. .5161 of consensus"
repeat_region 7678. .7969
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repeat_region 7970. .8091
repeat_region /note="L1 repeat: matches 5150. .5270 of consensus"
repeat_region 8094. .8396
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repeat_region 8400. .8615
repeat_region /note="L1M3 repeat: matches 47. .276 of consensus"
repeat_region 8616. .8733
repeat_region /note="AluJb repeat: matches 2. .121 of consensus"
repeat_region 8743. .8816
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repeat_region 8856. .9146
repeat_region /note="AluJb repeat: matches 2. .300 of consensus"
repeat_region 9152. .9362
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repeat_region 9365. .9667
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repeat_region 9668. .10289
repeat_region /note="L1M10 repeat: matches 297. .919 of consensus"
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repeat_region 10710. .11004
repeat_region /note="AluSx repeat: matches 7. .361 of consensus"
repeat_region 11299. .11939
repeat_region /note="L1M8 repeat: matches 271. .910 of consensus"
repeat_region 11983. .12087
repeat_region /note="L1M7 repeat: matches 6. .309 of consensus"
repeat_region 12100. .12401
repeat_region /note="AluSx repeat: matches 4. .302 of consensus"
repeat_region 12439. .12940
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repeat_region 13958. .14050
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14514. .14836
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15626. .15730
/note="AluJb repeat: matches 196. .300 of consensus"
16118. .16420
/note="AluJb repeat: matches 1. .290 of consensus"
complement(16828. .16935)
/note="FLAM-A repeat: matches 117. .6 of consensus"
complement(17160. .17224)
/note="MIR repeat: matches 149. .84 of consensus"
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complement(18124. .18827)
/note="match: GSSs B16853 B14990"
complement(19378. .19676)
/note="AluSp repeat: matches 303. .2 of consensus"
19901. .20160
/note="AluY repeat: matches 39. .298 of consensus"
complement(20716. .20882)
/note="MIR repeat: matches 260. .69 of consensus"
complement(20824. .21385)
/note="match: GSSs B94184 A010265"
21550. .23628
/note="putative CpG island"
complement(22542. .22581)
/note="MIR2 repeat: matches 134. .95 of consensus"
complement(23094. .24185)
/note="SVA repeat: matches 1101. .1 of consensus"
24186. .24231
/note="23 copies 2 mer aa 80% conserved"
24520. .24884
/note="L1PA5 repeat: matches 517. .890 of consensus"
complement(25504. .25687)
/note="MER20 repeat: matches 155. .1 of consensus"
26421. .26484
/note="32 copies 2 mer tt 83% conserved"
complement(26486. .26661)
26867. .27164
/note="AluJb repeat: matches 195. .5 of consensus"
27165. .27462
/note="AluY repeat: matches 3. .300 of consensus"
27165. .27462
/note="AluSp repeat: matches 2. .302 of consensus"
28080. .28392
/note="AluSx repeat: matches 1. .298 of consensus"
complement(28817. .29089)
/note="AluSx repeat: matches 298. .2 of consensus"
29122. .29252
/note="L1 repeat: matches 3151. .3280 of consensus"
complement(29957. .30200)
/note="MLT2_internal repeat: matches 5375. .5124 of consensus"
complement(30513. .30706)
/note="MLT2_internal repeat: matches 4754. .4572 of consensus"
30728. .31025
/note="AluSx repeat: matches 1. .299 of consensus"
31059. .31356
/note="AluSg repeat: matches 1. .296 of consensus"
31359. .31505
/note="MER4B repeat: matches 11. .148 of consensus"
32041. .32319
/note="AluSx repeat: matches 1. .287 of consensus"
complement(32381. .33599)
/note="MLT2_internal repeat: matches 4572. .3316 of consensus"
33603. .33906
/note="AluJb repeat: matches 1. .302 of consensus"
34020. .34321
/note="AluJb repeat: matches 1. .301 of consensus"
complement(34386. .34933)
```



```

repeat_region /note="LIP2 repeat: matches 900. 6144 of consensus"
63508..63541
/note="17 copies 2 mer aa 828 conserved"
63586..63668
/note="L1MD repeat: matches 738. 415 of consensus"
63917..64021
/note="L1MD repeat: matches 984. 108 of consensus"
complement(64074..64343)
/note="match: GSS: Em:AQ485350"
complement(66096..66577)
/note="match: GSS: Em:AQ511651"
69990..70342
/note="match: STS: Em:G21603"
complement(76094..76635)
/note="match: GSS: Em:AQ277578"
complement(76184..76636)
/note="match: GSS: Em:AQ812553"
complement(76460..76628)
/note="match: GSS: Em:AQ140871"
complement(88581..89052)
/note="match: GSS: Em:AQ201907"
89057..89594
/note="match: GSS: Em:AQ543464"
91625..91990
/note="THE1C repeat: matches 1..371 of consensus"
92079..92237
/note="LIP2 repeat: matches 5949. 6125 of consensus"
BASE COUNT 32991 a 18802 c 18896 g 27671 t
ORIGIN

```

```

Query Match 2.0%; Score 58; DB 9; Length 98360;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCCACTGCGCCAGC 1244
|||||
DB 18635 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCCACTGCGCCAGC 18578
|||||

```

```

RESULT 24
AL611933/c 141273 bp DNA linear PRI 11-JUN-2002
LOCUS Human DNA sequence from clone RP11-374C13 on chromosome 1, complete
sequence.
DEFINITION
AL611933
ACCESSION AL611933
VERSION AL611933.30 GI:21425229
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Peck, A.
1 (bases 1 to 141273)
Direct Submission
Submitted (11-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Jun 13, 2002 this sequence version replaced gi:21261816.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e. paired quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats: all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: EMBL, EMBL; SWISS,

```

```

SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/NGP/Chrl
RP11-374C13 is from the library RP11-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6.
FEATURES             Location/Qualifiers
     source            1..141273
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP11-374C13"
                     /clone_lib="RP11-11.2"
BASE COUNT 35351 a 32122 c 33734 g 40066 t
ORIGIN

```

```

Query Match 2.0%; Score 58; DB 9; Length 141273;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCCACTGCGCCAGC 1244
|||||
DB 4256 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCCACTGCGCCAGC 4199
|||||

```

```

RESULT 25
AC107939/c 145264 bp DNA linear PRI 31-MAR-2002
LOCUS Homo sapiens chromosome 11, clone RP11-4809, complete sequence.
DEFINITION
AC107939
ACCESSION AC107939.5 GI:19849381
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Birren, H., Linton, L., Nusbaum, C. and Lander, E.
1 (bases 1 to 145264)
Homo sapiens chromosome 11, clone RP11-4809
Unpublished
2 (bases 1 to 145264)
Birren, H., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bozulavsky, I., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choe, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArclano, K., Dewar, K., Diaz, J. S., Dodge, S., Faró, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lechoczy, J., Levine, R., Liu, G., MacLean, C.,
Maddison, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
Mienka, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainou, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
1 (bases 1 to 145264)
Birren, H., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

```



```

/rpt_family="(TTTGTG)n"
complement(16631..16909)
/rpt_family="AluSq"
complement(16910..17040)
/rpt_family="AluSq"
complement(17245..17300)
/rpt_family="Alu"
complement(17308..17573)
/rpt_family="Alu"
complement(17921..18226)
/rpt_family="AluSx"
complement(18706..19030)
/rpt_family="L2"

```

```

Query Match: 2.0% Score 56; DB 9; Length 14524;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0; Inserts 0; Gaps 0;
QY 1187 CTGTCACCTGGGCTCCCAAGTCTGGGATTACAGGCATGACGACGATCGGTCACG 1244
DB 7484: CTGCCACCTGGGCTCCCAAGTCTGGGATTACAGGCATGACGACGATCGGTCACG 74786

```

```

RESULT 26
AC015494 146312 bp DNA linear HTG 26 MAY-2001
DEFINITION Homo sapiens clone RP11-21E12, WORKING DRAFT SEQUENCE, 12 unordered
pieces.
AC015494
VERSION AC015494.6 GI:14209771
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 146312)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-21E12
Unpublished
2 (bases 1 to 146312)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Bozulackiy,L., Boukhvalter,R.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collins,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donnelly,R., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,K., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hughes,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Liu,C., Locke,K., MacDonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,I., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,K., Roy,A., Santos,F., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wex,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 26, 2001 this sequence version replaced g1:1443216.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: t3990
Center clone name: 21_E12
----- Summary Statistics
Sequencing vector: M13; M7815; 1% of reads
Sequencing vector: plasmid; n/a; 97% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads

```

```

Assembly program: Phrap; version 0.960731
Consensus quality: 142529 bases at least Q40
Consensus quality: 14014 bases at least Q30
Consensus quality: 144580 bases at least Q20
Insert size: 128000; agarose-fp
Insert size: 145212; sum-of-contigs
Quality coverage: 9.4 in Q20 bases; agarose-fp
Quality coverage: 8.3 in Q20 bas.

```

* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1742: contig of 1732 bp in length
1733 1842: gap of 100 bp
1833 2945: contig of 1113 bp in length
2946 3045: gap of 100 bp
3046 4116: contig of 1071 bp in length
4117 4216: gap of 100 bp
4217 5757: contig of 1541 bp in length
5758 5857: gap of 100 bp
5858 7545: contig of 1688 bp in length
7546 7645: gap of 100 bp
7646 11527: contig of 3882 bp in length
11528 11627: gap of 100 bp
11628 55477: contig of 43850 bp in length
55478 55577: gap of 100 bp
55578 66767: contig of 11190 bp in length
66768 68667: gap of 100 bp
68668 83973: contig of 17106 bp in length
83974 84073: gap of 100 bp
84074 107174: contig of 23101 bp in length
107175 107274: gap of 100 bp
107275 137395: contig of 30121 bp in length
137396 137495: gap of 100 bp
137496 146312: contig of 8817 bp in length.

FEATURES

	Location/Qualifiers	source
	1..146312	/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="RP11-21E12"
		/clone_lib="RPC1-11 Human Male BAC"
misc_feature	1..1732	/note="assembly_fragment"
		clone_end:SP6
		vector_side:left
misc_feature	1833..2945	/note="assembly_fragment"
misc_feature	3046..4116	/note="assembly_fragment"
misc_feature	4217..5757	/note="assembly_fragment"
misc_feature	5858..7545	/note="assembly_fragment"
misc_feature	7646..11527	/note="assembly_fragment"
misc_feature	11628..115477	/note="assembly_fragment"
misc_feature	55578..66767	/note="assembly_fragment"
misc_feature	66868..83973	/note="assembly_fragment"
misc_feature	84074..107174	/note="assembly_fragment"
misc_feature	107275..137395	/note="assembly_fragment"
misc_feature	137496..146312	/note="assembly_fragment"
		clone_end:T7
		vector_side:right


```

Query Match
Best Local Similarity 100.0%; Score 58; DB 2; Length 15645;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGCATACAGGATGAGCACTGCGGCTAGC 1244
|||||
DB 64066 CTGCCACCTTGGCTCCCAAGTCTGGCATACAGGATGAGCACTGCGGCTAGC 64066

RESULT 30
AC093737
LOCUS
DEFINITION
Homo sapiens chromosome 2 clone RP11-21M2, WORKING DRAFT
2 unordered pieces.
ACCESSION
AC093737
VERSION
AC093737.1 GI:15529775
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 162419)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 162419)
Waterston,R.H.
Direct Submission
Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/usc/index.shtml
Center project name: H.MH0021M02
Drafting center: QC core
----- Summary Statistics -----
Sequencing vector: M13; 36%
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.960319
Consensus quality: 162004 bases at least Q40
Consensus quality: 162155 bases at least Q30
Consensus quality: 162211 bases at least Q20
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 70250: contig of 70250 bp in length
* 70251 70350: gap of unknown length
* 70351 162419: contig of 92069 bp in length.
FEATURES
source
1..162419
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-21M2"
misc-feature
1..70250
/note="assembly_name:Contig13
clone_end:7
vector_side:right"
misc-feature
70351..162419

```

```

/note="assembly_name:Contig14
clone_end:SP6
vector_side:right"
BASE COUNT
50019 a 30933 c 30950 g 50417 t 100 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 58; DB 2; Length 162419;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGCATACAGGATGAGCACTGCGGCTAGC 1244
|||||
DB 52046 CTGCCACCTTGGCTCCCAAGTCTGGCATACAGGATGAGCACTGCGGCTAGC 52103

RESULT 31
AC019307
LOCUS
DEFINITION
Homo sapiens chromosome 8 clone RP11-359P11 map 8, WORKING DRAFT
33 unordered pieces.
ACCESSION
AC019307
VERSION
AC019307.3 GI:7249157
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 166011)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G., Castle,A.,
Choquel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArillano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Kiehn,J.,
Landers,T., Lebecky,J., Levine,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrum,J., Meneses,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severi,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo.A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 16, 2000 this sequence version replaced gi:6721260.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center -----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L5223
Center clone name: 359_P11
----- Summary Statistics -----
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150247 bases at least Q40
Consensus quality: 157501 bases at least Q30
Consensus quality: 159942 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 162811; sum-of-contigs

```

Quality coverage: 3.9 in Q20 bases; agarose-gp
Quality coverage: 4.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1042: contig of 1042 bp in length
1043 1142: gap of 100 bp
1143 2142: contig of 1000 bp in length
2143 2242: gap of 100 bp
2243 3710: contig of 1468 bp in length
3711 3810: gap of 100 bp
3811 5057: contig of 1247 bp in length
5058 5157: gap of 100 bp
5158 6697: contig of 1540 bp in length
6698 6797: gap of 100 bp
6798 7389: contig of 592 bp in length
7390 7489: gap of 100 bp
7490 8708: contig of 1219 bp in length
8709 8808: gap of 100 bp
8809 10176: contig of 1368 bp in length
10177 10276: gap of 100 bp
10277 11738: contig of 1462 bp in length
11739 11838: gap of 100 bp
11839 14084: contig of 2246 bp in length
14085 14184: gap of 100 bp
14185 15991: contig of 1807 bp in length
15992 16091: gap of 100 bp
16092 18891: contig of 2800 bp in length
18892 18991: gap of 100 bp
18992 21414: contig of 2423 bp in length
21415 21514: gap of 100 bp
21515 23808: contig of 2394 bp in length
23809 23908: gap of 100 bp
23909 25419: contig of 1511 bp in length
25420 25519: gap of 100 bp
25520 28063: contig of 2544 bp in length
28064 28163: gap of 100 bp
28164 32741: contig of 4578 bp in length
32742 32841: gap of 100 bp
32842 37294: contig of 4453 bp in length
37295 37394: gap of 100 bp
37395 42230: contig of 4836 bp in length
42231 42330: gap of 100 bp
42331 47685: contig of 5456 bp in length
47686 47785: gap of 100 bp
47786 52553: contig of 4768 bp in length
52554 52653: gap of 100 bp
52654 59378: contig of 6725 bp in length
59379 59478: gap of 100 bp
59479 64583: contig of 5105 bp in length
64584 64683: gap of 100 bp
64684 72618: contig of 7945 bp in length
72619 72718: gap of 100 bp
72719 78416: contig of 5698 bp in length
78417 78516: gap of 100 bp
78517 85048: contig of 6532 bp in length
85049 85148: gap of 100 bp
85149 91596: contig of 6448 bp in length
91597 91696: gap of 100 bp
91697 98785: contig of 7089 bp in length
98786 98885: gap of 100 bp
98886 108615: contig of 9730 bp in length
108616 108715: gap of 100 bp
108716 120908: contig of 12193 bp in length
120909 121008: gap of 100 bp
121009 131478: contig of 10470 bp in length
131479 131578: gap of 100 bp

* 131579 144378: contig of 12800 bp in length
* 144379 144478: gap of 100 bp
* 144479 166011: contig of 21533 bp in length.
FEATURES
Source
1. 166011
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8"
/clone="RP11-359P11"
/clone_lib="RPC1-11 Human Male BAC"
1. 1042
/note="assembly_fragment"
1143. 2142
/note="assembly_fragment"
2243. 3710
/note="assembly_fragment"
3811. 5057
/note="assembly_fragment"
5158. 6697
/note="assembly_fragment"
6798. 7389
/note="assembly_fragment"
clone_end:T7
vector_side:right
7490. 8708
/note="assembly_fragment"
8809. 10176
/note="assembly_fragment"
10277. 11738
/note="assembly_fragment"
11839. 14084
/note="assembly_fragment"
14185. 15991
/note="assembly_fragment"
16092. 18891
/note="assembly_fragment"
18992. 21414
/note="assembly_fragment"
21515. 23808
/note="assembly_fragment"
23909. 25419
/note="assembly_fragment"
clone_end:SP6
vector_side:right
25520. 28063
/note="assembly_fragment"
28164. 32741
/note="assembly_fragment"
32842. 37294
/note="assembly_fragment"
37395. 42230
/note="assembly_fragment"
42331. 47685
/note="assembly_fragment"
47786. 52553
/note="assembly_fragment"
52654. 59378
/note="assembly_fragment"
59479. 64583
/note="assembly_fragment"
64684. 72618
/note="assembly_fragment"
72719. 78416
/note="assembly_fragment"
78517. 85048
/note="assembly_fragment"
85149. 91596
/note="assembly_fragment"
91697. 98785
/note="assembly_fragment"

Query Match

2.0%; Score 58; DB 2; Length 166011;

```

Best Local Similarity 100.0%; Pred. NO. 1.7e-20; Gaps 0;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCCATGCTGGCCAGC 1244
|||||
Db 51649 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCCATGCTGGCCAGC 51649

RESULT 32
AC069120/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AC069120 177533 bp DNA linear HTG 15-NOV-2001
Homo sapiens chromosome 8 clone RP11-675F6 map 8, *** SEQUENCING IN
PROGRESS ***, 15 unordered pieces.
AC069120
HTG: HTGS_PHASE1; HTGS_FULLTOP: HTGS_ACTIVE.FIN.
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177533)
Birren, B., Linton, L., Nusbaum, C., and Lander, E.
Homo sapiens chromosome 8, clone RP11-675F6
Unpublished
2 (bases 1 to 177533)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F.,
Bonuskavly, L., Boukhallier, B., Brown, A., Buckett, G.,
Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
Cody, S., Cooke, P., DeArillano, K., Dewar, K., Diaz, J., S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Haque, B., Heaford, A., Herton, B.,
Howland, J. C., Iliev, I., Johnson, K., Jones, C., Karn, J., Karatas, A.,
Klein, J., Larocque, K., Lamazares, K., Landers, T., Lebecky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, J., Marquis, N.,
McCarthy, M., McEwan, P., McGowan, A., McKenna, K., McKeeters, R.,
McLaird, J., Meneus, L., Mihova, T., Miranda, C., Mienda, V., Morrow, J.,
Murphy, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, R.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, R., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (18-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02142, USA
On Nov 15, 2001 this sequence version replaced with 51649.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
***** Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
***** Project Information:
Center project name: L9305
Center clone name: 675_F_6
*****
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1253: contig of 1253 bp in length;
* 1254 1353: gap of 100 bp
* 1354 26734: contig of 25381 bp in length

```

```

26735 26834: gap of 100 bp
26835 60661: contig of 33827 bp in length
60662 60761: gap of 100 bp
60762 91265: contig of 30504 bp in length
91266 91365: gap of 100 bp
91366 108600: contig of 17235 bp in length
108601 108700: gap of 100 bp
108701 114249: contig of 5549 bp in length
114250 114349: gap of 100 bp
114350 128608: contig of 12459 bp in length
128609 128608: gap of 100 bp
128609 137847: contig of 10939 bp in length
137848 137947: gap of 100 bp
137948 140143: contig of 2196 bp in length
140144 140243: gap of 100 bp
140244 143309: contig of 3066 bp in length
143310 143409: gap of 100 bp
143410 145669: contig of 2260 bp in length
145670 145769: gap of 100 bp
145770 154154: contig of 8385 bp in length
154155 154254: gap of 100 bp
154255 15634: contig of 2180 bp in length
156343 156534: gap of 100 bp
156535 168277: contig of 9743 bp in length
168278 166377: gap of 100 bp
166378 177533: contig of 11156 bp in length.
Location/Qualifiers
1. 177533
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-675F6"
/clone.lib="RPC1-11 Human Male BAC"
/a 40970 c 39158 g 49339 t 1505 others

BASE COUNT 46561 a 40970 c 39158 g 49339 t 1505 others
ORIGIN

Query Match 2.0%; Score 58; DB 2: Length 177533;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCCATGCTGGCCAGC 1244
|||||
Db 123261 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCCATGCTGGCCAGC 123204

RESULT 33
AC013281
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AC013281 188820 bp DNA linear HTG 10-SEP-2000
Homo sapiens chromosome 15 clone RP11-528M4, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
AC013281
HTG: HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188820)
The sequence of Homo sapiens clone
Waterston, R.H.
Unpublished
2 (bases 1 to 188820)
Waterston, R.H.
Direct Submission
Submitted (05-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 10, 2000 this sequence version replaced with 123261.
*****
Center: Washington University Genome Sequencing Center
Center code: WUGSC

```

Web site: <http://genome.wustl.edu/gsc/index.shtml>
 ----- Project Information -----
 Center project name: H_NH0528N04
 ----- Summary Statistics -----
 Sequencing vector: M13; 76%
 Chemistry: Dye-primer EL: 76% of reads
 Chemistry: Dye-terminator Big Dye; 24% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 179527 bases at least Q40
 Consensus quality: 182913 bases at least Q30
 Consensus quality: 184575 bases at least Q20
 Insert size: 203000; agarose-fp
 Insert size: 189063; sum-of-contigs
 Quality coverage: 4.28 in Q20 bases; agarose-fp
 Quality coverage: 4.60 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 2415: contig of 2415 bp in length
 * 2416 2515: gap of unknown length
 * 2516 5539: contig of 3024 bp in length
 * 5540 5639: gap of unknown length
 * 5640 12163: contig of 6524 bp in length
 * 12164 12663: gap of unknown length
 * 12664 22743: contig of 10480 bp in length
 * 22744 22843: gap of unknown length
 * 22844 36050: contig of 13207 bp in length
 * 36051 38150: gap of unknown length
 * 38151 47862: contig of 1712 bp in length
 * 47863 47962: gap of unknown length
 * 47963 62123: contig of 14161 bp in length
 * 62124 62223: gap of unknown length
 * 62224 75585: contig of 13362 bp in length
 * 75586 75685: gap of unknown length
 * 75686 90351: contig of 14566 bp in length
 * 90352 90451: gap of unknown length
 * 90452 110259: contig of 19838 bp in length
 * 110260 110359: gap of unknown length
 * 110360 140334: contig of 24975 bp in length
 * 140335 140434: gap of unknown length
 * 140435 188820: contig of 48381 bp in length.
 Location/Qualifiers
 1..188820
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="15"
 /clone="RP11-528N4"
 1..2415
 /note="assembly_name:Contig15"
 2516..5539
 /note="assembly_name:Contig16"
 5640..12163
 /note="assembly_name:Contig17"
 12264..22743
 /note="assembly_name:Contig18"
 22844..36050
 /note="assembly_name:Contig19
 clone_end:SP6
 vector_side:right
 36151..47862
 /note="assembly_name:Contig10"
 47963..62123
 /note="assembly_name:Contig11"
 62224..75585
 /note="assembly_name:Contig12"
 75686..90351

FEATURES

source

misc_feature
 /note="assembly_name:Contig13"
 90452..110259
 /note="assembly_name:Contig14"
 110360..140334
 /note="assembly_name:Contig15"
 140435..188820
 /note="assembly_name:Contig16"
 48904 a 45259 c 44833 g 48717 t 1107 others
 ORIGIN
 Query Match 2.0% Score 58; DB 2: Length 188820;
 Best Local Similarity 100.0%; Pred. No. 1.7e-20;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCCTGCGCCVAGC 1244
 Db 123691 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCCTGCGCCAGC 123748
 RESULT 34
 AC012668/c 192396 bp DNA linear PRI 09-JAN-2002
 LOCUS Homo sapiens BAC clone RP11-458D8 from 2, complete sequence.
 DEFINITION AC012668
 ACCESSION AC012668.1 GI:14589741
 VERSION HTG.
 KEYWORDS Homo sapiens.
 SOURCE Homo sapiens.
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99083792
 PUBMED 9847074
 2 (bases 1 to 192396)
 REFERENCE Waligorski, J., Cotton, M. and Elliott, G.
 AUTHORS The sequence of Homo sapiens BAC clone RP11-458D8
 TITLE unpublished (2001)
 JOURNAL
 REFERENCE 3 (bases 1 to 192396)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 192396)
 REFERENCE Waterston, R.H.
 AUTHORS Direct Submission
 JOURNAL Submitted (03-JUL-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 5 (bases 1 to 192396)
 REFERENCE Waterston, R.
 AUTHORS Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jul 3, 2001 this sequence version replaced gi:13411202.
 COMMENT

 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics -----

 Center project name: H_NH0458D08

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:


```

clone_end:T7
vector_side:right*
BASE COUNT 51569 a 46564 c 45000 g 48977 t 1234 others
ORIGIN

Query Match 2.0%; Score 58; DB 2; Length 1434;
Best Local Similarity 100.0%; Pred. NO. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACACGACGACGACG 1244
      |||||||
DB 87925 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACGACGACGACG 87982

RESULT 36
HSBA425M5/C
LOCUS
DEFINITION
    HSBA425M5 194433 bp. DNA. linear. 191.14.MAR.2001
    Human DNA sequence from clone RP11-425M5 on chromosome 20. Contains
    a GLRX (glutaredoxin (thioltransferase)) pseudogene, a PPIA
    (peptidylprolyl isomerase A (cyclophilin A)) pseudogene, the NNAT
    gene for neurexin, the BLCAP gene for bladder cancer 10 kD
    protein BC10, a putative novel transcript, BSIs, SIs, GSSs and
    three putative CpG islands, complete sequence.
ACCESSION
    AL109614
VERSION
    AL109614.28 GI:8745190
KEYWORDS
    HTG; BC10; BLCAP; CpG island; cyclophilin; GLRX; neurexin; NNAT;
    PPIA.
SOURCE
    human.
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 194433)
    Phillimore, B.
    Direct Submission
    Submitted (06-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
    CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
    requests: clonerequest@sanger.ac.uk
    On Jun 26, 2000 this sequence version replaced gi:7329727.
    During sequence assembly data is compared from overlapping clones.
    Where differences are found these are annotated as variations
    together with a note of the overlapping clone name. Note that the
    variation annotation may not be found in the sequence submission
    corresponding to the overlapping clone, as we submit sequences with
    only a small overlap as described above.
    The following abbreviations are used to associate primary accession
    numbers given in the feature table with their source databases:
    Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPeP; Inf,
    on the WormPeP database can be found at
    http://www.sanger.ac.uk/Projects/h/c/oligos/accomp This sequence
    was generated from part of bacterial clone RP11-425M5 from
    chromosome 20, constructed by the Sanger Centre, Hinxton, Cambridgeshire 20
    Mapping Group. Further information can be found at
    http://www.sanger.ac.uk/HGP/Chr20
    This sequence was finished as follows unless otherwise noted: all
    regions were either double-stranded or sequenced with an alternate
    chemistry or covered by high quality data (i.e., phred quality >
    30); an attempt was made to resolve all sequencing problems, such
    as compressions and repeats; all regions were covered by at least
    one plasmid subclone or more than one M13 subclone; and the
    assembly was confirmed by restriction digest. RP11-425M5 is from
    the library RP11-11.2 constructed by the group of Pieter de Jong.
    For further details see
    http://www.chori.org/bacpac/home.htm
    VECTOR: pBAC3.6
    This sequence is the entire insert of clone RP11-425M5. The true
    left end of clone RP4-640H8 is at 176187 in this sequence. The true
    right end of clone RP4-592G19 is at 59744 in this sequence.
FEATURES
    Location/Qualifiers
        1..194433
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="20"
            /clone="RP11-425M5"

```

```

/clone_lib="RPC111.2"
9..86
/note="AluJ/FLAM repeat: matches 3..80 of consensus"
424..701
/note="MLT1-INTERNAL repeat: matches 308..583 of
consensus"
901..1251
/note="MLT1F repeat: matches 170..540 of consensus"
1528..1827
/note="AluSx repeat: matches 1..299 of consensus"
1960..2174
/note="LIME2 repeat: matches 5746..6163 of consensus"
2375..2513
/note="AluSg/x repeat: matches 175..308 of consensus"
2516..2541
/note="U2 repeat: matches 5..33 of consensus"
2542..2738
/note="AluSg repeat: matches 1..201 of consensus"
2741..3206
/note="LIME2 repeat: matches 5283..5748 of consensus"
3207..3525
/note="AluJb repeat: matches 1..303 of consensus"
3526..3551
/note="LIME2 repeat: matches 5258..5283 of consensus"
3559..3856
/note="LIM4 repeat: matches 4669..4987 of consensus"
3857..4157
/note="AluSg repeat: matches 1..299 of consensus"
4158..4286
/note="LIM4 repeat: matches 4541..4669 of consensus"
4521..4624
/note="MIR repeat: matches 47..152 of consensus"
4674..4804
/note="L2 repeat: matches 581..713 of consensus"
5623..5850
/note="L2 repeat: matches 1312..1557 of consensus"
5861..6031
/note="FAM repeat: matches 8..176 of consensus"
6420..6487
/note="L2 repeat: matches 2648..2710 of consensus"
6762..7013
/note="L16C repeat: matches 133..387 of consensus"
7292..8014
/note="LIME1 repeat: matches 5444..6163 of consensus"
8053..8364
/note="AluJo repeat: matches 1..302 of consensus"
8384..8590
/note="LIME3 repeat: matches 5545..5755 of consensus"
8770..9137
/note="LIME3 repeat: matches 5763..6134 of consensus"
9165..9444
/note="AluJo repeat: matches 40..312 of consensus"
9706..10153
/note="L2 repeat: matches 1057..1554 of consensus"
10598..10799
/note="L2 repeat: matches 2111..2358 of consensus"
10862..10958
/note="MLTIC repeat: matches 1..98 of consensus"
10959..11266
/note="AluSx repeat: matches 1..308 of consensus"
11267..11298
/note="MLTIC repeat: matches 98..129 of consensus"
11299..11721
/note="MSTA repeat: matches 1..426 of consensus"
11722..12061
/note="MLTIC repeat: matches 129..466 of consensus"
12065..12411
/note="L2 repeat: matches 2389..2706 of consensus"
13039..13353
/note="AluJo repeat: matches 1..312 of consensus"
complement(14182..14645)
/note="match: GSS: Em:AQ719314"
14310..14793
misc_feature
misc_feature

```

```
/note="match; GSS: Em:A0812308"
15382..15581
/note="MIR repeat: matches 39..244 of consensus"
15547..15599
/note="L2 repeat: matches 2692..2745 of consensus"
15598..16111
/note="L2 repeat: matches 1119..2029 of consensus"
16314..16444
/note="L2 repeat: matches 2092..2221 of consensus"
16445..16851
/note="L1M4 repeat: matches 5014..5402 of consensus"
16956..17162
/note="L2 repeat: matches 2174..2380 of consensus"
17502..17852
/note="L1M6 repeat: matches 5394..5628 of consensus"
18164..18298
/note="L1P repeat: matches 4879..5012 of consensus"
L1P repeat: matches 4879..5012 of consensus"
18608..18952
/note="match; GSS: Em:A005989"
21158..21213
/note="L2 repeat: matches 2066..2119 of consensus"
21214..21538
/note="AluX repeat: matches 1..312 of consensus"
21539..22081
/note="L2 repeat: matches 2119..2792 of consensus"
22089..22510
/note="L2 repeat: matches 1148..1567 of consensus"
22514..22831
/note="L1M4 repeat: matches 4532..4834 of consensus"
23524..23826
/note="L1M6 repeat: matches 5525..5817 of consensus"
24119..24589
/note="match; GSS: Em:A058890"
24205..24250
/note="L23 copies 2 mer 11 78% conserved"
24271..24576
/note="AluX repeat: matches 1..304 of consensus"
24594..24655
/note="L1 copies 2 mer 3a 67% conserved"
24667..24943
/note="L1 repeat: matches 4727..4988 of consensus"
25177..25275
/note="MIR repeat: matches 49..115 of consensus"
25336..25689
/note="L2 repeat: matches 2426..2700 of consensus"
25676..25699
/note="L2 repeat: matches 2151..2172 of consensus"
25700..26011
/note="AluX repeat: matches 1..112 of consensus"
26012..26841
/note="L2 repeat: matches 1249..2151 of consensus"
complement(27254..27711)
/note="match; GSS: Em:A081244"
27511..27796
/note="L2 repeat: matches 1339..1602 of consensus"
27797..28088
/note="AluX repeat: matches 1..293 of consensus"
28089..28720
/note="L2 repeat: matches 1602..2325 of consensus"
28727..28984
/note="AluY repeat: matches 49..307 of consensus"
29196..29339
/note="L2 repeat: matches 2278..2425 of consensus"
29381..29418
/note="L2 repeat: matches 2556..2593 of consensus"
29419..29747
/note="AluJ repeat: matches 1..308 of consensus"
29748..29842
/note="L2 repeat: matches 2593..2687 of consensus"

Query Match 2.0%; Score 58; DB 9; Length 14443;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
```

```
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1187 CTCCACACCTTGGCTCCCAAGTCTGGATTACAGGCATGAGCCACTGCCGCCAGC 1244
|||||
Db 148147 CTCCACACCTTGGCTCCCAAGTCTGGATTACAGGCATGAGCCACTGCCGCCAGC 148090
|||||

RESULT 37
AL805961/C
LOCUS
DEFINITION Homo sapiens chromosome 1 clone RP11-718D19, *** SEQUENCING IN
PRXRESS ***, in ordered pieces.
ACCESSION AL805961
VERSION AL805961.12 GI:22204675
KEYWORDS HTGS_PHASE2; HTGS_ACTIVIFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 195386)
Van Heilmond, Z.
Direct Submission
Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:2200315.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA718D19
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 195288 bases at least Q40
Consensus quality: 195341 bases at least Q30
Consensus quality: 195366 bases at least Q20
Insert size: 195386; sum-of-contigs
Insert size: 181232; 9.2% error; agarose-fp
Quality coverage: 12.04x in Q20 bases; sum-of-contigs Quality
coverage: 13.15x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
location/Qualifiers
source
1..195386
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-718D19"
/clone_lib="RPCT-11.3"
1..195386
misc_feature
1..195386
/note="assembly fragment:04211"
BASE COUNT 48905 a 47558 c 50028 g 48895 t
ORIGIN

Query Match 2.0%; Score 58; DB 2; Length 195386;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1187 CTCCACACCTTGGCTCCCAAGTCTGGATTACAGGCATGAGCCACTGCCGCCAGC 1244
|||||
Db 168811 CTCCACACCTTGGCTCCCAAGTCTGGATTACAGGCATGAGCCACTGCCGCCAGC 168754
|||||

RESULT 38
AC083830/C
LOCUS
DEFINITION Homo sapiens chromosome UL clone RP11-495K24, WORKING DRAFT
```


misc_feature
/note=-assembly_fragment:05572.0*
190925..201197
/note=-assembly_fragment:03857
clone_end:T7
vector_side:right*

BASE COUNT 55207 a 43266 c 43712 g 57504 t 1538 others
ORIGIN

Query Match 2.0%; Score 58; DB 2; Length 20197;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
UY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATAGCATATGTCGTCACGC 1244
DB 60280 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATAGCATATGTCGTCACGC 1244

RESULT 40
AC027176 292703 bp DNA linear HTG 19-AUG-2002
LOCUS Homo sapiens chromosome 20 clone RP11-493E3 map 20. *** SEQUENCING
IN PROGRESS ***, 6 unordered pieces.
AC027176
AC027176.11 GI:22297423
HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVATED; IN
human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 292703)
Birren, B., Nusbaum, C., and Lander, E.
Homo sapiens chromosome 20, clone RP11-493E3.
Unpublished
2 (bases 1 to 292703)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Aldrich, H., Allen, N.,
Anderson, S., Baldwin, J., Bara, N., Bastien, V., Beck, E.,
Boyslavsky, L., Boukhalter, B., Brown, A., Burkett, S.,
Campiano, A., Caserio, A., Choquet, Y., Choudhury, S., Collins, S.,
Collamore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, V., Fitzpatrick, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hades, H., Heath, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, G., Kahn, L., Karatas, A.,
Klein, J., Lacroque, K., Lamazares, K., Landers, T., Lechoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, E., Marquis, N.,
McCarthy, M., McEwan, P., McGuire, K., McKernan, K., McPherson, R.,
McElroy, J., Meneus, L., Mihova, I., Miranda, J., Miranda, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, E., O'Connor, T., Osborne, L., P.,
O'Neill, D., Olivier, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, K., Rong, P., Rottman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Theodore, J., Tirrell, A., Travers, S. M., Tripathi, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 292703)
Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Bozulavsky, L., Boukhalter, B.,
Camara, J., Chang, J., Chazaro, B., Choquet, Y., Cullis, A.,
Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Farf, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
Gardyna, S., Ginde, S., Graham, L., Grand-Pierre, N., Hades, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, G., Kanat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lischad, T., K.,
Liu, G., Maclean, C., MacDonald, P., Maier, C., Matthews, C.,
McCarthy, M., McElroy, J., Meneus, L., Mihova, I., Miranda, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norman, E., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliveira, S., Peterson, K.,
Pisani, C., Pierre, N., Raymond, C., Rella, K., Rong, P., Roy, A.,
Roman, J., Roy, A., Schauer, S., Schupbach, K., Seeman, S., Severy, P.,

TITLE
JOURNAL

COMMENT

Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (19-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 19, 2002 this sequence version replaced gi:22213416.
All repeats were identified using RepeatMasker.
Smith, A. F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6996
Center clone name: 493_E_3

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N. But the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 14452: contig of 14452 bp in length
14453 14552: gap of 100 bp
14553 26924: contig of 12372 bp in length
26925 27024: gap of 100 bp
27025 139971: contig of 112947 bp in length
139972 140071: gap of 100 bp
140072 151044: contig of 10973 bp in length
151045 151144: gap of 100 bp
151145 179656: contig of 28512 bp in length
179657 179757: gap of 100 bp
179757 292703: contig of 112947 bp in length.

FEATURES
SOURCE

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/db_xref="taxon:9606"
/chromosome="20"
/map="20"

/clone="RP11-493E3"

/clone_lib="RP11-11 Human Male BAC"

BASE COUNT 83142 a 66391 c 66021 g 76579 t 570 others

ORIGIN

Query Match 2.0%; Score 58; DB 2; Length 292703;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATAGCATATGTCGTCACGC 1244

DB 9771 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATATGTCGTCACGC 9828

RESULT 41

AK094822/c

LOCUS

AK094822

DEFINITION

Homo sapiens cDNA FLJ37503 fis, clone BRAWH2016679.

ACCESSION

AK094822

VERSION

AK094822.1 GI:21753958

KEYWORDS

oligo capping; fis (full insert sequence).

SOURCE

Homo sapiens brain cDNA to mRNA, clone LIB: BRAWH2

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 Suzuki, T., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,

TITLE

Direct Submission
Submitted (30-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE

Waterston, R.

AUTHORS

Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 30, 2001 this sequence version replaced 4 314778789.

COMMENT

..... Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/qsc>
Contact: sapiens@watson.wustl.edu
..... Summary Statistics
.....
Center project name: H_NH9616K02

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NIGMS Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson at the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GIB/CHR7>, send <mailto:cgreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/qsc>

SOURCE INFORMATION:

The RPCL11 human BAC library was made from the blood of one male donor, as described by Osoeckwa, K., Wom, T. Y., Zhao, B., Friedman, E., Tatenio, M., Catanesi, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP5 99785, 203 bp overlap; the clone sequenced to the right is RP11-757A2, 2036 bp overlap. Actual start of this clone is at base position 1-427; of RP5-997N5, actual end is at base position 44275 of RP11-54E23.

FEATURES

Source

Location/Qualifiers

1..38958
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7"

/clone="RP11-616K2"

/clone_lib="RPCL11"

10..1288

/rpt_family="L2"

2206..2486

/rpt_family="MaLR"

3076..3290

/rpt_family="L2"

3416..3442

/rpt_family="(TA)n"

repeat_region 3443..3487
/rpt_family="(CA)n"
repeat_region 3527..3778
/rpt_family="L2"
repeat_region 4302..4592
/rpt_family="L2"
repeat_region 4752..5129
/rpt_family="MaLR"
repeat_region 5489..5509
/rpt_family="AT-rich"
repeat_region 6218..6301
/rpt_family="MaLR"
repeat_region 6366..6401
/rpt_family="GA-rich"
repeat_region 6456..6558
/rpt_family="MaLR"
repeat_region 6665..6818
/rpt_family="L2"
repeat_region 7679..7707
/rpt_family="(TG)n"
repeat_region 9052..9381
/rpt_family="Alu"
repeat_region 9170..9216
/rpt_family="(TAAAA)n"
repeat_region 9471..9406
/rpt_family="(TAAA)n"
repeat_region 9446..9521
/rpt_family="MIR"
repeat_region 9514..1011
/rpt_family="MIR"
repeat_region 11924..11974
/rpt_family="(TATATG)n"
repeat_region 12057..12085
/rpt_family="MER2_type"
repeat_region 12086..12393
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repeat_region 12394..13529
/rpt_family="MER2_type"
repeat_region 12812..12847
/rpt_family="AT-rich"
repeat_region 12882..12905
/rpt_family="AT-rich"
repeat_region 12956..13033
/rpt_family="AT-rich"
repeat_region 13542..13571
/rpt_family="(TA)n"
repeat_region 13574..14658
/rpt_family="L1"
repeat_region 14706..15418
/rpt_family="L1"
repeat_region 15025..15140
/rpt_family="CT-rich"
repeat_region 15604..16018
/rpt_family="ERVL"
repeat_region 17729..17946
/rpt_family="L2"
repeat_region 17818..17867
/rpt_family="(TTTTG)n"
repeat_region 18111..18285
/rpt_family="L1"
repeat_region 18286..19823
/rpt_family="ERVL"
repeat_region 19864..19893
/rpt_family="(T)n"
repeat_region 20322..20521
/rpt_family="MER1_type"
repeat_region 20580..20619
/rpt_family="(T)n"
repeat_region 20592..20897
/rpt_family="Alu"
repeat_region 23205..23501
/rpt_family="Alu"
repeat_region 23502..23591


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repeat_region      /rpt_family="(TTA)n"
                    25228..25597
repeat_region      /rpt_family="MALR"
                    25916..26051
repeat_region      /rpt_family="ERVL"
                    26089..26270
repeat_region      /rpt_family="LI"
                    26277..26837
repeat_region      /rpt_family="LI"
                    26742..26765
repeat_region      /rpt_family="(TG)n"
                    26858..27440
repeat_region      /rpt_family="LI"
                    27948..28316
repeat_region      /rpt_family="LI"
                    28837..28875
repeat_region      /rpt_family="LI"
                    29272..29490
repeat_region      /rpt_family="LI"
                    29491..29831
repeat_region      /rpt_family="MALR"
                    29832..30496
misc_feature        /rpt_family="LI"
                    30510..31152
                    /note="similar to EST AA843681 (NID:2993097) ak01c11.s1"

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Query Match      2.0%; Score 57; DB 9; Length 54958;
Best Local Similarity 100.0%; Pred. No. 5,8e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

UY 1187 CTGCCACCTGGCCCTCCCAAGTCTGGGATACAGACGATGAGTCAGTGTGCTGAG 1243
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2015 CTGCCACCTGGCCCTCCCAAGTCTGGGATACAGACGATGAGTCAGTGTGCTGAG 2017

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```

RESULT 44
AC131566/c      91907 bp DNA linear; PRI 24-AUG-2002
LOCUS      Homo sapiens chromosome 16 clone RP11-141N14; complete sequence.
DEFINITION      AC131566 AC017012
ACCESSION      AC131566.1 GI:22474847
VERSION      HTG.
KEYWORDS      human.
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 91907)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratories.
TITLE      Direct Submission
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 91907)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE      Direct Submission
JOURNAL      Submitted (24-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT      On Aug 24, 2002 this sequence version replaced gi:8569822.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >40 99.6% of sequence;
Estimated Total Number of Errors is 0.2.

```

```

FEATURES
    source
        1..91907
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="16"
            /clone="RP11-141N14"

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```

BASE COUNT      26999 a 20814 c 19555 g 24539 t
ORIGIN

```

```

Query Match      2.0%; Score 57; DB 9; Length 91907;
Best Local Similarity 100.0%; Pred. No. 6e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

UY 1025 CTCACGTAACTCTGCTCCCGGTTCAAGCGATTCTCCTGCGCTCAGCTCTCTGAG 1081
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Db 916 CTCACGTAACTCTGCTCCCGGTTCAAGCGATTCTCCTGCGCTCAGCTCTCTGAG 860

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```

RESULT 45
AC069314      104906 bp DNA linear PRI 09-JAN-2002
LOCUS      Homo sapiens BAC clone CTD-2300122 from 2, complete sequence.
DEFINITION      AC069314
ACCESSION      AC069314.5 GI:18042324
VERSION      HTG.
KEYWORDS      Homo sapiens.
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 104906)
AUTHORS      Sulston, J.E. and Waterston, R.
TITLE      Toward a complete human genome sequence
JOURNAL      Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE      99063792
PUBMED      9847074
REFERENCE      2 (bases 1 to 104906)
AUTHORS      Desai, A., Meyer, R. and Boyer, E.
TITLE      The sequence of Homo sapiens BAC clone CTD-2300122
JOURNAL      Unpublished (2001)
REFERENCE      3 (bases 1 to 104906)
AUTHORS      Waterston, R.H.
TITLE      Direct Submission
JOURNAL      Submitted (26-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE      4 (bases 1 to 104906)
AUTHORS      Waterston, R.H.
TITLE      Direct Submission
JOURNAL      Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE      5 (bases 1 to 104906)
AUTHORS      Waterston, R.
TITLE      Direct Submission
JOURNAL      Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT      On Jan 3, 2002 this sequence version replaced gi:16924147.
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplensew@wustl.edu
Summary Statistics
Center project name: H_MS2300122

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/us09>

SOURCE INFORMATION:

Clone CTD-2300122 is from a release of the human BAC library CID. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); D.-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. (<http://www.resgen.com>).
VECTOR: pBelBAC11
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-498M11, 2000 bp overlap; the clone sequenced to the right is AF225899, 2000 bp overlap.
Actual start of this clone is at base position 342435 of RP11-498M11.

FEATURES

Source

Location/Qualifiers
1..104906
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone="CTD-2300122"
/clone_lib="C:D"
607..892
/rpt_family="L2"
893..937
/rpt_family="(TG)n"
937..1251
/rpt_family="MIR"
1376..1424
/rpt_family="MIR"
1599..1909
/rpt_family="Alu"
1880..1902
/rpt_family="(CAAA)n"
2027..2621
/note="Similar to Mus musculus ES: B6E2008
(NID:g16496123)"
2737..2760
/rpt_family="AT-rich"
2751..3006
/rpt_family="L1"
3526..3561
/rpt_family="MIR"
4670..4696
/rpt_family="(T)n"
6431..6627
/rpt_family="MIR"
7465..7710
/rpt_family="Alu"
8016..8092
/rpt_family="L2"
8316..8420
/rpt_family="(CT-rich"
8380..8415
/note="Similar to Homo sapiens EST S597527
(NID:g12340042)"
8708..8743
/rpt_family="AT-rich"
8874..9191
/rpt_family="Alu"
9177..9221
/rpt_family="(CAAA)n"
9217..9318
/rpt_family="Mariner"
9319..9607
/rpt_family="Alu"
9579..9517

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9608..9737
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10967..10998
/rpt_family="(T)n"
repeat_region
10685..11002
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repeat_region
11040..11347
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repeat_region
11318..11352
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repeat_region
11353..11375
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repeat_region
12077..12096
/rpt_family="(CAAA)n"
repeat_region
12184..12495
/rpt_family="Alu"
repeat_region
12467..12489
/rpt_family="(TAAA)n"
repeat_region
14337..14615
/rpt_family="Alu"
repeat_region
14615..14660
/rpt_family="(CA)n"
repeat_region
14966..15383
/rpt_family="L1"
repeat_region
15535..15577
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repeat_region
15549..15680
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repeat_region
16050..16086
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repeat_region
16302..16354
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repeat_region
16326..16402
/rpt_family="L2"
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17576..18132
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repeat_region
18319..18621
/rpt_family="Alu"
repeat_region
19730..19766
/rpt_family="T-rich"
repeat_region
19735..20044
/rpt_family="Alu"
repeat_region
21134..21354
/rpt_family="MIR"
repeat_region
22103..22169
/rpt_family="L2"
repeat_region
22391..22506
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repeat_region
22364..22386
/rpt_family="AT-rich"
repeat_region
22370..22646
/rpt_family="Alu"
repeat_region
22804..23026
/rpt_family="MIR"
repeat_region
23156..23176
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repeat_region
24638..24749
/rpt_family="MIR"
repeat_region
24815..24933
/rpt_family="MIR"
repeat_region
24991..25071
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25007..25071
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repeat_region
25189..25484
/rpt_family="Alu"
repeat_region
25604..25983

Query Match 4.0% Score 57; DB 9; Length 164936;
Best Local Similarity 100.0%; Pred. No. 6e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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repeat_region 150..530
repeat_region /rpt_family="L1"
repeat_region 498..649
repeat_region /rpt_family="L1"
repeat_region 673..1096
repeat_region /rpt_family="MAlu"
repeat_region 3188..3348
repeat_region /rpt_family="L1"
repeat_region 3605..3726
repeat_region /rpt_family="(TA)n"
repeat_region 3845..4563
repeat_region /rpt_family="L1"
repeat_region 5641..6075
repeat_region /rpt_family="Retroviral"
repeat_region 6133..6433
misc_feature /rpt_family="Alu"
7110..8040
7872..40218
/notes="CpG island (MGC-69.1, o/e=0.80, #pCs 93)"
7872..40218
/genes="WUGSC:H.RG437L15.1"
join(7872..8044,12642..12795,15154..15404,15584..19741,
21552..21601,22478..22638,29862..29975,33955..33944,
36395..36488,39123..39284,39881..40218)
/genes="WUGSC:H.RG437L15.1"
/notes="serine/threonine kinase KICK: Match to protein
AF027706 (PID:g3123887) and mRNA AF327706 (NID:g3123886);
H.RG437L15.1"
/codon_start=1
/evidence=not_experimental
/protein_id="AAC24561.1"
/db_xref="GI:3264574"
/translation="MNCEAICSAIPTIPYKHLAD:RYLSKSGAGSIVSSARHADRWQV
AVKHLIHPLDSEKDLREAEILIKARFVYLPILGNEPFFLGVTEYMPNGS
LNELLIRKTEYPOVAPNLRERILHETALGVNHHNTPGLHHDLKTONILLONEFHV
KIADGLSKWRMSLSQSRSSKSAPEGGLIYMPHNYEYKSKSRAS:KHUIYSYAVI
IWEVLSRKOPEDYTNPIOLMYSVSQCHRPVINEESLPYIPEKARM:SLIESCHQSN
PDERPSFLACILEBPLR:FEETIEAVICUKTKATGVSVAIHITDKKMLSESN
IPVNHQSCSSQHLHENSQSPETSRLPAQNDFTSRKAQDCYFKLHHCPONH
SWSTISGSOARAACDHKTPCSSALINPLSTAGNSERLQPGIACQGIOSKREDIVNQ
MTEACLNQSDALLKOLINKKEYELVSKPTPTSKVRQLITIDTQGEFEAKVIVQK
LKONKQGLQPYPEILWRSRPSLNLQNKSM"
8463..8770
repeat_region /rpt_family="MER1_type"
repeat_region 10435..10540
repeat_region /rpt_family="MIR"
repeat_region 11433..11538
repeat_region /rpt_family="Alu"
repeat_region 11790..12003
repeat_region /rpt_family="Alu"
repeat_region 12466..12557
repeat_region /rpt_family="MIR"
repeat_region 15579..16292
repeat_region /rpt_family="L1"
repeat_region 16292..16429
repeat_region /rpt_family="L1"
repeat_region 16460..16991
repeat_region /rpt_family="L1"
repeat_region 22863..23483
repeat_region /rpt_family="L2"
repeat_region 23575..23750
repeat_region /rpt_family="L1"
repeat_region 23761..23924
repeat_region /rpt_family="Alu"
repeat_region 23929..24439
repeat_region /rpt_family="L1"
repeat_region 24471..24960
repeat_region /rpt_family="L2"
repeat_region 24967..25285
repeat_region /rpt_family="Alu"
repeat_region 25337..25671
repeat_region /rpt_family="L2"
repeat_region 26151..26280
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repeat_region 26268..26500
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repeat_region 26611..27000
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repeat_region 28128..29109
repeat_region /rpt_family="L1"
repeat_region 29128..29434
repeat_region /rpt_family="Alu"
repeat_region 29435..29752
repeat_region /rpt_family="L1"
repeat_region 30205..30341
repeat_region /rpt_family="Alu"
repeat_region 31170..31344
repeat_region /rpt_family="Alu"
repeat_region 31466..31688
repeat_region /rpt_family="MER2_type"
repeat_region 31761..31955
repeat_region /rpt_family="Alu"
repeat_region 31956..32225
repeat_region /rpt_family="MER2_type"
repeat_region 32429..32460
repeat_region /rpt_family="Alu"
repeat_region 33155..33281
repeat_region /rpt_family="MIR"
repeat_region 33380..33437
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repeat_region 34433..34514
repeat_region /rpt_family="MER2_type"
repeat_region 34525..34939
repeat_region /rpt_family="MAlu"
repeat_region 34999..35256
repeat_region /rpt_family="Alu"
repeat_region 35388..35477
repeat_region /rpt_family="MER2_type"
repeat_region 35994..36286
repeat_region /rpt_family="Alu"
repeat_region 36686..36985
repeat_region /rpt_family="Alu"
repeat_region 37488..37673
repeat_region /rpt_family="L2"
repeat_region 37862..38161
repeat_region /rpt_family="Alu"
repeat_region 38297..38599
repeat_region /rpt_family="Alu"
repeat_region 41954..42006
repeat_region /rpt_family="L2"
repeat_region 42596..42777
repeat_region /rpt_family="MER1_type"
repeat_region 43357..43658
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repeat_region 44088..44386
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Best Local Similarity 100.0%; Prod. No. 6.1e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 CTCACGTAACTCTGCTCCCGGGTTCAGCGATTCTTCCTCAGCCTCCTGAG 1081
|||||
DB 44313 CTCACGTAACTCTGCTCCCGGGTTCAGCGATTCTTCCTCAGCCTCCTGAG 44257
|||||

RESULT 48

HS329A5/c

LOCUS

DEFINITION

Human DNA sequence from clone RP3-329A5 on chromosome 6p21.1-21.33
Contains a pseudogene similar to ribosomal protein L55a, ZNF76
(zinc finger protein 76 (expressed in testis)), part of the gene
for KIAA0646 protein, an EST, SIF5, GSSS and CpG islands.b,
complete sequence.

ACCESSION

297832

VERSION

297832.1

KEYWORDS

HTG; CpG island; KIAA0646; ribosomal protein L55a; ZNF76.

SOURCE Homo sapiens.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 117026)
 Williams.S.
REFERENCE Direct Submission
AUTHORS Submitted (01-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
TITLE CB10 ISA, UK. E-mail enquiries: humquerry@sanger.ac.uk
JOURNAL requests: clonerequest@sanger.ac.uk
 On Oct 19, 1999 this sequence version replaced a 150,6482.
COMMENT This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information
 on the WormPEP database can be found at
<http://www.sanger.ac.uk/projects/Celegans/wormpep> RP3-329A5 is
 from the library RP3-3 constructed at the Roswell Park Cancer
 Institute by the group of Pieter de Jong. For further details see
<http://bacpac.med.buffalo.edu/>
VECTOR pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
 RP3-329A5. It may be shorter because we only sequence overlapping
 sections once, or longer because we arrange for a small overlap
 between neighbouring submissions.
 The true left end of clone RP3-329A5 is at 1,6427 in this sequence. The
 true left end of clone RP1-109F14 is at 1,6427 in this sequence.
 This sequence was generated from part of bacterial clone contigs of
 human chromosome 6, constructed by the Sanger Centre Chromosome 6
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/chr6>.
 Location/Qualifiers

FEATURES

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1. 117026
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 /db_xref="taxon:9606"
 /chromosome="6"
 /map="p21.1-21.33"
 /clone="RP3-329A5"
 /clone_lib="RP3-3"
 /note="4427..5878"
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 /note="CpG island"
 /evidence=not_experimental
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 4926..5045
 /note="40 copies 3 mer aa 78% conserved"
repeat_region
 4927..5092
 /note="83 copies 2 mer aa 57% conserved"
repeat_region
 5006..5089
 /note="21 copies 4 mer gaqa 69% conserved"
repeat_region
 8314..8371
 /note="29 copies 2 mer ga 81% conserved"
repeat_region
 8622..8681
 /note="15 copies 4 mer tate 70% conserved"
repeat_region
 9342..9381
 /note="20 copies 2 mer gt 77% conserved"
misc_feature
 11477..11646
 /note="match: STS: Em:G22405"
misc_feature
 11523..11730
 /note="match: STS: Em:G15403"
misc_feature
 complement(17952..18500)
 /note="match: GSS: Em:AQ416819"
misc_feature
 18510..18912
 /note="match: GSS: Em:AQ762444"

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 /note="MER91A repeat: matches 90..196 of consensus"
misc_feature
 21086..21547
 /note="match: GSS: Em:AQ506253"
misc_feature
 25158..25441
 /note="match: GSS: Em:AQ771827"
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 /note="3 copies 19 mer 87% conserved"
repeat_region
 30570..30726
 /note="3 copies 19 mer 86% conserved"
repeat_region
 30703..30732
 /note="15 copies 2 mer ga 86% conserved"
repeat_region
 31101..31220
 /note="MER91A repeat: matches 52..175 of consensus"
misc_feature
 35578..35884
 /note="match: GSS: Em:AQ167878"
misc_feature
 complement(38569..38704)
 /note="match: GSS: Em:AQ455275"
repeat_region
 39952..40009
 /note="29 copies 2 mer ct 69% conserved"
repeat_region
 41817..41842
 /note="13 copies 2 mer tt 92% conserved"
repeat_region
 45456..45517
 /note="Charlie2 repeat: matches 72..133 of consensus"
repeat_region
 46451..46459
 /note="Charlie2 repeat: matches 174..285 of consensus"
repeat_region
 46481..47711
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repeat_region
 47781..47913
 /note="Charlie2 repeat: matches 3427..3554 of consensus"
repeat_region
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repeat_region
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repeat_region
 48516..48678
 /note="Charlie2 repeat: matches 3577..3760 of consensus"
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 /note="CpG island"
repeat_region
 53027..53413
 /note="MER39 repeat: matches 6..419 of consensus"
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 /note="match: GSS: Em:AQ138905"
misc_feature
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misc_feature
 57730..57793
 /note="match: GSS: Em:AQ106757"
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 59592..59621
 /note="15 copies 2 mer aa 86% conserved"
repeat_region
 60651..60960
 /note="7SK repeat: matches 5..110 of consensus"
repeat_region
 63578..63629
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 64340..64598
 /note="Single clone region. Small insert library of pUC
 clone"
repeat_region
 64853..64937
 /note="FIAM_C repeat: matches 27..111 of consensus"
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 complement(66719..67074)
 /note="match: GSS: Em:AQ128487"
misc_feature
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 /note="match: GSS: Em:AQ782452"
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 complement(join(70250..70485,70840..70936))
 /gene="d3329A5.1"
CDS
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 /note="similar to ribosomal protein L35a)
 match: cDNAs: Em:X52966
 match: proteins: Wp:P02434 Sw:P18077 Sw:O55142
 Sw:P04645"
 /pseudo

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/misc_feature
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/complement(70136..70387)
/gene="dJ329A5.1"
/note="match: GSS: Em: AQ14959;"
/complement(71855..71986)
/note="match: GSS: Em: AQ12216"
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/note="match: GSS: Em: AQ80983"
72158..87093
/gene="ZNF76"
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81749..81824,82386..82511,82666..82845,83533..83895,
83989..84152,84859..85023,85564..85677,86252..87093)
/gene="ZNF76"
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testis))"
/note="match: CDNAS: Em: M61592"
/evvidence-not_experimental
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81749..81824,82386..82511,82666..82845,83533..83895,
83989..84152,84859..85023,85564..85677,86252..86456)
/gene="ZNF76"
/note="match: proteins: Sw: P36502"
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testis))"
/protein_id="CAB65621.1"
/db_xref="GI:668774"
/translation="MESLGLHTVTSIGTAYVQDAVKSEKILETOVIOLENGITAYI
HQVTVREGDPTSLERVLQLEDSATIHPPVAVPSESTSLAVL:EVGLDELAAEIDQ
GFSADVALEQVASKVLHDSQTPHNGQGVGRHAPGCKRGRLEYTAHILAVHE
RAHGTGDFPCDFSCGAKATGYGLKSHVHTTEKPYSDLELCSAKFTSGDQK
HVRTHTERPEFQCFEGCGSFTTSNIRKVVHVTHTGERVYTCQEPHCQGETSATNY
KNHVRITSEQSVLPDPPSGSFTNPVPHCPISLEFLASSHHUPHSPVSGKPPVQ
TVPCGGRFRFTEYSLKHVVHHTCKPYCTCKTKYRQTSILAMHKBHAGCELEATE
ESGALTEQOQLPEASAAESPPKPRRTAYLSVKEFERLD:PAQYAMVTEELGAPV
ALITDGAQVQVSPEDLQALGASISMTVHGSTTITITSPDALGCTGTHTVHMVSA
DGTOPTVTITISGAVVDSVASLRHQVALLATANGPHIAVG:EEQVITLEAINTV
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73128..73240
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/note="MER53 repeat: matches 1..122 of consensus"
73478..73545
repeat_region
/note="MER53 repeat: matches 122..129 of consensus"
Query Match 2.0% Score 57: 18 9: Length 11702+
Best Local Similarity 100.0%: Pred. No. 5,10-20:
Matches 57: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 1025 CTCACGTGAAGCTCGCTCCGGCTCAAGCGATCTGCTGCTCAGCTCCACAG 1081
DB 46222 CTCACGTGAAGCTCGCTCCGGGTCAAGCGATTTTCCTGGCTCAGCTCTCAG 46166

RESULT 49
AL360017
LAC2S
AL360017 118603 bp DNA linear: FIG 10-JUL-2001
DEFINITION Homo sapiens chromosome 1 clone RP11-57B11. *** SEQUENCING IN
PROGRESS ***, 30 unordered pieces.
ACCESSION AL360017
VERSION AL360017.5 GI:10040034
KEYWORDS HTG: HTGS_PHASE1: HTGS_CANCELLED.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118603)
McLay, K.
Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk clone
requests: clonerequest@sanger.ac.uk

```

On Sep 9, 2000 this sequence version replaced gi:9864236.

----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA57B11
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 5% of reads
Sequencing vector: plasmid: 108752; 94% of reads
Chemistry: Dye-terminator ET-amersham; 28% of reads Chemistry:
Dye-terminator Big Dye; 71% of reads
Consensus quality: 108370 bases at least Q40
Consensus quality: 112350 bases at least Q30
Consensus quality: 114458 bases at least Q20
Insert size: 115703: sum-of-contigs
Insert size: 198549: 0.6% error; agarose-fp
Quality coverage: 3.40x in Q20 bases; sum-of-contigs Quality
coverage: 2.66x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 2887: contig of 2887 bp in length
* 2888 2987: gap of 100 bp
* 2988 6254: contig of 3267 bp in length
* 6255 6454: gap of 100 bp
* 6355 8455: contig of 2101 bp in length
* 8456 8555: gap of 100 bp
* 8556 10953: contig of 2398 bp in length
* 10954 11053: gap of 100 bp
* 11054 15632: contig of 4579 bp in length
* 15633 15732: gap of 100 bp
* 15733 17940: contig of 2208 bp in length
* 17941 18040: gap of 100 bp
* 18041 21589: contig of 3549 bp in length
* 21590 21689: gap of 100 bp
* 21690 24423: contig of 2734 bp in length
* 24424 24523: gap of 100 bp
* 24524 26757: contig of 2234 bp in length
* 26758 26857: gap of 100 bp
* 26858 29230: contig of 2373 bp in length
* 29231 29330: gap of 100 bp
* 29331 31453: contig of 2223 bp in length
* 31454 31553: gap of 100 bp
* 31554 33568: contig of 2015 bp in length
* 33569 33668: gap of 100 bp
* 33669 36828: contig of 3160 bp in length
* 36829 36928: gap of 100 bp
* 36929 39734: contig of 2806 bp in length
* 39735 39834: gap of 100 bp
* 39835 43884: contig of 4050 bp in length
* 43885 43984: gap of 100 bp
* 43985 46407: contig of 2423 bp in length
* 46408 46507: gap of 100 bp
* 46508 49182: contig of 2675 bp in length
* 49183 49282: gap of 100 bp
* 49283 51741: contig of 2459 bp in length
* 51742 51841: gap of 100 bp
* 51842 55628: contig of 3787 bp in length
* 55629 55728: gap of 100 bp
* 55729 66859: contig of 11131 bp in length
* 66860 66959: gap of 100 bp
* 66960 70916: contig of 3957 bp in length
* 70917 71016: gap of 100 bp
* 71017 74767: contig of 3751 bp in length

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* 74768 74867: gap of 100 bp
* 74868 78453: contig of 3586 bp in length
* 78454 78553: gap of 100 bp
* 78554 84138: contig of 5585 bp in length
* 84139 84238: gap of 100 bp
* 84239 91281: contig of 7043 bp in length
* 91282 91381: gap of 100 bp
* 91382 96604: contig of 5223 bp in length
* 96605 96704: gap of 100 bp
* 96705 105604: contig of 8900 bp in length
* 105605 105704: gap of 100 bp
* 105705 108501: contig of 2797 bp in length
* 108502 108601: gap of 100 bp
* 108602 112331: contig of 3730 bp in length
* 112332 112431: gap of 100 bp
* 112432 118603: contig of 6172 bp in length
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        11054..15632
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        39835..43884
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    /note="assembly_fragment:01178"
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    /note="assembly_fragment:01299"
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BASE COUNT 29046 a 29214 c 28605 g 28835 t 2903 others
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Best Local Similarity 100.0%; Pred. NO. 6.1e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1025 CTCACGTAACTCTCCCTCCGGGTTCAAGCGATTCTCGCTCAGCGCTCTGAG 1081
|||||
Db 7041 CTCACGTAACTCTCCCTCCGGGTTCAAGCGATTCTCGCTCAGCGCTCTGAG 7047

RESULT 50
AP003555/c
LOCUS AP003555 121600 bp DNA linear PRI 08-DEC-2001
DEFINITION Homo sapiens genomic DNA, chromosome 11q, clone:RP11-626H12,
complete sequence.
ACCESSION AP003555
VERSION AP003555.2 GI:17426126
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:RP11-626H12.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Published Only in Database (2001)
REFERENCE 2 (bases 1 to 121600)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
TITLE Submitted (27-APR-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suhiro-chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Dec 7, 2001 this sequence version replaced gi:13528404.
FEATURES
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        /map="11q"
        /clone="RP11-626H12"
BASE COUNT 30736 a 29421 c 29985 g 31456 t

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DB 20160 TCGGCTGCTCTAGGAGCTCTGGGAGCTCAGGCTGGAATCTCAAGGTAATAGGTTGGC 28159
QY 2264 TATCAAAATCAAGCTCAGGCTTCTGCGGGGAAATCAAAATCAAGCTCAATCAAGGTT 2423
DB 20160 TATCAAAATCAAGCTCAGGCTTCTGCGGGGAAATCAAAATCAAGCTCAATCAAGGTT 28219
QY 2324 ATGTGCGGCTTCCCTCAGCCAGCTAGGCTTTGAAGAGAAATCAAGGTTCAAGGTT 2463
DB 20220 ATGTGCGGCTTCCCTCAGCCAGCTAGGCTTTGAAGAGAAATCAAGGTTCAAGGTT 28279
QY 2384 AAGATTCGGCTCTGAGGAGATTCAGCTTAGAGCTTCTGCTGAGGAAATCAAGGTT 2443
DB 20280 AAGATTCGGCTCTGAGGAGATTCAGCTTAGAGCTTCTGCTGAGGAAATCAAGGTT 28339
QY 2444 GCGCTGAGCAACTAACAAGGAAATCAAGGTTCAAGGTTCAAGGTTCAAGGTT 2503
DB 20440 GCGCTGAGCAACTAACAAGGAAATCAAGGTTCAAGGTTCAAGGTTCAAGGTT 28499
QY 2504 ATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2563
DB 20440 ATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 28499
QY 2564 AGCTGAGGCTTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2623
DB 20460 AGCTGAGGCTTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 28519
QY 2624 GCGGAGCTTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2683
DB 20520 GCGGAGCTTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 28579
QY 2684 CTAACTGCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2743
DB 20580 CTAACTGCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 28639
QY 2744 CTGCACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2803
DB 20640 CTGCACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 28599
QY 2804 GAGAGAGAGACACAGGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2863
DB 20700 GAGAGAGAGACACAGGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 28699
QY 2864 ATAAAGAACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2923
DB 20760 ATAAAGAACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 28719
QY 2924 GAG 2983
DB 20820 GAG 28779
QY 2984 GCGAG 3043
DB 20880 GCGAG 28839
QY 3044 TTTTCTCCCTTCTCGGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCT 3103
DB 20940 TTTTCTCCCTTCTCGGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCT 28999
QY 3104 GTGGAACAGAGTATGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCT 3163
DB 20900 GTGGAACAGAGTATGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCT 29059
QY 3164 GCGAGAGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCT 3223
DB 20960 GCGAGAGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCT 29119
QY 3224 CAGACTT 3231
DB 209120 CAGACTT 29127

RESULT 3

AAD37267

ID AAD37267 standard: DNA: 2910 bp.

XX AAD37267;

XX AC 21-AUG 2002 (first entry)

XX DE Human: ABC1 Transcription regulatory DNA #3.

XX KW Human: ATP binding cassette 1; ABC1 gene regulation; atherosclerosis;
cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT protein_bind 12..24

FT /tag: d

FT /bound_moiety: "LM2COM/MYOD"

FT protein_bind 97..107

FT /tag: b

FT /bound_moiety: "deltaE1"

FT protein_bind 110..125

FT /tag: c

FT /bound_moiety: "Sb/NKX2.5"

FT protein_bind 196..211

FT /tag: d

FT /bound_moiety: "S8"

FT protein_bind 228..247

FT /tag: p

FT /bound_moiety: "GATA"

FT protein_bind 399..410

FT /tag: f

FT /bound_moiety: "IK2"

FT protein_bind 412..420

FT /tag: d

FT /bound_moiety: "LYF1"

FT protein_bind 528..539

FT /tag: h

FT /bound_moiety: "LM2COM/MYOD/DeltaE1"

FT protein_bind 549..556

FT /tag: j

FT /bound_moiety: "LYF1"

FT protein_bind 558..558

FT /tag: j

FT /bound_moiety: "deltaE1"

FT protein_bind 590..596

FT /tag: k

FT /bound_moiety: "LKX2.5"

FT protein_bind 598..620

FT /tag: j

FT /bound_moiety: "NFY/CAAT"

FT protein_bind 709..715

FT /tag: m

FT /bound_moiety: "MZF1"

FT protein_bind 723..730

FT /tag: e

FT /bound_moiety: "MZF1"

FT protein_bind 771..785

FT /tag: o

FT /bound_moiety: "HFH2/SRY/EV1"

FT protein_bind 803..812

FT /tag: p

FT /bound_moiety: "CREB1/VBP"

FT protein_bind 831..837

FT /tag: r

FT /bound_moiety: "NKX2.5"

FT protein_bind 1076..1089

FT /tag: s

FT /bound_moiety: "GATA"

FT protein_bind 1173..1188

FT	/*tag=	l	/*tag=	l	/*tag=	l		
FT	/bound_moliety=	"LXRa:pha/deltaEFL"	1189..1209	/*tag=	u	/*tag=	u	
FT	protein_bind			/bound_moliety=	"DeltaEFL/.LYF1/IK2"	1483..1491	/*tag=	v
FT	protein_bind			/bound_moliety=	"AP4"	1498..1514	/*tag=	w
FT	protein_bind			/bound_moliety=	"LMo2-OM/NMYC/deltaEFL/EA3"	1524..1545	/*tag=	x
FT	protein_bind			/bound_moliety=	"ZiE/deltaEFL"	1597..1607	/*tag=	y
FT	protein_bind			/bound_moliety=	"betaEFL"	1622..1627	/*tag=	z
FT	protein_bind			/bound_moliety=	"PPAR"	1632..1637	/*tag=	aa
FT	protein_bind			/bound_moliety=	"PPAR"	1685..1698	/*tag=	ab
FT	protein_bind			/bound_moliety=	"USF/NMYC/NYCMAX"	1787..1797	/*tag=	ac
FT	protein_bind			/bound_moliety=	"betaEFL"	1809..1819	/*tag=	ad
FT	protein_bind			/bound_moliety=	"betaEFL"	1822..1833	/*tag=	ae
FT	protein_bind			/bound_moliety=	"SKY"	1840..1850	/*tag=	af
FT	protein_bind			/bound_moliety=	"AP1"	1942..1956	/*tag=	ag
FT	protein_bind			/bound_moliety=	"HNFbeta"	1978..1985	/*tag=	ah
FT	protein_bind			/bound_moliety=	"NKX2.5"	2008..2016	/*tag=	ai
FT	protein_bind			/bound_moliety=	"PPAR/NKX2.5/PPAR"	2019..2024	/*tag=	aj
FT	protein_bind			/bound_moliety=	"PPA3/NKX2.5/PPA3"	2051..2059	/*tag=	ak
FT	protein_bind			/bound_moliety=	"GATA"	2104..2111	/*tag=	al
FT	protein_bind			/bound_moliety=	"SOX5"	2114..2152	/*tag=	am
FT	protein_bind			/bound_moliety=	"SYR/HNF/HNFbeta"	2221..2228	/*tag=	an
FT	protein_bind			/bound_moliety=	"WZF1"	2234..2249	/*tag=	ao
FT	protein_bind			/bound_moliety=	"IKZ/NF-kappaB/cREL"	2259..2272	/*tag=	ap
FT	protein_bind			/bound_moliety=	"LMo2/OM/GATA"	2289..2306	/*tag=	aq
FT	protein_bind			/bound_moliety=	"WZF1/SKY"	2313..2318	/*tag=	ar
FT	protein_bind							

FT	protein_bind	/bound_moiety=	"PPAR"
FT		/*tag=	as
FT		/bound_moiety=	"PPAR"
FT	protein_bind	2335..2442	
FT		/*tag=	at
FT		/bound_moiety=	"MZF1"
FT	protein_bind	2361..2384	
FT		/*tag=	au
FT		/bound_moiety=	"HNF3beta/SRY/EV11"
FT	protein_bind	2426..2433	
FT		/*tag=	av
FT		/bound_moiety=	"MZF1"
FT	protein_bind	2442..2451	
FT		/*tag=	aw
FT		/bound_moiety=	"AP4"
FT	protein_bind	2455..2466	
FT		/*tag=	ax
FT		/bound_moiety=	"SRY"
FT	protein_bind	2491..2498	
FT		/*tag=	ay
FT		/bound_moiety=	"STAT"
FT	protein_bind	2524..2534	
FT		/*tag=	az
FT		/bound_moiety=	"STAT/PPAR"
FT	protein_bind	2536..2541	
FT		/*tag=	ba
FT		/bound_moiety=	"PPAR"
FT	protein_bind	2589..2600	
FT		/*tag=	bb
FT		/bound_moiety=	"AP2"
FT	protein_bind	2613..2617	
FT		/*tag=	bc
FT		/bound_moiety=	"MZF1"
FT	protein_bind	2634..2648	
FT		/*tag=	bd
FT		/bound_moiety=	"LMO2COM/MYOD/E47"
FT	protein_bind	2657..2672	
FT		/*tag=	be
FT		/bound_moiety=	"RREB1"
FT	protein_bind	2680..2698	
FT		/*tag=	bt
FT		/bound_moiety=	"MZF1/CMVB"
FT	protein_bind	2728..2740	
FT		/*tag=	bd
FT		/bound_moiety=	"SP1/SC"
FT	protein_bind	2743..2757	
FT		/*tag=	ba
FT		/bound_moiety=	"USF/NNYC/ARNT"
FT	protein_bind	2768..2773	
FT		/*tag=	bi
FT		/bound_moiety=	"NFE2AP1"
FT	protein_bind	2774..2787	
FT		/*tag=	bj
FT		/bound_moiety=	"XFD1/HFH"
FT	protein_bind	2794..2806	
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FT		/bound_moiety=	"SC/SP1/MZF1"

	Query Match	90.1%	Score 2910;	DB 24;	Length 2910;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2910;	Conservative	Mismatches	0;	Indels
				0;	Gaps
Qy	1	ACAGGCACTGCTGGAGGCGCTGTAACTTCAGTTACTCGGGAGGTGGAGGTTCGAATGA	60		
Lb	1	ACAGCGATCGCTGGCAGGTCGCTGTAACTTCAGTTACTCGGGAGGTGGAGGTTCGAATGA	60		
Qy	61	GGCCAGATGGTAACATCTGACATCGAGCTGGGCCAACAAAAGGTGAAACTCCATCTCAATT	120		
Lb	61	GAGCGAGATGGCAACATTGTACTTCAGCTTGGGCAACAAAAGGTGAAACTCCATCTCAATT	120		
Qy	121	AAAAAATAAATAATATATATTTGGTGGTGGACTTCAAATAGGTAGGAGGAAGGAGGAGAGG	180		

121 AAAAAAAAAAAGATGATTTTGGTGGTGGACTTCAAAATAGTAGAGGAGAAATAAGAGAGAG 180
181 AGATGAGGCTCAGGAGATCTAAATTAAGTCTTAATAATCATGCTAGAGAGAGAGAGAGAG 240
182 AAAAAAAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
183 AGATGAGGCTCAGGAGATCTAAATTAAGTCTTAATAATCATGCTAGAGAGAGAGAGAGAG 240
241 TTAATAAACACTCTGCTCTTTTATACATCACTATCTGAGAGAGAGAGAGAGAGAGAGAGAG 400
242 TTAATAAACACTCTGCTCTTTTATACATCACTATCTGAGAGAGAGAGAGAGAGAGAGAGAG 400
301 AAGTTCACCTTTCAGAAAGCCCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
302 AAGTTCACCTTTCAGAAAGCCCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
303 AAGTTCACCTTTCAGAAAGCCCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
361 AAGATGAAGAAACAGGCGGAGCAATGCTAATGCTTAAATGCTTAAATGCTTAAATGCTTAA 420
362 AAGATGAAGAAACAGGCGGAGCAATGCTAATGCTTAAATGCTTAAATGCTTAAATGCTTAA 420
421 CTGAGGCTCAGAGGATCGCTTGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 480
422 CTGAGGCTCAGAGGATCGCTTGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 480
481 AAGTTCACCTTTCAGAAAGCCCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
482 AAGTTCACCTTTCAGAAAGCCCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
541 CTGAGGCTCAGAGGATCGCTTGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 600
542 CTGAGGCTCAGAGGATCGCTTGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 600
601 CTGAGGCTCAGAGGATCGCTTGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 660
602 CTGAGGCTCAGAGGATCGCTTGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 660
661 AAAAAAGAAATCAAG 720
662 AAAAAAGAAATCAAG 720
721 GAGGAGGAG 780
722 GAGGAGGAG 780
781 GATGAG 840
782 GATGAG 840
841 GATGAG 900
842 GATGAG 900
901 GATGAG 960
902 GATGAG 960
961 TTAATTTTCTTGACAGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
962 TTAATTTTCTTGACAGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
1021 TCGAGTCACTGTAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1022 TCGAGTCACTGTAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1081 GATAAGAGGCGCGGAG 1140
1082 GATAAGAGGCGCGGAG 1140
1141 TCAATCATGTTGGCAGGAGTGGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1142 TCAATCATGTTGGCAGGAGTGGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1201 CTGCGAAGTGTGGGATACAGGCTATGAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAG 1260
1202 CTGCGAAGTGTGGGATACAGGCTATGAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAG 1260

1261 CTAGGGCTAAACAGAGTCCATGCTCAAGAGGGGCTATGCCACCCAGAGCTATGAGTACCTGG 1320
1262 CTAGGGCTAAACAGAGTCCATGCTCAAGAGGGGCTATGCCACCCAGAGCTATGAGTACCTGG 1320
1321 GACTGCAAAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1322 GACTGCAAAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1381 TCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1382 TCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1441 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1442 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1501 TCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1502 TCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1561 GGGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
1562 GGGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
1621 GGGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
1622 GGGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
1681 GGGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
1682 GGGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
1741 GTTCTATGAAATCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
1742 GTTCTATGAAATCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
1801 TGGCCAGAAATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
1802 TGGCCAGAAATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
1861 TGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
1862 TGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
1921 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
1922 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
1981 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
1982 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
2041 GTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
2042 GTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
2101 CATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
2102 CATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
2161 TCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
2162 TCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
2221 CTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2222 CTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2281 CAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
2282 CAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340

[illegible]

CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH0146 to AAH1828 and
 CC AAH1833 to AAH18742 represent human cDNA sequences; AAH92445 to
 CC AAH95893 represent human amino acid sequences; and AAH1829 to AAH18542
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 763 BP; 337 A; 205 C; 260 G; 158 T; 3 other;

Query Match 10.4%; Score 336; DB 22; Length 763;
 Best Local Similarity 100.0%; Pred. No. 1.5e-61;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2896 AATTGCGAGTCAGAGTACGTGGGCGCGGAGCGGACAGCGAGCGAGCGAGTCTCTCC 2955

DB 1 AATTGCGAGTCAGAGTACGTGGGCGCGGAGCGGAGCGAGCGAGCGAGTCTCTCC 60

QY 2956 GGGCTGCGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 4215

DB 61 GGGCTGCGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 120

QY 4016 TATGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCG 4075

DB 121 TATGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCG 380

QY 4076 GTAGAGCAAGAGACCGCAACACAAAGTGGAAACAAAGTGGAAACAAAGTGGAAACAAAGTGG 4145

DB 181 GGTAGAGCAAGAGACCGCAACACAAAGTGGAAACAAAGTGGAAACAAAGTGGAAACAAAGTGG 240

QY 3136 TACTTGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCG 3195

DB 241 TACTTGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCG 300

QY 4196 GGGACTTGATCGCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 4211

DB 401 GGGACTTGATCGCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 336

RESULT 8

AAH17451

XX AAH17451; standard; cDNA; 1750 BP.

XX AAH17451;

XX 26 JUN 2001 (first entry)

XX Human cDNA sequence SEQ ID NO:16745

XX Purcag; primer; detection; diagnosis; antisense therapy; gene therapy; SS.

XX Homo sapiens.

XX EP1074517-A2.

XX 07 FEB 2001.

XX 28 JUN 2000; 2000EP-0116126.

XX 29 JUN 1999; 95JP-0248036.

XX 27 AUG 1999; 95JP-0300253.

XX 1 JAN 2000; 2000JP-0118776.

XX 02 MAY 2000; 2000JP-0183767.

XX 09 JUN 2000; 2000JP-0241899.

XX (HELI-) HELIX RES INSL.

XX Ota T, Isoai I, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI: 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PI full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -

PS Claim 8: SEQ ID 16905; 2537pp - CD ROM: English.

XX The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH0166 to AAH1628 and
 CC AAH1633 to AAH18742 represent human cDNA sequences; AAH92445 to
 CC AAH95893 represent human amino acid sequences; and AAH1829 to AAH18632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 1750 BP; 291 A; 489 C; 586 G; 384 T; 0 other;

Query Match 10.4%; Score 336; DB 22; Length 1750;
 Best Local Similarity 100.0%; Pred. No. 1.5e-61;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2896 AATTGCGAGTCAGAGTACGTGGGCGCGGAGCGGAGCGGAGCGGAGCGGAGTCTCTCC 2955

DB 1 AATTGCGAGTCAGAGTACGTGGGCGCGGAGCGGAGCGGAGCGGAGCGGAGTCTCTCC 60

QY 2956 GGGCTGCGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 4215

DB 61 GGGCTGCGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 120

QY 4016 TATGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCG 4075

DB 121 TATGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCG 380

QY 4076 GTAGAGCAAGAGACCGCAACACAAAGTGGAAACAAAGTGGAAACAAAGTGGAAACAAAGTGG 4145

DB 181 GGTAGAGCAAGAGACCGCAACACAAAGTGGAAACAAAGTGGAAACAAAGTGGAAACAAAGTGG 240

QY 3136 TACTTGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCG 3195

DB 241 TACTTGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCGCGCGTATGTTTTCG 400

QY 4196 GGGACTTGATCGCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 3231

DB 401 GGGACTTGATCGCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 336

RESULT 9

AAH05355

XX AAH05355; standard; DNA; 20645 BP.

XX AA:05455;

XX

DI 21 NOV-2001 (first entry)
XX Human reproductive system related antigen DNA SEQ ID NO: 6643
XX human reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX Homo sapiens.
XX W4200155320-A2.
XX 62 AUG 2001.
XX 17 JAN 2001; 2001WO-0501339.
XX 31 JAN-2000; 2000US-0179065.
XX 04 FEB-2000; 2000US-0180628.
XX 24 FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0186874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198124.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214386.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217497.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 20-JUL-2000; 2000US-0220963.
XX 25-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 14-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226661.
XX 22-AUG-2000; 2000US-0226866.
XX 24-AUG-2000; 2000US-0227182.
XX 30-AUG-2000; 2000US-0227059.
XX 01-SEP-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
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PR 08-DEC-2000; 2000US-0251868.

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PR 06-DEC-2000: 2000US-0251985.
PR 11-DEC-2000: 2000US-0251950.
PR 05-JAN-2001: 2001US-0250578.
XX
XX (HUMA) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-041565/60.
XX
XX Nucleic acids encoding 1224 human nervous system antigen polypeptides,
XX useful for preventing, diagnosing and/or treating nervous system
XX cancers and metastases -
XX
XX Disclosure: SEQ ID NO 9032; 1701pp - Sequence has been English.
XX
XX The invention relates to novel genes (A641144, A642154) and proteins
XX (A641478-A641800) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (antibodies) are used
XX in the diagnosis, treatment and prevention etc. (a) cancer, e.g. breast
XX and ovarian cancer and other cancers of the adrenal gland, bone, bone
XX marrow, breast, gastrointestinal tract, liver, lung or thyroid;
XX (b) immune disorders e.g. Addison's disease, allergic autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX disease, multiple sclerosis, rheumatoid arthritis and myasthenia

CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic form directly
CC from WIPO at http://wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5075 BP: 1417 A: 1054 C: 1197 G: 1397 T: 0 other;

Query Match 10.1%; Score 325.8; DB 22; Length 3075;
Best Local Similarity 64.7%; Pred. No. 2.9e-59;
Matches 584; Conservative 0; Mismatches 302; Indels 17; Gaps 6;

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DB 3102 CTAATAAATACAAAAATTAGCCAGGATGGTGGCAGGCGCTGTAAATCCAGCTACTCAGG 3043
QY 555 AGGCTAAGCTGGAGGATCGTTGAGCCAGAGGAGTCAAGTCTACACTGAGCCATGATG 614
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QY 615 GATCAGTGCAGCTCCAGGCTG---GGTAGACAGAGCAAGACCTGTCTCAAAAAGAGAA 671
DB 2982 GCGCACTGGATTCGAGGCTGGATGATAGAGGAGGAGCACTGTCTCAAAAAGAGAGAG 2923
QY 672 TCAG 731
DB 2922 AG 2863
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DB 2852 AAGTCAAG 2803
QY 792 GGCAG 851
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QY 852 AATTAATGAG 911
DB 2745 GGTGGTAG 2686
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DB 2685 AAGCTGAG 2626
QY 972 GATACAG 1031
DB 2625 GATACAG 2566
QY 1032 TAAATGAG 1083
DB 2565 CAACCTGTGAG 2506
QY 1084 AATACAG 1143
DB 2505 TATAG 2447
QY 1144 TCAATGAG 1203
DB 2445 GATATGAG 2387
QY 1204 GCAAG 1262
DB 2386 GCAAG 2327

cc medical conditions e.g. by protein or gene therapy. The genes are
cc isolated from a range of human tissues disclosed in the specification.
cc The nucleic acids, proteins, antibodies and (anti)agonists are useful
cc in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
cc and ovarian cancer and cancers of the adrenal gland, bone, bone
cc marrow, breast, gastrointestinal tract, liver, lung, or prostate;
cc (b) immune disorders e.g. Addison's disease, allergies, autoimmune
cc haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
cc disease, multiple sclerosis, rheumatoid arthritis and osteoporosis;
cc (c) cardiovascular disorders such as myocardial ischaemia;
cc (d) wound healing; (e) neurological diseases e.g. cerebral ammonia and
cc epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
cc and parasitic infections.
cc Note: The sequence data for this patent did not form part of the
cc printed specification, but was obtained from Genbank and is directly
cc from WIP0 at http://wipo.int/pub/publicised_pat_sequences.

XX Sequence 23934 bp; 7785 A; 4761 C; 4365 G; 7923 T; 9 others.

Query Match 9.9%; Score 320.4; 56 22; 14676 2094;
Best Local Similarity 64.2%; Pred. No. 60-58;
Matches 592; Conservative 0; Mismatches 296; Indels 6; 109 52

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DB 21341 TTTCTACATAAAGACCTTACTTAGAGCGTCAGATGTCGTGCTATCTGATAAGAGAA 21292
QY 438 GTACCTTGGAGCGGTGAGGCGAGAGATGCTTCTAGCTCTAGAGCTTCTAGCTAGCTT 437
DB 21281 GCACTTGGAGCGGTGAGGCGGTGGAGATGCTTCTAGCTCTAGAGCTTCTAGCTAG 21222
QY 478 AATACATGAGAAACCGCTGCTCTACAAAGAAATATATAAAATATATATATATATATAT 477
DB 21223 GCAATGAGAAACCGCTGCTCTACAAAGAAATATATAAAATATATATATATATATAT 21164
QY 528 ATCTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 527
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Job time : 1122.17 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run On: May 9, 2003, 12:47:56 : Search time 5422.82 Seconds
(without alignment:s)
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Title: US-09-846-456-1

Perfect score: 3231

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Scoring table: IDENTITY_NUC

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Maximum Match 100%

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 8: em_estc:*
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 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	237.8	7.4	289	10	AW748338
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4	221.2	6.8	457	10	AW816516
5	219.4	6.8	577	17	AQ265389
6	218.6	6.8	544	17	AQ418551

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10	214.4	6.6	423	14	BM991096
11	214.2	6.6	581	17	AQ347610
12	213.4	6.6	338	10	AW023111
13	213.4	6.6	666	17	AG075934
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15	213.2	6.6	622	17	AQ537948
16	213	6.6	514	9	A1754653
17	213	6.6	739	17	AQ200209
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19	213	6.6	1183	13	BM564264
20	212.8	6.6	484	17	AQ314669
21	212.8	6.6	487	17	AQ414845
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25	212.2	6.6	448	17	AQ634562
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27	212	6.6	575	17	AQ587429
28	211.4	6.5	577	10	AW973181
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34	210.6	6.5	388	10	AW069227
35	210.6	6.5	437	9	AA644090
36	210.6	6.5	546	14	BM697526
37	210.6	6.5	551	9	AL698703
38	210.6	6.5	605	17	AQ412598
39	210.4	6.5	547	9	AL698654
40	210.4	6.5	552	9	AL712937
41	210.4	6.5	684	17	AG102895
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ACCESSION	AU121731				
VERSION	AU121731.1	GI:10936966			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 763)				
AUTHORS	Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y., Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and Isoami.T.				
TITLE	HRI human cdna project				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Takao Isogai				
	Genomics Laboratory				
	Helix Research Institute				
	1532-3 Yana, Kisarazu, Chiba 292-0812, Japan				
	Tel: 81-438-52-3975				
	Fax: 81-438-52-3986				
	Email: genomics@hri.co.jp				
	HRI human cdna project: 5'- & 3'-end one pass sequencing: Helix				
	Research Institute: cdna library construction: Department of				
	Virology, Institute of Medical Science, University of Tokyo, and				
	Helix Research Institute.				


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Site_2: Small; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
a 95 c 115 g 90 t

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Db	397	GTGATCTCAACICACTGCAAGCTCTGCTCCCGGGTTCAAGCGATTCTCCTGCCICAGCC	338
QY	1075	TCCTGA-----GATACAGGCGCGGCGACACATCTCGCTAAATTTTTGTATTTTAG	1127
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QY	1188	TGCGCACTCTGGCTTGGCAAAAGTCTGGGATTACAGGCATGAGCCACTCGGCCAGCTCA	1247
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QY	1248	GATCTCA	1253
Db	157	TCTTCA	152

[illegible]

Journal
COMMENT

unpublished (1996)
Other_GSSS: CITHI-El-2509o10.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
7912 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/human/bac_end_search.html.
Seq primer: M13 2;
Class: BAC ends.

FEATURES
source

Location/Qualifiers
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Caltech Human BAC Library D"

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QY 1016 TGATCTGACCTACTGTAACCTCTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCT 1075
DB 370 CGATCTCGCTCTCACTCAACCTCTGCTCCAGGTTCAAGTGATTCTCTGCTCAGCT 311
QY 1076 CTGCA-----CATACAGGCGCCGCCACCATCTAGCTAAATTCTGATTTAG 1127
DB 310 CCGAGTAATCTAGACTACAGGCAACCGCCAGGCTGCTAAATTCTGATTTAG 25;
QY 1128 TAAGACTGGGTTTCATCATCTGGCCAGGTTGGTTTGGAACTCTGAGCTGAGTGA 1187
DB 250 TAGACAGGGGTTTCAACATCTTCTGTCAGGCTGCTCTGAACTCTGATCTAGCGATC 191
QY 1188 TGTTCACCTTGCTCCCAAGCTGCTGATTAAGCAATGAGGCTATGTAAGAG 1247
DB 190 CAGCTGCTGCTGCTCCCAAGCTGCTGATTAAGCAATGAGGCTATGTAAGCAAT 191
QY 1248 GATGATCCCTTTCTAAGGCAACAGCTCTATGCTGTAAGAGGCTATGTAAGAG 1306
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RESULT 6
LOCUS A0418551
DEFINITION RP11-11-203K4.TJ RP11-11 Homo sapiens cDNA clone
A0418551
VERSION A0418551.1 GI:4476275
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 544)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.D.
Use of BAC End Sequences from library RP11-11 for Sequence Ready
Map Building
Unpublished (1997)
Other GSSs: RP11-11-203K4.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hwe@tigr.org
Clones are derived from the human BAC library RP11-11. For BAC
library availability, please contact Pieter de Jong
(peter.dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/education) or from
Research Genet cs (info@resgen.com) BAC end search page:

http://www.tigr.org/ldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1. .544
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RP11-11-203K4"
/sex="male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"

BASE COUNT 207 a 86 c 165 g 85 t

ORIGIN

Query Match 6.8%; Score 218.6; DB 17; Length 544;
Best Local Similarity 70.5%; Pred. No. 3.3e-15;
Matches 306; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

QY 353 CCATTTTAAAGTAGAAGAAAGCGCGGCGACAAATGGCTGTATCCAGCACT 412
DB 81 CCATTAAGAAATAAAGGAAGAGCGCCAGGAGTAGTGGCTATGCTGTAATTCGAGCACT 140
QY 413 TTGGAGGCTCAGCGGAGGAGTGGCTTGGAGCTCCAGAGTTTTCAGACCAAGCTGGATAAC 472
DB 141 TTGGAGGCTCAGCGGAGGAGTGGCTTGGAGCTCCAGAGTTTTCAGACCAAGCTGGATAAC 200
QY 473 ATGCCAAACCCCTGTCTCTACAAAAAATACAAAAATAGATGGGTGGGATGCA 532
DB 201 ATGCTGAACCCCTGTCTCTATAAAA---ATACAAAAATAGCGAGCGGTGGTGGCA 257
QY 533 CCTGTGTCAGCTACTTGGAGGCTAAGTGGAGGATCGCTTGGAGCCAGGAGTCA 592
DB 258 CCTGTATCCAGCTTCTCAGGAAGCTGAGGAGGAGGATCCTTACCTGGGAGCA 317
QY 593 AGTCTACACTGAGCTATGATTTGGATCCTCCTCAGCTGGGTAGACAGAGCAAGACC 652
DB 318 AGTTGAGTGGCTGAGGAGATGTGCCACTGCTCAGCTGCGCTGCAACAAGCAAGACTC 377
QY 653 CTGTCTCAAAAAAAGAAATCAAGAAAGAAAGAAAGAGAGAGAGAGAGATGAGG 712
DB 378 CAAAAAGAAAAAAGAAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 437
QY 713 GATGAGGAGAGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 772
DB 438 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497
QY 773 AAAAACAAGATGAA 786
DB 498 AAGAGCAGCAGAA 511

RESULT 7
LOCUS BQ775487
DEFINITION BQ775487 620 bp mRNA linear EST 26-JUL-2002
UT-H-FH0-bc1-1-24-0-UI.s1 NCI-CCAP_FH0 Homo sapiens cDNA clone
UT-H-FH0-bc1-1-24-0-UI.3', mRNA sequence.
ACCESSION BQ775487
VERSION BQ775487.1 GI:21983963
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 620)
NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ccap@tmail.nih.gov

Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 17-306, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA-Yes

FEATURES
Source Location/Qualifiers
1..620
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-H-FHO-bc1-1-24-0-01"
/clone_lib="NCL CGAP-FHO"
/tissue_type="Human Chondrosarcoma Cell Line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Bone; Vector: p773-Pac (Plasmid) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCL CGAP-FHO is a cDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line. The library was constructed according to Bonaldi, Benson and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCGGC. The cell line was provided by Dr. James Martin from University of Iowa
TAG LIB=UI-H-FHO
TAG TISSUE=Human Chondrosarcoma Cell Line CSE - Grade 1 Chondrosarcoma
TAG_SEQ=AGAATCGGC"

BASE COUNT 118 a 154 c 159 g 185 t 4 others
Query Match 6.7%; Score 217; DB 14; Length 620;
Best Local Similarity 85.6%; Pred No. 4.4e-15;
Matches 256; Conservative 0; Mismatches 15; Indels 8; Gaps 1;
QY 954 TTCCTTTTATTTTTCAGACGAGTCTTCCTTGTGTAATGAGTGGATGACATGG 1013
DB 7 TTTTTCCTTGTTCAGATGAGTCTTCCTTGTGTAATGAGTGGATGACATGG 66
QY 1014 CATGATCTGACATCACTGTAACCTTCGCTCCGAGTTCAGAGCACTCCGCTGAGG 1073
DB 67 CATGATCTGCTGCTGACATCACTGTAACCTTCGCTCCGAGTTCAGAGCACTCCGCTGAGG 126
QY 1074 CTC-----CTGAGATAACAGGGGGGGGGGACCAATGATGATTAATTTT 1125
DB 127 CTCGATGATGCTGAGATACAGGGGGGGGGGACCAATGATGATTAATTTT 185
QY 1126 AGTAAGACATGGGTTTCATCATGTTGGCCAGGTTGGTTTCAGAGTTCATGATGAGGCA 1185
DB 187 AGTAGAGTGGGGTTTCATCATGTTGGCCAGGTTGGTTTCAGAGTTCATGATGAGGCA 246
QY 1186 GTGCTCAGCTTGGGCTCCCAAGTGTGGGATACAGGCAATGAGTATTCGCTGAGG 1244
DB 247 TCCTGCTACCTTGGCTCCCAAGTGTGGGATACAGGCAATGAGTATTCGCTGAGG 305
RESULT 8
BM803650
LOCUS BM803650 990 bp mRNA linear EST 05-MAR-2002
DEFINITION AGENCOURT_6439541 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5520297
ACCESSION 5', mRNA sequence.
VERSION BM803650
BM803650.1 GI:19120473

KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens
REFERENCE Eukaryota: Metazoa, Chordata: Craniata; Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 990)
NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cyapts@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12184 row: b column: 10
High quality sequence stop: 632.

FEATURES
Source Location/Qualifiers
1..990
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5520297"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="PH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
BASE COUNT 170 a 277 c 268 g 275 t

Query Match 6.7%; Score 216.4; DB 14; Length 990;
Best Local Similarity 80.7%; Pred. No. 3.5e-15;
Matches 248; Conservative 0; Mismatches 56; Indels 8; Gaps 1;
QY 942 GAGATCATCCCTTCTTTTATTTTCTTGACACGAGTCTTGTCTGTCTACAGCT 1001
DB 15 GAGCGCGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 74
QY 1002 GGAGTCGATGGCATCATCTGACCTGACTGCTTAACTCTGCTCCCGGTTCAAGCGATC 1061
DB 75 GGAGTCGATGGCATCATCTGACCTGACTGCTTAACTCTGCTCCCGGTTCAAGCGATC 134
QY 1062 TCCTGCTCAGCTCTC-----CTGAGATAACAGCGCGCGCCACCATCTGCTCTAAT 1113
DB 135 TCCTGCTCAGCTCTC-----CTGAGATAACAGCGCGCGCCACCATCTGCTCTAAT 194
QY 1114 TTTTGATTTTAAAGAACTGGTTTCATCATGTTGGCCAGGTTGGTTTCGAATCCT 1173
DB 195 TTTTGATTTTAAAGAACTGGTTTCATCATGTTGGCCAGGTTGGTTTCGAATCCT 254
QY 1174 GAGTCGATGGCATCATCTGACCTGACTGCTTAACTCTGCTCCCGGTTCAAGCGATC 1233
DB 255 GAGTCGATGGCATCATCTGACCTGACTGCTTAACTCTGCTCCCGGTTCAAGCGATC 314
QY 1234 CTGCGGCCAGTTCAGATGATCCCTTTCTTAAG 1265
DB 315 CCGGCCAGTTCAGATGATCCCTTTCTTAAG 346

RESULT 9
AQ475181/c
LOCUS AQ475181 715 bp DNA linear GSS 23-APR-1999
DEFINITION CITBI-E: 2589H9.TF CITBI-E1 Homo sapiens genomic clone 2589B9, DNA sequence.
ACCESSION AQ475181
VERSION AQ475181.1 GI:4657300
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
 Mammalia: Eutheria; Primates; Catarrhini; Homidae: Homo.
 1 (bases 1 to 719)
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M., and
 Venter, J.C.
 Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other_GSSs: CITBI-E1-2589B9.TR
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 938 0200
 Fax: 301 938 0208
 Email: hbe@tigr.org
 Clones are available from Research Genetics (http://resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humden/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES source

Location/Qualifiers
 1..719
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2589B9"
 /clone_lib="CITBI-E1"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"

BASE COUNT 228 a 162 c 180 g 149 t
 ORIGIN

Query Match: 6.7%; Score 215.2; DB 17; Length 719;
 Rest Local Similarity 75.7%; Pred. No. 6.1e-15;
 Matches 283; Conservative 0; Mismatches 83; Indels 8; Gaps 1;

QY 893 TGGCTCTCTGGGCTTGGGCTTTAGAACCTCATCTCTGGCTTTCTGAGATCCATCC 952
 DB 443 TCCATCTCAGAGCCCTCCGAGCACTGGTTATCTCTATAAATGATCCATCTTT 372
 QY 953 CTCTCTTTTATTTCTGACACGAGTCTTCTCTGCTGCTGACTAGACTGACGACG 1012
 DB 111 312
 DB 371 TTTCTTTTCTTTTGGACACAGATCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 312
 QY 1013 ATATGATCTGACCTGACTGATACCTCTGCTCTGCTGCTGCTGCTGCTGCTGCT 1072
 DB 111 252
 DB 311 GATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 252
 QY 1073 CT 1124
 DB 251 CT 192
 QY 1125 TAGTAAGACTGGTTTCTATCATGTGGCAGGTGGTTTCTGAAATCTGAGCTGAGGTG 1184
 DB 111 132
 DB 191 TAGTAAGACTGGTTTCTATCATGTGGCAGGTGGTTTCTGAAATCTGAGCTGAGGTG 132
 QY 1185 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1244
 DB 131 ATCT 72
 QY 1245 TACATCTCATCTCT 1258
 DB 71 CTGATCTCATCTCT 58

RESULT 10
 BM991096/c
 LOCUS
 DEFINITION
 IMAGE:5862692 3', mRNA sequence.
 ACCESSION
 BM991096

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BM991096.1 GI:19710485
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
 Mammalia: Eutheria; Primates; Catarrhini; Homidae: Homo.
 1 (bases 1 to 423)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs.rem.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 1-21, >AT-rich; Low_complexity 77-366, >ALU
 Seq primer: M13 FORWARD
 POLYA: Yes.

FEATURES source

Location/Qualifiers
 1..423
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5862692"
 /clone_lib="NCI-CGAP_D10"
 /tissue_type="Lung Focal Fibrosis"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI-CGAP_D10 is a cDNA library containing the following
 tissue(s): A pool of Lung Focal Fibrosis. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dr primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 ATACCGGGTC.

TAG_L1B-01-H-D10
 TAG_TISSUE-Lung with fibrosis
 TAG_SEQ-ATACCGGGTC"

BASE COUNT 111 a 100 c 111 g 101 t
 ORIGIN

Query Match: 6.6%; Score 214.4; DB 14; Length 423;
 Best Local Similarity 76.8%; Pred. No. 1.1e-14;
 Matches 278; Conservative 0; Mismatches 76; Indels 8; Gaps 1;

QY 911 GGCTTTAGAAAGCTCATCTCTGGCTTTCTGAGATCCATCTCTTTCTTTTCTTTCT 970
 DB 419 GAGGTTTACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 971 TGACAGGAGCTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1030
 DB 359 TGACAGGAGCTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 1031 GTAACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1082
 DB 299 GCAACCTCCACCTCCCGGTTCAAGTGATCTCTCTCTGCTGCTGCTGCTGCTGCT 240
 QY 1083 TAACAGCGCGCGCCACCACATCTGCTAAATTTTGTATTTTGTAAAGACTGGGTTC 1142
 DB 239 TTACAGCGCGCGCCACCACCGCGCTAAATTTTGTATTTTGTAAAGACTGGGTTC 180
 QY 1143 ATCATGTGGCAGGTTGTTTTCGAACCTCTGACCTGAGGTGAGCTGCCACCTTGGCT 1202


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/cell_type="Sperm"
/Note="Vector: pBeloBAC11; Site_1: Hind.II; Site_2:
Hind.III."
BASE COUNT 90 a 160 c 102 g 140 t 1 others 1
ORIGIN
Query Match 6.6%; Score 213.2; DB 17; Length 622;
Best Local Similarity 79.9%; Pred. No. 1.4e-14;
Matches 267; Conservative 0; Mismatches 58; Indels 9; Gaps 1;
QY 946 TCATCGCTTCTTTTATTTCTTGACACGGAGCTTCCTCTCTCACTTAACTGAG 10-5
DB 32 TCCTCTCTTTTTTTTTTTTGGACGGTGTCTCTCTCACTTAACTGAG 91
QY 1006 TGGAGTGGATGATCTCGACTCACTGTAACCTTCTGCTCCGAGGTTCAGAGATCTCT 1065
DB 92 TGAATGGGTGATCTCAGCTCACTGCAACCTCTGCTCCGAGGTTCAGATCTCTCT 151
QY 1066 GCCTACGCTTCTTCTGAG-----ATAACAGGCGCGCGCCACGACATCTGCTAAATTT 1116
DB 152 GCCTACGCTTCTTCTGAGTATCTGGGATTACAGCGCGCGCCACGACGACGCTAAATTT 211
QY 1117 TGATTTTAGTAAGACTGGGTTTCATCATGTTCGCGAGGTTCGTAATCTCTGAC 1176
DB 212 TGTATTTTAGTAGGACGGGATTTCACCATCTTGGCGAGGTTCGTAATCTCTGAC 271
QY 1177 CTGAGTGAGCTGCCACCTTGGCTCCGAAATGTCGAGGATTCAGGACGACGACATG 1246
DB 272 CTGAGTGAGCTGCCCGCTGAGCTCCGAAATGTCGAGGATTCAGGACGACGACATG 341
QY 1237 GCGCACTCAGATCCCTCTTCTAAAGGCAA 1270
DB 132 GCGCGCGCTCAGCCCTAACTTCAATGACAA 165

RESULT 15
A0537948/G
LOCUS
DEFINITION
A0537948
VERSION
A0537948.1 GI:4849638
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Zhao,S., Adams,M.D., Nierman,W., Mulek,J., de Jong,P. and Venter
,J.C.
Use of BAC End Sequences from Library RPC1-11 for Sequence Ready
Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1..622
/organism="Homo sapiens"
/db_xref="GDH:7623762"
/db_xref="taxon:9606"
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/clone="RPC1-11-323E19"
/clone.lib="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/Note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC library"
BASE COUNT 123 a 178 c 103 g 218 t
ORIGIN
Query Match 6.6%; Score 213.2; DB 17; Length 622;
Best Local Similarity 73.2%; Pred. No. 1.1e-14;
Matches 300; Conservative 0; Mismatches 108; Indels 2; Gaps 2;
QY 361 AAGATGAAGAAACAGCGCGGACCAATGGCTAATGCGCTGTATCCGACACTTTGGGAGG 420
DB 462 AAAATATTTCATCAGCGCGGACAGTGGCTACACCTGTATATCGCAGCACTTTGGGAGG 403
QY 421 CTGAGCGCCAGAGATTCGCTTGAGCTCCAGAGTTTGAGACACGAGCTGGATACATGSCAAA 480
DB 402 CCAGGCGAGAGAAATGCTTGAGCTCCAGAGTTTCAAGACACGCTGGGCAACATGGTGAG 343
QY 481 ACCCTGCTCTTACAAAATAATACAAAATTAGATGGGTGGTGGCATGCACTGTGGT 540
DB 342 ACCTCATCACTAAAAATAATTTTAAAAAATAGCCAGGCATGGTGGCATGGCTGTCT 283
QY 541 CCCAGCTACTTGGAGGCTAAGTGGGAGGATCGCTTCAGCCCGAGGGAGTCAAGTCTACA 600
DB 282 CCAGCTACTTCAAGAGGCTGAGATGAGAGGATCAGCTGAGCTGAGGCGGCTGAGGCTGTA 223
QY 601 CTGAGCGCATGTTGATCACTCACTCCAGCTGGGTAGACAGAGCAAGACCTTCTCTCA 660
DB 222 GTCAGCCAAAGATCATGCCATCCATTCAGGCTTGGT-GACAGAATAAGACCTCTCTTA 164
QY 661 AAAAAAGAAATGAA-AGAGAAGAAAGAAAGAGAGAGAGAGAGATGAGGGGAGGAG 719
DB 163 AGAAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 104
QY 720 GAGAGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 769
DB 103 GAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 54

Search completed: May 9, 2003, 17:54:54
Job time : 5438.82 secs
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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 12:19:31 ; Search time 174.597 Seconds
(without alignments)
5671.939 Million cell updates/sec

Title: US-09-846-456-1
Perfect score: 3231
Sequence: 1 acaggcaggtgcagggtg.....gccccacatcccaactt 3231

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTOUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297.6	9.2	43950	US-09-735-934A-3	Sequence 3, Appl
2	292.6	9.1	162450	US-09-345-882-1	Sequence 1, Appl
3	285.4	8.8	20674	US-09-641-638-651	Sequence 651, App
4	278.2	8.6	84495	US-09-797-906-3	Sequence 3, Appl
5	277.2	8.6	84495	US-09-797-906-3	Sequence 3, Appl
6	271.8	8.4	15297	US-09-817-180-3	Sequence 3, Appl
7	271.6	8.4	162450	US-09-345-882-1	Sequence 1, Appl
8	271.2	8.4	43950	US-09-735-934A-3	Sequence 3, Appl
9	269.4	8.3	28720	US-09-341-587-7	Sequence 7, Appl
10	268	8.3	38564	US-09-734-673-3	Sequence 3, Appl
11	267.6	8.3	81001	US-09-750-580-1	Sequence 1, Appl
12	267	8.3	45716	US-08-965-048-5	Sequence 5, Appl
13	267	8.3	45989	US-08-965-048-6	Sequence 6, Appl
14	261.6	8.1	18073	US-09-078-294-12	Sequence 12, Appl
15	257.8	8.0	246240	US-08-724-394A-20	Sequence 20, Appl
16	257.8	8.0	246240	US-08-724-394A-21	Sequence 21, Appl
17	257.8	8.0	246240	US-08-724-394A-22	Sequence 22, Appl
18	253.6	7.8	20674	US-09-641-638-651	Sequence 651, App
19	253	7.8	6719	US-09-740-235-16	Sequence 36, Appl
20	253	7.8	8021	US-09-740-235-2	Sequence 2, Appl
21	253	7.8	162450	US-08-724-394A-20	Sequence 20, Appl
22	253	7.8	246240	US-08-724-394A-21	Sequence 21, Appl
23	253	7.8	246240	US-08-724-394A-22	Sequence 22, Appl
24	252.2	7.8	35060	US-08-814-095-7	Sequence 7, Appl
25	251.4	7.8	7680	US-09-210-748A-3	Sequence 3, Appl
26	250.2	7.7	21234	US-09-810-671-3	Sequence 3, Appl
27	249.6	7.7	81001	US-09-750-580-1	Sequence 1, Appl

28	246.4	7.6	38564	4	US-09-734-673-3	Sequence 3, Appl
29	243.4	7.5	7210	2	US-08-257-963B-10	Sequence 10, Appl
30	243.4	7.5	7210	4	US-08-367-841A-10	Sequence 10, Appl
31	243.4	7.5	7210	5	PCT-US95-07201-12	Sequence 43, Appl
32	243.4	7.5	22481	4	US-08-367-841A-43	Sequence 43, Appl
33	243.4	7.5	22481	5	PCT-US95-07201-43	Sequence 43, Appl
34	243.4	7.5	22484	4	US-09-875-223-2	Sequence 2, Appl
35	243.4	7.5	176373	3	US-09-128-155-17	Sequence 17, Appl
36	242.4	7.5	72604	4	US-09-268-992-7	Sequence 7, Appl
37	242.4	7.5	72604	4	US-09-657-474-7	Sequence 7, Appl
38	242	7.5	21234	4	US-09-810-671-3	Sequence 3, Appl
39	240.2	7.4	14796	4	US-08-975-080-35	Sequence 35, Appl
40	240.2	7.4	14796	4	US-09-630-706-10	Sequence 10, Appl
41	240.2	7.4	14796	4	US-09-496-694B-3	Sequence 3, Appl
42	240	7.4	35060	3	US-08-814-095-7	Sequence 7, Appl
43	239	7.4	3507	1	US-08-832-883-67	Sequence 67, Appl
44	239	7.4	3507	2	US-08-832-877-67	Sequence 67, Appl
45	238.8	7.4	87350	3	US-08-781-891-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-735-934A-3
; Sequence 3, Application US/09735934A
; Patent No. 6372468
; GENERAL INFORMATION:
; APPLICANT: LI, JIAYIN et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000851
; CURRENT APPLICATION NUMBER: US/09/735,934A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 43950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-934A-3

Query Match	9.2%	Score	297.6;	DB 4;	Length	43950;			
Best Local Similarity	62.5%;	Pred. No.	1.6e-63;						
Matches	554;	Conservative	0;	Mismatches	314;	Indels	18;	Gaps	5;
QY	375	GGCCGGGCAACAATGGCTTAATGCCGTGTAATCCACGACCTTTGGGAGGCTGAGGCACAGGA	434						
Db	37664	GGCCAGGTGGTCTCTCATGCTGTAATCCACGACCTTTGGGAGGCTGAGGCAGGAGGA	37723						
QY	435	TCGCTTGAGCTCCAGAGTTTGAGACCAGCCTGGATACATGGCAAAACCCCTGCTCTACA	494						
Db	37724	ACACCTGAGCTCAGGAGCTTTGGGACCAACGCTGGCTGATGGTGAATGCTGCTCTAC-	37782						
QY	495	AAAAAATACAAAAATTAGATGGTGGTGGGCATGCACCTGTGGTCCGAGCTACTTGGG	554						
Db	37783	-TAAAAATACAAAAATTAGCAGGCACTGGTGGGGTCCCTGTGATCCAGCTATTCCGG	37841						
QY	555	AGGCTAAGTGGGAGGATCCCTTGAGCCAGGGAGTCAAGTCTACACTGAGCCATGATTG	614						
Db	37842	AGGCTAGGCAAGAGAAATTCCTTGAACCCGGGAGGAGGTTGCAGTGAGCCAAAGTCA	37901						
QY	615	GATCACTGCACTCCAGCTGGGTAGACAGAGCAAGACCCCTGCTCAAAAAAAGAAATGA	674						
Db	37902	CGTACTGCACTCCAGCTGGG-CGACAGAGCGAGACTCCGTCTCAAAAAAATAAACA	37960						
QY	675	A-----AGAGAAGAAAGAAAGAGGAGAGAGAGATGAGGGGAGGAGGGGGGG	728						
Db	37961	ATGAAGGAAAGGTAGGCATACACCATACTGCTGCCAGCTACCGCACTCAGCACCCTC	38020						
QY	729	GAGGAAGGAAGGAGGAGGAAAGGAAAAAAGATGAAAAAAGAAAAAAGATGAAC	788						


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DB 28132 ATTGAGGACACCCGCCACCCACCCGCTGTAATTTTGTATTTTGTGACACATCGGCTT 28191
OY 1141 TCATCATGTGTCAGGTTGTTTTCGAACCTGCTGACCTGAGGTGAGTACGTAATTTGTC 1200
DB 28192 TTGCAAGTGGCCAGGTTGTTCTGGACTGCTGACCTCAAGGCTTGCAGGCTGAC 28251
OY 1201 CTGCCAAAGTGTGGGATTACAGGCATGAGGCACCTGCTGCTGAGTACATGATGCTTT 1240
DB 28252 CTGCAAGTGTGGGATTACAGGTATGAGGCACTGCTGCTGAGTACAGGCTGCTTTC 28311
OY 1261 CTAAAGGCAACAGTCCATGG 1281
DB 28312 TGACAGTCCACACCGCTTATTTG 28332

RESULT 3
US-09-641-638-651/c
: Sequence: 651, Application US/09641638
: Patent No. 6412646
: GENERAL INFORMATION:
: APPLICANT: Blumenfeld, Marta
: APPLICANT: Bouqueleret, Lydie
: APPLICANT: Chumakov, Ilya
: APPLICANT: Cohen, Annick
: TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
: FILE REFERENCE: GENSET.051CPI
: CURRENT APPLICATION NUMBER: US/09/641.638
: PRIOR FILING DATE: 2000-08-16
: PRIOR APPLICATION NUMBER: US 09/502.330
: PRIOR FILING DATE: 2000-02-11
: PRIOR APPLICATION NUMBER: US 60/133.206
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: US 09/275.267
: PRIOR FILING DATE: 1999-03-23
: PRIOR APPLICATION NUMBER: US 60/119.917
: PRIOR FILING DATE: 1999-02-12
: NUMBER OF SEQ ID NOS: 1304
: SOFTWARE: Patent.pm
: SEQ ID NO: 651
: LENGTH: 20674
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1125..3123
: OTHER INFORMATION: 5' regulatory region
: NAME/KEY: exon
: LOCATION: 3124..3297
: OTHER INFORMATION: exon 1
: NAME/KEY: exon
: LOCATION: 3471..4072
: OTHER INFORMATION: exon 2
: NAME/KEY: exon
: LOCATION: 5552..5633
: OTHER INFORMATION: exon 3
: NAME/KEY: exon
: LOCATION: 5758..5880
: OTHER INFORMATION: exon 4
: NAME/KEY: exon
: LOCATION: 5996..6099
: OTHER INFORMATION: exon 5
: NAME/KEY: exon
: LOCATION: 6349..6509
: OTHER INFORMATION: exon 6
: NAME/KEY: exon
: LOCATION: 7379..7522
: OTHER INFORMATION: exon 7
: NAME/KEY: exon
: LOCATION: 8645..8854
: OTHER INFORMATION: exon 8
: NAME/KEY: exon
: LOCATION: 12254..12340
: OTHER INFORMATION: 3' regulatory region
: NAME/KEY: exon 9
: LOCATION: 12854..13023
: OTHER INFORMATION: exon 10
: NAME/KEY: exon
: LOCATION: 13308..13429
: OTHER INFORMATION: exon 11
: NAME/KEY: exon
: LOCATION: 16567..16667
: OTHER INFORMATION: exon 12
: NAME/KEY: exon
: LOCATION: 16775..16945
: OTHER INFORMATION: exon 13
: NAME/KEY: exon
: LOCATION: 17063..17594
: OTHER INFORMATION: exon 14
: NAME/KEY: misc_feature
: LOCATION: 17555..20674
: OTHER INFORMATION: 3' regulatory region
: NAME/KEY: allele
: LOCATION: 1128
: OTHER INFORMATION: 10-508-191 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 1182
: OTHER INFORMATION: 10-508-245 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 1359
: OTHER INFORMATION: 10-509-284 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 1570
: OTHER INFORMATION: 10-509-295 : deletion of C
: NAME/KEY: allele
: LOCATION: 1827
: OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTT
: NAME/KEY: allele
: LOCATION: 2048
: OTHER INFORMATION: 10-511-62 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 2323
: OTHER INFORMATION: 10-511-337 : insertion of T
: NAME/KEY: allele
: LOCATION: 2341
: OTHER INFORMATION: 10-512-36 : polymorphic base G or C
: NAME/KEY: allele
: LOCATION: 2623
: OTHER INFORMATION: 10-512-318 : polymorphic base A or G
: NAME/KEY: allele
: LOCATION: 2832
: OTHER INFORMATION: 10-513-250 : polymorphic base A or G
: NAME/KEY: allele
: LOCATION: 2844
: OTHER INFORMATION: 10-513-262 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 2934
: OTHER INFORMATION: 10-513-352 : polymorphic base A or G
: NAME/KEY: allele
: LOCATION: 2947
: OTHER INFORMATION: 10-513-355 : polymorphic base A or G
: NAME/KEY: allele
: LOCATION: 3802
: OTHER INFORMATION: 12-206-81 : polymorphic base A or G
: NAME/KEY: allele
: LOCATION: 4062
: OTHER INFORMATION: 10-543-241 : deletion of C
: NAME/KEY: allele
: LOCATION: 4088
: OTHER INFORMATION: 12-206-356 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 4109
: OTHER INFORMATION: 10-543-278 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 4370
: OTHER INFORMATION: 10-543-349 : polymorphic base G or T
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NAME/KEY: allele
 LOCATION: 5903 : polymorphic base A or G
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 NAME/KEY: allele
 LOCATION: 6019 : polymorphic base A or G
 OTHER INFORMATION: 10-346-141 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 6141 : polymorphic base G or C
 OTHER INFORMATION: 10-346-263 : polymorphic base G or C
 NAME/KEY: allele
 LOCATION: 6183 : polymorphic base C or T
 OTHER INFORMATION: 10-346-305 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 6338 : polymorphic base A or G
 OTHER INFORMATION: 10-347-74 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 6475 : polymorphic base G or C
 OTHER INFORMATION: 10-347-111 : polymorphic base G or C
 NAME/KEY: allele
 LOCATION: 6429 : polymorphic base C or T
 OTHER INFORMATION: 10-347-165 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 6467 : polymorphic base A or G
 OTHER INFORMATION: 10-347-203 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 6484 : polymorphic base A or G
 OTHER INFORMATION: 10-347-220 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 6534 : polymorphic base A or T
 OTHER INFORMATION: 10-347-271 : polymorphic base A or T
 NAME/KEY: allele
 LOCATION: 6611 : polymorphic base A or G
 OTHER INFORMATION: 10-347-348 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 7668 : polymorphic base A or G
 OTHER INFORMATION: 10-348-391 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 8608 : polymorphic base C or T
 OTHER INFORMATION: 10-349-47 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 8658 : polymorphic base A or G
 OTHER INFORMATION: 10-349-97 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 8703 : polymorphic base G or C
 OTHER INFORMATION: 10-349-142 : polymorphic base G or C
 NAME/KEY: allele
 LOCATION: 8777 : polymorphic base G or T
 OTHER INFORMATION: 10-349-216 : deletion of CIG
 NAME/KEY: allele
 LOCATION: 8785 : polymorphic base C or T
 OTHER INFORMATION: 10-349-224 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 8926 : polymorphic base C or T
 OTHER INFORMATION: 10-349-368 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 12171 : polymorphic base C or T
 OTHER INFORMATION: 10-350-72 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 12429 : polymorphic base C or T
 OTHER INFORMATION: 10-350-332 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 13341 : polymorphic base A or G
 OTHER INFORMATION: 10-507-170 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 13492 : polymorphic base A or G
 OTHER INFORMATION: 10-507-321 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 13524 : polymorphic base C or T
 OTHER INFORMATION: 10-507-353 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 13535

Query Match

8.8% Score 285.4 DB 4 Length 20674

Best Local Similarity 62.7%; Pred. No. 1.2e-60;
 Matches 556; Conservative 0; Mismatches 301; Indels 30; Gaps 6;
 QY 357 TTATAAGATCAAGAACAGCCGGGCACAAATGCTAATGCTTATCCACGACCTTTGG 416
 DB 16196 TTAAGATGAGGATGCGCGCGCGCGCTGCTACCGCTGTAGTCCAGCATGGG 16137
 QY 417 GAGGTCAGGCTCAGAGATGCTTGAGCTCCAGAGTTTGAGACCGCTGGAIAACATGG 476
 DB 16136 GAGGCCAAGATGGCGGATCAC--GAGGTCAGGAGATCGAGACCATCTCGCTGCTAACACGG 16079
 QY 477 CAAACGCTTCTCTACAAAAAATACAAAAATAGATGGTGTGGTGGCATGCACCTG 536
 DB 16078 TGAACGCGCTCTCTACTAAAAATA--CGAAAGATTAGCCAGGTGGTGGCGGSCACCTG 16020
 QY 537 TGGTCAGTACTTGGGAGGCTTAAGGTCGGAGGATCGCTTCAGCCAGGAGTCAAGTC 596
 DB 16019 TAGTCCAGGTACTCGGAGGCTGAGCGAGGAGATGGCGTGAACCCGGGAGAGAGCT 15960
 QY 597 TACACGAGGCTATGATGATCACTGCTCAGCTCCAGCTGGGTAGACAGCAGACGCTGT 656
 DB 15959 TCGAGCGAGCTGAGATCCCGCCACTGCTCAGCTCCAGCTGGG--CGACACACGAGAGCTCTGT 15901
 QY 657 CTCAAAAAAGAAATSAAGAGA-----AAGAAAGAAAGAGAGAGAGA 702
 DB 15900 CTCAAAAAAGAAATSAAGAGA-----AAGAAAGAAAGAGAGAGAGA 15841
 QY 703 GGAGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 762
 DB 15840 GCACCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15781
 QY 763 GAAAAAGAAAAAACAGATGAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 822
 DB 15780 TCTCTATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTT 15721
 QY 823 TGTGGTGTGCAAGCTTTGACCCCAAAACCAATTTATTGACCAAGGTTATCTTCACTGA 882
 DB 15720 ACAGATTACAGCTCTGGTTATATATGTTGGGATAGTCAATGATTCAGTGTCTAC 15661
 QY 883 GGCAGGGGTTCGCTCTCTCGGGGCTTGGGTTTAGAAGGTCATCTCTGCGCTT---- 938
 DB 15660 AGCTGAGAGGGGCTCGACAAAGGTTATCTCAGTCCACTCATTTTTCAGTGGATATGGG 15601
 QY 939 TCTGAGATCACT 998
 DB 15600 GCTCAGAGAGGAGTATCT 15541
 QY 999 GCTGAGTGTGAGTGGGATGCTGAGTCACTGTAACCTCTGCTCCCGGGTTCAGGCA 1058
 DB 15540 GCTGAGTGTGAGTGGGATGCTGAGTCACTGTAACCTCTGCTCCCGGGTTCAGGCA 15491
 QY 1059 TTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
 DB 15480 TTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15421
 QY 1111 AATTTTGTATTTTAGTAAGAGTGGTTCATCATGTGTTGCCAGGTTGGTTTTCGAAT 1170
 DB 15420 AATTTTGTATTTTAGTAAGAGTGGTTCATCATGTGTTGCCAGGTTGGTTTTCGAAT 15361
 QY 1171 CTTGACCTGAGTGAGCTGCCACCTTGGCTCCCAAGAGTGTGGGA 1217
 DB 15360 CTTGACCTGAGTGAGCTGCCACCTTGGCTCCCAAGAGTGTGGGA 15314

RESULT 4

US-09-797-906-3
 : Sequence 3, Application US/09797906
 : Patent No. 6329188
 : GENERAL INFORMATION:
 : APPLICANT: Zhanhe YAN, Karen A. KEICHUM, Valentina DIFRANCESCO, Ellen M. BEAS
 : TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
 : TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, A
 : TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001151CIP
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 84495
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match 8.6%; Score 278.2; DB 4; Length 84495;
Best Local Similarity 61.5%; Pred. No. 1.4e-58;
Matches 553; Conservative 0; Mismatches 328; Indels 18; Gaps 5;
DB 360 AAGATGAAGAAACAGCGCGGCACATGCTTAATGGCTGCTTAATCTAGCACTTGGGAG 419
DB 34817 AAAATTGACTTGGAGCGCGCGGCTGGCTCAGCGCTGTAATATCAACAGCTGGGAG 3476
QY 420 GTTGAGGCGAGAGGATCGCTGAGCTCCAGAGATTGTAATAGCTGATATATAGTAA 474
DB 44877 GCGGAGCGAGGTGGATCAC--GAGGTGAGCGGATGAGAGATATGATATAGATGTA 34934
QY 480 AATCTCTCTCTACAAAAAATACAAAAATGAGATGAGTGTGAGTGTGAGTGTGAG 549
DB 34545 AATCTCTCTCTACTAAAA--ATAAAAATAGCTGAGTGTGAGTGTGAGTGTGAGT 34590
QY 540 TCTGAGCTACTTGGAGGCTAAGTGTGAGGATGCTTTGAGTAACTTGAAGTAACTGAG 599
DB 34991 TCTGAGCTACTTGGAGGCTGAGGAGGAGATGCTGAGTAACTTGAAGTAACTGAG 35050
QY 600 ATGAGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 659
DB 35051 AAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 35109
QY 660 AAAAAAAGAAATGAAG 719
DB 35110 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 35159
QY 720 GAGGCGGAG 779
DB 35176 GCTAGATTAATATGCTACAGGAATACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 35229
QY 779 AAGATGAACAG 848
DB 35230 ACCAGATACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 35289
QY 835 GAGTCCAAACCCAAATTTATGACCAAGGTTATTTTCTGATGATGATGATGATGATG 899
DB 35286 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 35349
QY 899 CTGCTGGGCTTTGGGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 958
DB 35350 ATAGTAATCAAGTACATAGAGCTTATTGATGATGATGATGATGATGATGATGATGAT 35409
QY 959 TTTTATTTTCTTGGAGGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014
DB 35410 TTTTATTTTCTTGGAGGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 35469
QY 1019 TCTGAGCTACTTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
DB 35470 TCTGAGCTACTTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 35529
QY 1077 -----CTGAGATACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 35530 AAGTAAGTGGGATTAAGTGGGATTAAGTGGGATTAAGTGGGATTAAGTGGGATTAAGT 35589
QY 1131 AATACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194

DB 35590 AGAGCAAGGTTTCACTACGTGTGGCAGGCTGGTTTCGAATTCCTGACCTCAAGTGATGT 35649
QY 1189 GCCCAGCTTGGCTCCCAAGAGTCTGGGATTACAGCATGAGCCACTCGCCGACGCTCA 1247
DB 35650 GCTGTCTGGGCTCCCAAGAGTTCAGGAGATTACAGGTGTGAGCCACCGGCGCCCA 35708
RESULT 5
US-09-797-906-3/c
Sequence 3, Application US/09/797906
Patent No. 6429188
GENERAL INFORMATION:
APPLICANT: Zhanqin YAN, Karen A. KETCHUM, Valentina DIFFANCIO, Ellen M. BEA
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
FILE REFERENCE: CL001151CIP
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 84495
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match 8.6%; Score 277.2; DB 4; Length 84495;
Best Local Similarity 61.1%; Pred. No. 2.5e-58;
Matches 556; Conservative 0; Mismatches 338; Indels 16; Gaps 6;
DB 345 TCTTCTCTCATTTTAAAGATGAAGAACAGCGCGGCAATGGCTAATGCTGTATTC 404
DB 35736 TCATAATCTCTTTTAAATTAACAAATGGCTGGCGCGCTCACACC:GTAATC 35677
QY 405 CCAGCACTTGGAGGATGAGCCGAGAGATCGCTTGAGCTCCAGAGTTTTCAGACCAGCC 464
DB 35676 CTGCACTTGGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 35617
QY 465 TGATATATGAGTAAATCTCTCTACAAAAAATACAAAAATAGATGGCTGTGTT 524
DB 35616 TGCCCACTAG:GAAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35557
QY 525 GGTATGAGTGTGAGGAGGCTTACTGAGGAGGCTTACTGAGGAGGAGGAGGAGGAGG 584
DB 35556 GGTATGAGTGTGAGGAGGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 35497
QY 585 GGTATGAGTGTGAGGAGGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 644
DB 35496 GGTATGAGTGTGAGGAGGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 35438
QY 645 GGTATGAGTGTGAGGAGGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 704
DB 35437 GGTATGAGTGTGAGGAGGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 35378
QY 705 AGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 764
DB 35377 AGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 35318
QY 765 AAAAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 824
DB 35317 TTTTCTTCTTCTG:AAATATTTTGAAGAAATGAATTTGCTCCCTAGCACTTCTCACA 35258
QY 825 TGGTGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 884
DB 35257 T-TCTGAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 35199
QY 885 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 944


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: NAME/KEY: allele
: LOCATION: 90842
: OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 93714
: OTHER INFORMATION: 5-128-60 : polymorphic base deletion of G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97122
: OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97152
: OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99098
: OTHER INFORMATION: 5-130-257 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99117
: OTHER INFORMATION: 5-130-276 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 103806
: OTHER INFORMATION: 5-131-395 : polymorphic base A or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106940
: OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108106
: OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108149
: OTHER INFORMATION: 5-135-198 : polymorphic base insertion of G/T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108308
: OTHER INFORMATION: 5-135-357 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108471
: OTHER INFORMATION: 5-136-174 : polymorphic base C or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 134134
: OTHER INFORMATION: 5-140-120 : polymorphic base C or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 134362
: OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
: FEATURE:
: NAME/KEY: allele
: LOCATION: 134374
: OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
: FEATURE:
: NAME/KEY: allele
: LOCATION: 146328
: OTHER INFORMATION: 5-143-84 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 146345
: OTHER INFORMATION: 5-143-101 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 150329
: OTHER INFORMATION: 5-145-24 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 150031
: OTHER INFORMATION: 5-148-352 : polymorphic base G or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 72771..72817
: OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
: FEATURE:
: NAME/KEY: allele
: LOCATION: 72771..72817
: OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
: FEATURE:
: NAME/KEY: allele
: LOCATION: 88050..88096
: OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
: FEATURE:
: NAME/KEY: allele
: LOCATION: 88050..88096
: OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
: FEATURE:
: NAME/KEY: allele
: LOCATION: 90819..90865
: OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
: FEATURE:
: NAME/KEY: allele
: LOCATION: 90819..90865
: OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
: FEATURE:
: NAME/KEY: allele
: LOCATION: 93690..93736
: OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
: FEATURE:
: NAME/KEY: allele
: LOCATION: 93690..93736
: OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97099..97145
: OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97099..97145
: OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97130..97177
: OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97130..97177
: OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99075..99121
: OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99075..99121
: OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99094..99140
: OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99094..99140
: OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
: FEATURE:
: NAME/KEY: allele
: LOCATION: 103783..103828
: OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
: FEATURE:
: NAME/KEY: allele
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Best Local Similarity 62.6%  Pred. No. 5.8e-56;
Matches 581; Conservative 0; Mismatches 309; Indels 38; Gaps 9;
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DB 53994 TTTAAGAGGGAAGCTTGGCGGCACATGCTGCTCAGCGCTGTATATCCAGCAGCTTTGGG 53935

QY 418 AGGCTGAGGCACAGGATCGCTTGAGCTCCAGAGTTTGAGACCGCTGGGATACATGGC 477
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QY 538 GGTCCAGCTACTTGGGAGGCTAAGTGGGAGGATCGCTTGAGCCAGCGGAGTCAAGTCT 597
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 4 MEDIUM TYPE: Floppy disk
 5 COMPUTER: IBM PC compatible
 6 OPERATING SYSTEM: PC-DOS/MS-DOS
 7 SOFTWARE: Patent In Release #1.0, Version #1.30
 8 CURRENT APPLICATION DATA:
 9 APPLICATION NUMBER: US/08/724,394A
 10 FILING DATE: 01-OCT-1996
 11 CLASSIFICATION: 536
 12 ATTORNEY/AGENT INFORMATION:
 13 NAME: Fitts, Renee A.
 14 REGISTRATION NUMBER: 35,136
 15 REFERENCE/DOCKET NUMBER: 017957-000100
 16 TELECOMMUNICATION INFORMATION:
 17 TELEPHONE: 415-576-0200
 18 TELEFAX: 415-576-0300
 19 INFORMATION FOR SEQ ID NO: 20:
 20 SEQUENCE CHARACTERISTICS:
 21 LENGTH: 246240 base pairs
 22 TYPE: nucleic acid
 23 STRANDEDNESS: not relevant
 24 MOLECULE TYPE: cDNA
 25 FEATURE:
 26 NAME/KEY: misc_feature
 27 LOCATION: 1..246240
 28 OTHER INFORMATION: /note "HLA-B*CON1G"
 29 US: 08-724-394A-20

Query Match 8.0% Score 257.8; DB 2: length 246240;
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 QY 436 GCGTTGAGCTCCAGAGTTTGAGACCGAGCTGGATACAGCAAGCAAAATCTGCTACAA 495
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 QY 852 AATTATTGACCAAGGTTATTCTTTGACTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 911
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 Job time : 1489.7 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 11:21:45 ; Search time 461.057 Seconds
(without alignments)
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Perfect score: 3231
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1557708

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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17	2891.4	89.5	2893	9	US-09-846-827-153
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ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNY, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-3

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2281 CAGCTTGTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
2281 CAGCTTGTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
2341 CAGCTCAGCTTACGCTTCTTCAAGAGGAAACAAAAGAGCAACAAATGATTGGCGCTCTCTCA 2400

Db 2341 CACCCAGGCTAGGCTTTGAAAGCAAAACAAAGCAAGACAAATGATTCGGCTCTGA 2400
QY 2401 GGGAGATTAGGCTAGGCTCTCTCCGCCAATCCCTCCCTCCGGCTCAGGAACTAAC 2450
Db 2401 GGGAGATTAGGCTAGGCTCTCTCCGCCAATCCCTCCCTCCGGCTCAGGAACTAAC 2450
QY 2461 AAAGGAAAAAAATTTGGAAAGCAGGATTAGAGAAAGCAAAATTCGACTGTCGCTT 2520
Db 2461 AAAGGAAAAAAATTTGGAAAGCAGGATTAGAGAAAGCAAAATTCGACTGTCGCTT 2520
QY 2521 GGTCCGGGAGACGTGGACTAGAGAGTCTGGCGTCAGAGCCCGGAGCCGAGTCTTCCGG 2580
Db 2521 GGTCCGGGAGACGTGGACTAGAGAGTCTGGCGTCAGAGCCCGGAGCCGAGTCTTCCGG 2580
QY 2581 GGTCTTTAGCGCGGCGGCCCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Db 2581 GGTCTTTAGCGCGGCGGCCCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
QY 2641 GGTCTTTAGCGCGGCGGCCCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700
Db 2641 GGTCTTTAGCGCGGCGGCCCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700
QY 2701 TCGTGGCGGCTGACGCTGCGCGGTTTAAAGGGCGGCGCTCGGCTCCAGCTGCTTCGG 2760
Db 2701 TCGTGGCGGCTGACGCTGCGCGGTTTAAAGGGCGGCGCTCGGCTCCAGCTGCTTCGG 2760
QY 2761 TGAGTGACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2820
Db 2761 TGAGTGACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2820
QY 2821 GATTTGACGATAGTAACTCTGCGTTCGGTCCAGGCGCAATCTATATAAGGAACTAGTCC 2880
Db 2821 GATTTGACGATAGTAACTCTGCGTTCGGTCCAGGCGCAATCTATATAAGGAACTAGTCC 2880
QY 2881 GGGGAAAAACCCGTAATTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2940
Db 2881 GGGGAAAAACCCGTAATTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2940
QY 2941 GAGGCTTCTCTCCCGGGTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3000
Db 2941 GAGGCTTCTCTCCCGGGTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3000
QY 3001 GGTCTTCAGGCGGCTTCT 3060
Db 3001 GGTCTTCAGGCGGCTTCT 3060
QY 3061 GAGGCTTCT 3120
Db 3061 GAGGCTTCT 3120
QY 3121 GGTCTTCAGGCGGCTTCT 3180
Db 3121 GGTCTTCAGGCGGCTTCT 3180
QY 3181 AAGTCTTCGGGCTTCT 3240
Db 3181 AAGTCTTCGGGCTTCT 3240

RESULT 2

US-09-846-456-1

Sequence 1, Application US/09846456
Patent No. US20020146792A1
GENERAL INFORMATION:
APPLICANT: Rosier, Marie
APPLICANT: Prades, Catherine
APPLICANT: Lemoine, Cendrine
APPLICANT: Naudin, Laurent
APPLICANT: Benefie, Patrice
APPLICANT: Buvenger, Nicolas
APPLICANT: Brewer, Bryan
APPLICANT: Remaley, Alan

APPLICANT: Fojo, Silvia
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Mod
FILE REFERENCE: 3806.0505
CURRENT APPLICATION NUMBER: US/09/846,456
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3231
TYPE: DNA
ORGANISM: Homo sapiens
US-09-846-456-1

Query Match 100.0% Score 3231; DB 10; Length 3231;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGGGCATGTTGGCAGGTCCTGTATCTCAGTTACTCGGAGGTGGAGGTTCGAATGA 60
Db 1 ACAGGGCATGTTGGCAGGTCCTGTATCTCAGTTACTCGGAGGTGGAGGTTCGAATGA 60
QY 61 GCCAGATCCACCATTCGACTCCAGCTGGGCAACAAAGAGTGAACCTCCATCTCAATT 120
Db 61 GCCAGATCCACCATTCGACTCCAGCTGGGCAACAAAGAGTGAACCTCCATCTCAATT 120
QY 121 AAAAAAAGAAATGATTTTGGTGGCTTCAAAATAGTGGAGAGAGAGAGAGAGG 180
Db 121 AAAAAAAGAAATGATTTTGGTGGCTTCAAAATAGTGGAGAGAGAGAGAGAGG 180
QY 181 AGATGGAGGTGAGGAGATCTAATTACTCTCTAAATCATGCTAGGAAAGATACACCT 240
Db 181 AGATGGAGGTGAGGAGATCTAATTACTCTCTAAATCATGCTAGGAAAGATACACCT 240
QY 241 TTTAATAAAGTCTCTGCTTTTAAATCATCTTCCAGGAGCTCAAGGTTTCAACA 300
Db 241 TTTAATAAAGTCTCTGCTTTTAAATCATCTTCCAGGAGCTCAAGGTTTCAACA 300
QY 301 AAGTCTCTTTCAGAAACCCCTTTGAGGAAGACAGATATACATCTCTCTCCATTTA 360
Db 301 AAGTCTCTTTCAGAAACCCCTTTGAGGAAGACAGATATACATCTCTCTCCATTTA 360
QY 361 AAGATGAAGAAACAGCCCGGCACATGCTTAATGCTGTATCCAGCACTTCGGAGG 420
Db 361 AAGATGAAGAAACAGCCCGGCACATGCTTAATGCTGTATCCAGCACTTCGGAGG 420
QY 421 CTGAGGTCAGAGATTCGCTTCAGCTCCAGAGTTTGAGACCAGCTCGATACATGCAAA 480
Db 421 CTGAGGTCAGAGATTCGCTTCAGCTCCAGAGTTTGAGACCAGCTCGATACATGCAAA 480
QY 481 ACCCTGCTCTACAAAAAATACAAAATTAGTGGGTTCGGTGGCATCCACCTGTGGT 540
Db 481 ACCCTGCTCTACAAAAAATACAAAATTAGTGGGTTCGGTGGCATCCACCTGTGGT 540
QY 541 CCCAGTCTAGTGGAGGCTAAGTGGAGGATCGCTTGAGCCAGGAGTCAAGTCTACA 600
Db 541 CCCAGTCTAGTGGAGGCTAAGTGGAGGATCGCTTGAGCCAGGAGTCAAGTCTACA 600
QY 601 CTGAGGCTGATTTGGATTCGACTCCAGCTCGGCTGGGTAGACAGCAAGACCTGCTCA 660
Db 601 CTGAGGCTGATTTGGATTCGACTCCAGCTCGGCTGGGTAGACAGCAAGACCTGCTCA 660
QY 661 AAAAAAAGAAATGAG 720
Db 661 AAAAAAAGAAATGAG 720
QY 721 GAGGGGGAGGAG 780
Db 721 GAGGGGGAGGAG 780
QY 781 GATGAAGTGAAGGAG 840
Db 781 GATGAAGTGAAGGAG 840


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QY 3061 CGGTCTCAGGCGCTTTCGCTCTGTTTTCCTCCCGGTTCGTGTTTTCCTCTCCG 3060
DB 3061 CGGTCTCAGGCGCTTTCGCTCTGTTTTCCTCCCGGTTCGTGTTTTCCTCTCCG 3060
QY 3061 GAAGGCTTGTCAAGGGGTAGGAGCAACAGACACACACAAAGTGGAAACAGATAGA 3120
DB 3061 GAAGGCTTGTCAAGGGGTAGGAGCAACAGACACACACAAAGTGGAAACAGATAGA 3120
QY 3121 GGTCTCCAGTACCTTACTTGGCGGTATTGTTTTCGTAGGCTCAAGAGCTTGGG 3180
DB 3121 GGTCTCCAGTACCTTACTTGGCGGTATTGTTTTCGTAGGCTCAAGAGCTTGGG 3180
QY 3181 AAGTCTCGGTTTCGGGACTTTGATCCGAGCGCCACATATCTCAATCT 3241
DB 3181 AAGTCTCGGTTTCGGGACTTTGATCCGAGCGCCACATATCTCAATCT 3241
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RESULT 3

US-09-846-827-23

Sequence 23, Application US-09984827

Publication No. US20030056234A1

GENERAL INFORMATION:

APPLICANT: DENEFELE, PATRICE

APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE

APPLICANT: ARNOULD-REUIGNE, ISABELLE

APPLICANT: DUVERGER, NICOLAS

APPLICANT: CAMBIEN, FRANCOIS

TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN AKM1 GENE, THEIR USES, AND

FILE REFERENCE: 03806.0522-00000

CURRENT APPLICATION NUMBER: US-09/984,827

CURRENT FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 60/254,108

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: FR 00/14037

PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 161

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 23

LENGTH: 2893

TYPE: DNA

ORGANISM: Homo sapiens

US-09-846-827-23

Query Match 89.5%; Score 2893; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ACAGGGCATGGTGGCAGGTGGCTGTAATCTCAATTACTGGAGAGTGGAGGTGAATGA 60
QY 61 GCCCAGATCCGACCATTTGGCTCCAGCTCCAGCTGGGCAACAAAGGTGAACCTCAATTC 120
DB 61 GCCCAGATCCGACCATTTGGCTCCAGCTCCAGCTGGGCAACAAAGGTGAACCTCAATTC 120
QY 121 AAAAAAAGAGATGATTTGGTGGTGGACATCAATAGTAGGACACAGACAGAGAGAG 180
DB 121 AAAAAAAGAGATGATTTGGTGGTGGACATCAATAGTAGGACACAGACAGAGAGAG 180
QY 181 AGATGGAGGTTCAGGAGATCTAATTAATCTCTAAATCATCTAGGAGTTCAGAAATAC 240
DB 181 AGATGGAGGTTCAGGAGATCTAATTAATCTCTAAATCATCTAGGAGTTCAGAAATAC 240
QY 241 TTTAATAACTCTCTGCTTTTATAACATCAATCTGCTAAGGAGTTCAGAAATAC 300
DB 241 TTTAATAACTCTCTGCTTTTATAACATCAATCTGCTAAGGAGTTCAGAAATAC 300
QY 301 AAGTTCACCTTCAGAAACCCCTTTCAGGAAGACAGAAATATACATCTCTCTCAATTT 360
DB 301 AAGTTCACCTTCAGAAACCCCTTTCAGGAAGACAGAAATATACATCTCTCTCAATTT 360
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QY 361 AAGATGAAGAAACAGGCGGGCACAAATGGCTAATGCTGTATATCCAGCACTTTGGAGG 420
DB 361 AAGATGAAGAAACAGGCGGGCACAAATGGCTAATGCTGTATATCCAGCACTTTGGAGG 420
QY 421 CTGAGGCGCAGNGATCGCTTGAGCTCCAGAGTTTGAGACCAGGCTGGATTAACATGCA 480
DB 421 CTGAGGCGCAGNGATCGCTTGAGCTCCAGAGTTTGAGACCAGGCTGGATTAACATGCA 480
QY 481 ACCCTGTCTCTACAAAAAATACAAAAATAGATGGGTGTGGTGGCATGCACTTGTGT 540
DB 481 ACCCTGTCTCTACAAAAAATACAAAAATAGATGGGTGTGGTGGCATGCACTTGTGT 540
QY 541 CCGAGCTAATTGGAGGCTAAGGCGGAGGATCGCTTGAGCCAGGAGTCAAGTCTACA 600
DB 541 CCGAGCTAATTGGAGGCTAAGGCGGAGGATCGCTTGAGCCAGGAGTCAAGTCTACA 600
QY 601 CTGAGTCATGATTGGATCACTGCACCTCCAGCTGGGTAGACAGAGCAACACCTCTCT 660
DB 601 CTGAGTCATGATTGGATCACTGCACCTCCAGCTGGGTAGACAGAGCAACACCTCTCT 660
QY 661 AAAAAAGAAATGAACAGAAAGAAAGAGAGGAGGAGGAGATGAGGGAGGAGG 720
DB 661 AAAAAAGAAATGAACAGAAAGAAAGAGAGGAGGAGGAGATGAGGGAGGAGG 720
QY 721 GAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 721 GAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 781 GATCAAAACAGAGGACAAACACACTTACGTTAAATGCTCATCATGCTGCTCAATTTGA 840
DB 781 GATCAAAACAGAGGACAAACACACTTACGTTAAATGCTCATCATGCTGCTCAATTTGA 840
QY 841 CCCCCAACCCCAATTTATTGACCAAGGTTATTCTTTGACTGAGGCAAGGGGTGCGCTCT 900
DB 841 CCCCCAACCCCAATTTATTGACCAAGGTTATTCTTTGACTGAGGCAAGGGGTGCGCTCT 900
QY 901 CCGGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATCCATCCCTTCTTT 960
DB 901 CCGGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATCCATCCCTTCTTT 960
QY 961 TTATTTTCTTGACACAGGAGTCTGTCTCTCACTCAGGCTGGAGTGGAGTGGATGATC 1020
DB 961 TTATTTTCTTGACACAGGAGTCTGTCTCTCACTCAGGCTGGAGTGGAGTGGATGATC 1020
QY 1021 TCGACTCAGCTTAACCTCTGCTCCCGGTTCAAGCGATCTCCTGCTCCAGCTCCGCTGA 1080
DB 1021 TCGACTCAGCTTAACCTCTGCTCCCGGTTCAAGCGATCTCCTGCTCCAGCTCCGCTGA 1080
QY 1081 GATAACAGGCGCGCGCCACACATCTGGCTAATTTTGTATTTTATAGTAAAGACTGGGT 1140
DB 1081 GATAACAGGCGCGCGCCACACATCTGGCTAATTTTGTATTTTATAGTAAAGACTGGGT 1140
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DB 1141 TCATCATCTGTCGCGCAGGTTGGTTTTCGAACTCTCTGAGTGGAGTGGAGTGGAGTGG 1200
QY 1201 CTCCTCAAGTCTGGGATACAGGCATGAGGCTGCGCCAGCTCAGATCCATCCCTTT 1260
DB 1201 CTCCTCAAGTCTGGGATACAGGCATGAGGCTGCGCCAGCTCAGATCCATCCCTTT 1260
QY 1261 CTAGGCGCAACAGTCCATGCTGCTGAGTGGTCCAGAGGCGCATCCACCCAGAGTTATAGT 1320
DB 1261 CTAGGCGCAACAGTCCATGCTGCTGAGTGGTCCAGAGGCGCATCCACCCAGAGTTATAGT 1320
QY 1321 GACTCCAGAAATCTCTGCTGGTGGCTCCACATGACATCCAGGCGCTGCTGAGGCTC 1380
DB 1321 GACTCCAGAAATCTCTGCTGGTGGCTCCACATGACATCCAGGCGCTGCTGAGGCTC 1380
QY 1381 TCTATGCGTCTGCTGCTGAGTGGTGTATAGAACCACTGATGTAGTACCTGGGCTTGAGGC 1440
DB 1381 TCTATGCGTCTGCTGCTGAGTGGTGTATAGAACCACTGATGTAGTACCTGGGCTTGAGGC 1440
QY 1441 GTGCCCTGGAGATCTCTGTTGACTGTAGCATGAGGAGGGGCTTGTGCACTGAATGTGCA 1500
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1441 GTGGCTGGAGATCTGTGACTGTAGCATGGAGGGGCTGTGCAGCTGAATGCTTGA 1500
1501 TGCAGTGGTGGAGTCTGGAATATGATGGAGCTGGAGTGGGAAGAGAGTAGGCTTG 1560
1501 TGCAGTGGTGGAGTCTGGAATATGATGGAGCTGGAGTGGGAAGAGAGTAGGCTTG 1560
1561 GGGAGCTCTCTCATGTCACCTCAITCTGGCCAAACTCAAGTCAAACTGTGAAGAGCT 1629
1561 GGGAGCTCTCTCATGTCACCTCAITCTGGCCAAACTCAAGTCAAACTGTGAAGAGCT 1629
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1621 AAATGTGAATCTGCCCTTCAAGGTGGCTACAAAGTATCTTTGTCAAGSTAGGAGACTT 1680
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1861 TGGTGTAGGCTGCATCTCTACHTTGGCTTTTTHTGGCTCTGAGTCTTTTGGGT 1920
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1921 AGTTTGTCTCCCTACAGCCAAAGCAACAGAGAAAGTGGAGTCTGAGTCTGATAT 1980
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2041 GTCTGTGTTTATACAGAGGAGCTGATCAATATATGAATATAAAGAGGCTGCTG 2100
2041 GTCTGTGTTTATACAGAGGAGCTGATCAATATATGAATATAAAGAGGCTGCTG 2100
2101 CATATGTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 2160
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2161 TCTTCTCTCAATTTACAGAGAGTCAATACAGAGTCTGATGAGTCTGATGAGTCTG 2220
2161 TCTTCTCTCAATTTACAGAGAGTCAATACAGAGTCTGATGAGTCTGATGAGTCTG 2220
2221 CTGGGAGCTCAGCTGGGATCTCCAGGCTATACAGTCTGATGAGTCTGATGAGTCTG 2280
2221 CTGGGAGCTCAGCTGGGATCTCCAGGCTATACAGTCTGATGAGTCTGATGAGTCTG 2280
2281 CAGTTTGTGGGGGAAACAAAGAGAGCTATATATATATATATATATATATATATATAT 2340
2281 CAGTTTGTGGGGGAAACAAAGAGAGCTATATATATATATATATATATATATATATAT 2340
2341 CACCCAGCTAGGCTTTGAAGGAAACAAAGAGAGCTATATATATATATATATATATATAT 2400
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2401 GGCAGATTTCAGCTAGAGCT 2460
2401 GGCAGATTTCAGCTAGAGCT 2460
2461 AAAGGAAAAAATTCGGGAAGCAGGATTTAGAGAGAGTAAATTCACCTCTCTCTCTCTCT 2520
2461 AAAGGAAAAAATTCGGGAAGCAGGATTTAGAGAGAGTAAATTCACCTCTCTCTCTCTCT 2520
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Db 2521 GGCTCCGGAGCTGAGCTAGAGCTCTGGGAGAGTCTGAGGAGAGCTGAGGAGCTTCCGC 2580
QY 2581 GGCTCTTAGCG 2640
Db 2581 GGCTCTTAGCG 2640
QY 2641 CGTGTCTACCTTCCACCG 2700
Db 2641 CGTGTCTACCTTCCACCG 2700
QY 2701 TCGTGGCGGCTGAACTGCGCGCGTTTAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2760
Db 2701 TCGTGGCGGCTGAACTGCGCGCGTTTAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2760
QY 2761 TGACTCACTGAACACTAATAACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2820
Db 2761 TGACTCACTGAACACTAATAACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2820
QY 2821 GCTTTGACCGATAGTAACTCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 2880
Db 2821 GCTTTGACCGATAGTAACTCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 2880
QY 2881 CGGCAAAACCC 2893
Db 2881 CGGCAAAACCC 2893

RESULT 4

US-09-846-456-3
; Sequence 3, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine
; APPLICANT: Lemoine, Cendrine
; APPLICANT: Naudin, Laurent
; APPLICANT: Denelle, Patrice
; APPLICANT: Duverger, Nicolas
; APPLICANT: Brewer, Bryan
; APPLICANT: Romaley, Alan
; APPLICANT: Polo, Silvia
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifi
; FILE OF INVENTION: Activity and Therapeutic Uses
; FILE REFERENCE: 1806.0505
; CURRENT APPLICATION NUMBER: US/09/846,456
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,280
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-846-456-3

Query Match: 89.5%; Score 2893; DB 10; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGGGCATGCTGGCAGGTGCGCTGTAATCTCAGTTACTCGGAGGTGGAGGTGCAATGA 60
Db 1 ACAGGGCATGCTGGCAGGTGCGCTGTAATCTCAGTTACTCGGAGGTGGAGGTGCAATGA 60
QY 61 GCCCAGATCCACCATTTGCACCTCCAGCTGGGCAACAAAGGTGAACTCCATCTCAATT 120
Db 61 GCCCAGATCCACCATTTGCACCTCCAGCTGGGCAACAAAGGTGAACTCCATCTCAATT 120
QY 121 AAAAAAAGAAATGATTTTGGTGTGCTGACTTCAAAATAGTAGGAGAGAGAGAGAGG 180
Db 121 AAAAAAAGAAATGATTTTGGTGTGCTGACTTCAAAATAGTAGGAGAGAGAGAGAGG 180
QY 181 AGATGAGGCTGAGGAGAGATCTAAATTACTCTCTAAATAATCTAGTAAAGATAACACT 240

Query Match		89.5%	Score	2891.4	DB	9	Length	2893		
Best local Similarity		100.0%	Pred. No.	0						
Matches		2892	Conservative	0	Mismatches	1	Indels	0	Gaps	0
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DB	1	ACAGGCGATGGTGGCAGGTCCTGTAATCTCAAGTAACTCGGAGGTTGGAGTTGCATCA	60							
QY	61	GCCAGATCCACCAATTCGACTCCAGCTCGGCAAAACAAAGTCAAACTGATCTCAAT	120							
DB	61	GCCAGATCCACCAATTCGACTCCAGCTCGGCAAAACAAAGTCAAACTGATCTCAAT	120							
QY	121	AAAAAAAAGAGATGTTTTGGTGGTGGCTTCAAAATAGTACGAACAAAGAGAGAG	180							
DB	121	AAAAAAAAGAGATGTTTTGGTGGTGGCTTCAAAATAGTACGAACAAAGAGAGAG	180							
QY	181	AGATGGAGGTCAGGAGATCTAATTAATCTCTCAAAATCATGTAAGCAAAATACAC	240							
DB	181	AGATGGAGGTCAGGAGATCTAATTAATCTCTCAAAATCATGTAAGCAAAATACAC	240							
QY	241	TTTAAATACACTCTCTGCTTTTATAATCATCTCTGCAAGAGCTCAAAAGTTCAACA	300							
DB	241	TTTAAATACACTCTCTGCTTTTATAATCATCTCTGCAAGAGCTCAAAAGTTCAACA	300							
QY	301	AAGTTCACCTTCAGAAACCCCTTTGAGAGAGACAAATATACATCTCTGCAATTTA	360							
DB	301	AAGTTCACCTTCAGAAACCCCTTTGAGAGAGACAAATATACATCTCTGCAATTTA	360							
QY	361	AAGATGAAGAAACAGCGCGGCACAAATGGCTAAAGTGTGTAATGTGTAATGTGTA	420							
DB	361	AAGATGAAGAAACAGCGCGGCACAAATGGCTAAAGTGTGTAATGTGTAATGTGTA	420							
QY	421	CTGAGCCAGAGATCGCTTACGCTCCAGAGTTTGAGACACAGCTCGATTAAGATGCA	480							
DB	421	CTGAGCCAGAGATCGCTTACGCTCCAGAGTTTGAGACACAGCTCGATTAAGATGCA	480							
QY	481	ACCTGTCTCTACAAAAAATACAAAAATTAGATGCTGTGCTGGCACTGCACCTGCT	540							
DB	481	ACCTGTCTCTACAAAAAATACAAAAATTAGATGCTGTGCTGGCACTGCACCTGCT	540							
QY	541	CCAGCTACTTGGAGGCTAAGGTGGAGGATGCTTGAGCCAGGAGTCAAGCTTACA	600							
DB	541	CCAGCTACTTGGAGGCTAAGGTGGAGGATGCTTGAGCCAGGAGTCAAGCTTACA	600							
QY	601	CTGAGCCATGATTGGATCTGCTCCAGCTTGGAGTGGATGAGACAGATTAAGTCTG	660							
DB	601	CTGAGCCATGATTGGATCTGCTCCAGCTTGGAGTGGATGAGACAGATTAAGTCTG	660							
QY	661	AAAAAAGAAATGAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	720							
DB	661	AAAAAAGAAATGAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	720							
QY	721	GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780							
DB	721	GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780							
QY	781	GATCAAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	840							
DB	781	GATCAAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	840							
QY	841	CCCCAAACCAATTTATTGACCAAGGTTATTCTGACAGGAGGAGGAGGAGGAGG	900							
DB	841	CCCCAAACCAATTTATTGACCAAGGTTATTCTGACAGGAGGAGGAGGAGGAGG	900							
QY	901	CTGAGGCTTGGGCTTTAGAAAGCTATCTGAGGCTTCTGAGGAGGAGGAGGAGG	960							
DB	901	CTGAGGCTTGGGCTTTAGAAAGCTATCTGAGGCTTCTGAGGAGGAGGAGGAGG	960							
QY	961	TTATTTCCTGACACGGAGCTTGGCTCTGTCATCAATCAATCAATCAATCAATCA	1020							
DB	961	TTATTTCCTGACACGGAGCTTGGCTCTGTCATCAATCAATCAATCAATCAATCA	1020							
QY	1021	TCGACTCACTGTAACTCTGCTCCGGGTTCAAGCGATTCTCTGCCTCAGCTCCCTGA	1080							
DB	1021	TCGACTCACTGTAACTCTGCTCCGGGTTCAAGCGATTCTCTGCCTCAGCTCCCTGA	1080							
QY	1081	GATAACAGGCGCCGCCACCATCTGCTAAATTTTGTATTTTGTAGTAAAGACTGGGT	1140							
DB	1081	GATAACAGGCGCCGCCACCATCTGCTAAATTTTGTATTTTGTAGTAAAGACTGGGT	1140							
QY	1141	TCATCATGTTGCCCAGGTTGCTTTCGAACCTCTGACCTGAGTGAGCTGCCACCTGGC	1200							
DB	1141	TCATCATGTTGCCCAGGTTGCTTTCGAACCTCTGACCTGAGTGAGCTGCCACCTGGC	1200							
QY	1201	CTCCCAAACTGCTGGGATTCAGGATTCAGGCTGAGGCTGCCGCCAGCTCAATCCCTT	1260							
DB	1201	CTCCCAAACTGCTGGGATTCAGGATTCAGGCTGAGGCTGCCGCCAGCTCAATCCCTT	1260							
QY	1261	CTAAGGCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1320							
DB	1261	CTAAGGCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1320							
QY	1321	GACTCCAGAAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1380							
DB	1321	GACTCCAGAAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1380							
QY	1381	TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1440							
DB	1381	TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1440							
QY	1441	GTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1500							
DB	1441	GTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1500							
QY	1501	TGCAAGTGGTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1560							
DB	1501	TGCAAGTGGTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1560							
QY	1561	GGCGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1620							
DB	1561	GGCGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1620							
QY	1621	AAATGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1680							
DB	1621	AAATGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1680							
QY	1681	GTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1740							
DB	1681	GTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1740							
QY	1741	CTTCTATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1800							
DB	1741	CTTCTATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1800							
QY	1801	TGCGCAATGAAGTGGATTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1860							
DB	1801	TGCGCAATGAAGTGGATTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1860							
QY	1861	TGCTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1920							
DB	1861	TGCTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1920							
QY	1921	AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1980							
DB	1921	AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1980							
QY	1981	AAATTTACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2040							
DB	1981	AAATTTACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2040							
QY	2041	GTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2100							
DB	2041	GTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2100							
QY	2101	CAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2160							

QY 901 CTTGGGCTTGGCTTTAGAAAGCTCATCTCTGGGCTTTCTCAGATCCATCCCTTCTTT 960
DB 901 CTTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTCAGATCCATCCCTTCTTT 960
QY 961 TATTCTTTGACAGGAGCTTCTCTGTACACAGCTGAGCTGAGTGGAGTGGCAATGATC 1020
DB 961 TATTCTTTGACAGGAGCTTCTCTGTACACAGCTGAGCTGAGTGGAGTGGCAATGATC 1020
QY 1021 TCACTACTGTAACTCTGCCCTCCCGGTTCAAGGATTTCTCTGGCTCAGTCCCTGA 1080
DB 1021 TCACTACTGTAACTCTGCCCTCCCGGTTCAAGGATTTCTCTGGCTCAGTCCCTGA 1080
QY 1081 GATAACAGGCGCGCCGACACATCTGGCTAATTTTGTATTTTGTAGTAAAGAGTGGT 1140
DB 1081 GATAACAGGCGCGCCGACACATCTGGCTAATTTTGTATTTTGTAGTAAAGAGTGGT 1140
QY 1141 TCATCATGTTGGCAGGTTGGTTTCCAACTCCGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1200
DB 1141 TCATCATGTTGGCAGGTTGGTTTCCAACTCCGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1200
QY 1201 CTCCTCAAGTGTGGGATACAGGATGAGGCTAGGCTGAGGCTGAGGCTGAGGCTGAGG 1260
DB 1201 CTCCTCAAGTGTGGGATACAGGATGAGGCTAGGCTGAGGCTGAGGCTGAGGCTGAGG 1260
QY 1261 CTAAAGGCAACAGCTCCATGCTGCAAGGCGCTATGCAAGGCTGAGCTGAGCTGAGCTGAG 1320
DB 1261 CTAAAGGCAACAGCTCCATGCTGCAAGGCGCTATGCAAGGCTGAGCTGAGCTGAGCTGAG 1320
QY 1321 GATCTCAGAAATCTTGGCTTGGCTGCTCAGATGCTTCCAGGCTGAGCTGAGCTGAGCTGAG 1380
DB 1321 GATCTCAGAAATCTTGGCTTGGCTGCTCAGATGCTTCCAGGCTGAGCTGAGCTGAGCTGAG 1380
QY 1381 TTCTATGCTGCTGCTGAGTGTGATAGACACATGATGAGTACCTGAGCTGAGCTGAGCTGAG 1440
DB 1381 TTCTATGCTGCTGCTGAGTGTGATAGACACATGATGAGTACCTGAGCTGAGCTGAGCTGAG 1440
QY 1441 GTGGCTGAGATCTGTTGACTGTAGCTGAGGAGGCTGAGCTGAGCTGAGCTGAGCTGAG 1500
DB 1441 GTGGCTGAGATCTGTTGACTGTAGCTGAGGAGGCTGAGCTGAGCTGAGCTGAGCTGAG 1500
QY 1501 TGCAGTGTGGGAGTCTTGGAAATATGATGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1560
DB 1501 TGCAGTGTGGGAGTCTTGGAAATATGATGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1560
QY 1561 GGGGAGCTGCTCATGCGAGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
DB 1561 GGGGAGCTGCTCATGCGAGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 1621 AAATGTGAATCTGCTTCAAGTGTGCTAATAAGTGTGCTAATAAGTGTGCTAATAAGTGTG 1680
DB 1621 AAATGTGAATCTGCTTCAAGTGTGCTAATAAGTGTGCTAATAAGTGTGCTAATAAGTGTG 1680
QY 1681 GTGGCTTCAAGTGTGCTTCAAGTGTGCTTCAAGTGTGCTTCAAGTGTGCTTCAAGTGTGCT 1740
DB 1681 GTGGCTTCAAGTGTGCTTCAAGTGTGCTTCAAGTGTGCTTCAAGTGTGCTTCAAGTGTGCT 1740
QY 1741 CTCTATGAATCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAG 1800
DB 1741 CTCTATGAATCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAG 1800
QY 1801 TGCCAGAAATAGGTGACATTTAGTTGTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCT 1860
DB 1801 TGCCAGAAATAGGTGACATTTAGTTGTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCT 1860
QY 1861 TGTGTGTAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAG 1920
DB 1861 TGTGTGTAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAG 1920
QY 1921 AGTTTGTCTCCCTACAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAG 1980
DB 1921 AGTTTGTCTCCCTACAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAGGCTGCTTCAAG 1980

QY 1981 AATTTTACAGACTGCAATCTCTGGCTGCACTTCCAAATGCTATACAAATGCTATACAAATGCT 2040
DB 1981 AATTTTACAGACTGCAATCTCTGGCTGCACTTCCAAATGCTATACAAATGCTATACAAATGCT 2040
QY 2041 GTCTCTGTCTTTTATCAGAGGAGGCTGATCAATATATGAAATGAAATGAAATGAAATGAAAT 2100
DB 2041 GTCTCTGTCTTTTATCAGAGGAGGCTGATCAATATATGAAATGAAATGAAATGAAATGAAAT 2100
QY 2101 CATATTGCTCTGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2160
DB 2101 CATATTGCTCTGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2160
QY 2161 TCTCTCTCTCTCAATTTATGAGAGAGGAGTAAAGATGTTCTCTCTGGGCTCTCTGAGGGA 2220
DB 2161 TCTCTCTCTCTCAATTTATGAGAGAGGAGTAAAGATGTTCTCTCTGGGCTCTCTGAGGGA 2220
QY 2221 CTTGGGAGCTCAGCTGAGGATCTCCAAAGCAGTGTGCTGCTATCAAAATCAAAATCAAAAT 2280
DB 2221 CTTGGGAGCTCAGCTGAGGATCTCCAAAGCAGTGTGCTGCTATCAAAATCAAAATCAAAAT 2280
QY 2281 CAGTTTGTGGGGGAAACAAAGCAGGCTATACCCAGAGGAGTGTCCGCTTCCGCT 2340
DB 2281 CAGTTTGTGGGGGAAACAAAGCAGGCTATACCCAGAGGAGTGTCCGCTTCCGCT 2340
QY 2341 CACCCAGCTGAGGCTTGAAGGAAACAAAGCAGGCTATACCCAGAGGAGTGTCCGCTTCCGCT 2400
DB 2341 CACCCAGCTGAGGCTTGAAGGAAACAAAGCAGGCTATACCCAGAGGAGTGTCCGCTTCCGCT 2400
QY 2401 CGGAGTTACGCTAGAGCTCTCTCTCCCAATCCCTCCCTCCGCTGAGGAGTAAAC 2460
DB 2401 CGGAGTTACGCTAGAGCTCTCTCTCCCAATCCCTCCCTCCGCTGAGGAGTAAAC 2460
QY 2461 AAGGAAATAAATAATGCGGAAGCAGGATTTAGAGGAGGAGTTCACCTGCTGCTT 2520
DB 2461 AAGGAAATAAATAATGCGGAAGCAGGATTTAGAGGAGGAGTTCACCTGCTGCTT 2520
QY 2521 GCTGCTGAGGAGGCTGAGGCTGAGGAGTCTGCGGAGCAGGCTGAGGAGGAGGAGGAGGAG 2580
DB 2521 GCTGCTGAGGAGGCTGAGGCTGAGGAGTCTGCGGAGCAGGCTGAGGAGGAGGAGGAGGAG 2580
QY 2581 GCTGCTGAGGAGGCTGAGGCTGAGGAGTCTGCGGAGCAGGCTGAGGAGGAGGAGGAGGAG 2640
DB 2581 GCTGCTGAGGAGGCTGAGGCTGAGGAGTCTGCGGAGCAGGCTGAGGAGGAGGAGGAGGAG 2640
QY 2641 CTTGCTGAGGCTGAGGCTGAGGCTGAGGAGTCTGCGGAGCAGGCTGAGGAGGAGGAGGAG 2700
DB 2641 CTTGCTGAGGCTGAGGCTGAGGCTGAGGAGTCTGCGGAGCAGGCTGAGGAGGAGGAGGAG 2700
QY 2701 TCTGCTGAGGCTGAGGCTGAGGCTGAGGAGTCTGCGGAGCAGGCTGAGGAGGAGGAGGAG 2760
DB 2701 TCTGCTGAGGCTGAGGCTGAGGCTGAGGAGTCTGCGGAGCAGGCTGAGGAGGAGGAGGAG 2760
QY 2761 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2820
DB 2761 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2820
QY 2821 GCTTTGAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2880
DB 2821 GCTTTGAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2880
QY 2881 CGGCAAAACCC 2893
DB 2881 CGGCAAAACCC 2893

RESULT 8

US-09-984-827-141
; Sequence 141, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEPIER, PATRICE
; APPLICANT: ROSTIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

[illegible]

RESULT 9
US-09-984-827-142
: Sequence 142. Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFLÉ, PATRICE
: APPLICANT: ROSIER-MONTIUS, MARIE-FRANÇOISE
: APPLICANT: ARNOULD-REQUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANÇOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES
: FILE REFERENCE: 03806, 0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: CURRENT FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 142
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-984-827-142

Query Match 89.5%; Score 2891.4; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0;

QY	1	ACAGGCGATGUTGCGAGTGCCTGCTAATCTCAGTTACTCGGAGGTGGAGGTTGCCAATGA	60
DB	1	ACAGGCGATGUTGCGAGTGCCTGCTAATCTCAGTTACTCGGAGGTGGAGGTTGCCAATGA	60
QY	61	GCCAGATGCGACCAATTCACCTCCAGCTGGGCAACAAAAGGTCAAACTCATCTCAATT	120
DB	61	GCCAGATGCGACCAATTCACCTCCAGCTGGGCAACAAAAGGTCAAACTCATCTCAATT	120
QY	121	AAAAAAAAGAAATCATTTTGGTGGTCGACTTCAATTAGTGGAGAAAGAGGAGAGG	180
DB	121	AAAAAAAAGAAATCATTTTGGTGGTCGACTTCAATTAGTGGAGAAAGAGGAGAGG	180
QY	181	AGATGGAGGTCAGGAGATCTAATTAATCTCTAAATCATGCTAGGAAGATATACACCT	240
DB	181	AGATGGAGGTCAGGAGATCTAATTAATCTCTAAATCATGCTAGGAAGATATACACCT	240
QY	241	TTAATAACATCTCTGCTTTTATAACATCATCTCGCAAGGAGCTCAAAAGGTCTCAAGA	300
DB	241	TTAATAACATCTCTGCTTTTATAACATCATCTCGCAAGGAGCTCAAAAGGTCTCAAGA	300
QY	301	AAGTTCACTTTCAGAAAACCCCTTTGAGGAGAGCAGAAATATACATCTTCTCTCCATTTTA	360
DB	301	AAGTTCACTTTCAGAAAACCCCTTTGAGGAGAGCAGAAATATACATCTTCTCTCCATTTTA	360
QY	361	AAGATGAAGAACAGGCTGGGCACAATGGCTTAATGCCCTGTAATCCCGAGCACTTTGGAGG	420
DB	361	AAGATGAAGAACAGGCTGGGCACAATGGCTTAATGCCCTGTAATCCCGAGCACTTTGGAGG	420
QY	421	CTGAGGTCACAGGATCGCTTGAGCTCCAGAGTTTGAGACAGGCTGGATAACTGGCAAA	480
DB	421	CTGAGGTCACAGGATCGCTTGAGCTCCAGAGTTTGAGACAGGCTGGATAACTGGCAAA	480
QY	481	ACCTGTGCTTACAAAAAAAATACAAAAATTTAGATGGGTGTGGTGATGCACTGTGGT	540
DB	481	ACCTGTGCTTACAAAAAAAATACAAAAATTTAGATGGGTGTGGTGATGCACTGTGGT	540
QY	541	CCCAGCTACTTGGCAGGCTAAGGTGGGAGGATCGCTTGAGCCGAGGAGTCAAGTCTACA	600
DB	541	CCCAGCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCGAGGAGTCAAGTCTACA	600
QY	601	CTGAGGCAAGATTGGATTCATGTCACCTCCAGCCTGGGTAGACAGAGCAAGACCTGTCTCA	660

QY	361	AAAGTGAAGAAACAGCCGGGCACAAATGGCTTAATGCCCTGTAAATCCCGAGCACCTTGGGAGG	420
DB			
QY	361	AAGATCAACAAACAGCCGGGCACAAATGGCTTAATGCCCTGTAAATCCCGAGCACCTTGGGAGG	420
DB			
QY	421	CTGAGACCCAGAGGATCGCTTGAGCTCCAGAGTTTGACACCCAGGCTCGATATATATGCCAAA	480
DB			
QY	421	CTGAGGCCAGAGGATCGCTTGAGCTCCAGAGTTTGACACCCAGGCTCGATATATATGCCAAA	480
DB			
QY	481	ACCCCTGTCTCTACAAAAAAAATACAAAAATTAGATGGGTGTGGTGGCATATGAACTGTGGT	540
DB			
QY	481	ACCCCTGTCTCTACAAAAAAAATACAAAAATTAGATGGGTGTGGTGGCATATGAACTGTGGT	540
DB			
QY	541	CTCAGGCTACTTGGGAGGCTTAAGTGGGAGGATCGCTTGAAGCTCAGAGAGTGAAGCTATACA	600
DB			
QY	541	CTCAGGCTACTTGGGAGGCTTAAGTGGGAGGATCGCTTGAAGCTCAGAGAGTGAAGCTATACA	600
DB			
QY	601	CTGAGTCATGATTGATCATCGCTCCAGGCTGGGTAGACACAGTAAGACCCGTGTCTCA	660
DB			
QY	601	CTGAGGCTGATTGGATCACTGCTCCAGGCTGGGTAGACACAGTAAGACCCGTGTCTCA	660
DB			
QY	661	AAAAAAGAAATGAAGAGAAAGAAAGAACAGGAGAGAGAGAGATGACGGAGGAGG	720
DB			
QY	661	AAAAAAGAAATGAAGAGAAAGAAAGAACAGGAGAGAGAGAGATGACGGAGGAGG	720
DB			
QY	721	GAGGGGGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
DB			
QY	721	GAGGGGGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
DB			
QY	781	GATCAACACAGAGCCAGAAAGACTTTACGTTAAATTCCTCATCATCTGTTGTGAAGTTTCA	840
DB			
QY	781	GATCAACACAGAGCCAGAAAGACTTTACGTTAAATTCCTCATCATCTGTTGTGAAGTTTCA	840
DB			
QY	841	CCCCAAACCCCAATTATTGACCAAGTTATCTTTGACCTAGGACGAGGGGTCCGCTCT	900
DB			
QY	841	CCCCAAACCCCAATTATTGACCAAGTTATCTTTGACCTAGGACGAGGGGTCCGCTCT	900
DB			
QY	901	CCTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGCTTTCTTGAGATCCATGCTCTCTTT	960
DB			
QY	901	CCTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGCTTTCTTGAGATCCATGCTCTCTTT	960
DB			
QY	961	TTATTTTCTTGACAGGAGTCTTCTCTGTGACATATAGCTGGAGTGGAGTGGCATGATC	1020
DB			
QY	961	TTATTTTCTTGACAGGAGTCTTCTCTGTGACATATAGCTGGAGTGGAGTGGCATGATC	1020
DB			
QY	1021	TGCACCTCACTGTAACTCTGCTCCGGGTTTAAGGCAATCTGCTGCTCTCAAGCTCTCA	1080
DB			
QY	1021	TGCACCTCACTGTAACTCTGCTCCGGGTTTAAGGCAATCTGCTGCTCTCAAGCTCTCA	1080
DB			
QY	1081	GATACAGGCGCCGCCACCATCTGCTTAATTTTCTATTTTCTATTTTCTATTTTCTATTT	1140
DB			
QY	1081	GATACAGGCGCCGCCACCATCTGCTTAATTTTCTATTTTCTATTTTCTATTTTCTATTT	1140
DB			
QY	1141	TCATCATGTTGGCCAGTGGTTTCGAAATGCTGATGAGTGAAGCTGGCTGGCTACCTGGG	1200
DB			
QY	1141	TCATCATGTTGGCCAGTGGTTTCGAAATGCTGATGAGTGAAGCTGGCTGGCTACCTGGG	1200
DB			
QY	1201	CTCCCAAAGTGTGGGATTACAGGATGAGGCATGGACCTGGACCTCAGATCATCCCTTT	1260
DB			
QY	1201	CTCCCAAAGTGTGGGATTACAGGATGAGGCATGGACCTGGACCTCAGATCATCCCTTT	1260
DB			
QY	1261	CTAAGGCAACACAGTCCATCGTGCAAAGGGGTAATATCAAGACAGATATATCACTACCTGG	1320
DB			
QY	1261	CTAAGGCAACACAGTCCATCGTGCAAAGGGGTAATATCAAGACAGATATATCACTACCTGG	1320
DB			
QY	1321	CACCTCCAGAAATTCCTTGGCTTGGCTTCACATGCAATTCACAGGAGCTGTGTGGGCTC	1380
DB			
QY	1321	CACCTCCAGAAATTCCTTGGCTTGGCTTCACATGCAATTCACAGGAGCTGTGTGGGCTC	1380
DB			
QY	1381	TTCTATCGGCTCTGCTCTGAGTGTGATAGAAGCACTGATGTGAGTACCTGAGCTTGAAGC	1440
DB			
QY	1381	TTCTATCGGCTCTGCTCTGAGTGTGATAGAAGCACTGATGTGAGTACCTGAGCTTGAAGC	1440
DB			

QY	1441	GTGGCCCTGGAGATCCTGTTGACTGTAGCATGAGAGGGGCTTGTGCAAGCTGAATGCTGTGCA	1500
DB	1441	GTGGCCCTGGAGATCCTGTTGACTGTAGCATGAGAGGGGCTTGTGCAAGCTGAATGCTGTGCA	1500
QY	1501	TGCAGGTGGTGGGAGTCTGTGGAATAATGATGGAGCTGGAGGTGGGAAGAAGTAGTACGCTTG	1560
DB	1501	TCCAGGTGGTGGGAGTCTGTGGAATAATGATGGAGCTGGAGGTGGGAAGAAGTAGTACGCTTG	1560
QY	1561	GGGAGGCTCTCTCATGCCACTCATCTTCTGGCCAAAACCTCAGGTCAAACCTGTGAAGAGTCT	1620
DB	1561	GGGAGGCTCTCTCATGCCACTCATCTTCTGGCCAAAACCTCAGGTCAAACCTGTGAAGAGTCT	1620
QY	1621	AAATGTGAATCTGCCCTTCAAGTGGCTACAAAGTATCTTTGTCAAGGTAGGAGACCTT	1680
DB	1621	AAATGTGAATCTGCCCTTCAAGTGGCTACAAAGTATCTTTGTCAAGGTAGGAGACCTT	1680
QY	1681	GTGGCCCTCAGCTGGCACTTCAGAGGCTGCTTGGGCCCTCTCTACGGGTCTGTCTCGTCACT	1740
DB	1681	GTGGCCCTCAGCTGGCACTTCCAGGGCTGCTTGGGCCCTCTCTACGGGTCTGTCTCGTCACT	1740
QY	1741	CTTCTATGAATCCTTCAGGCGAGTTCATATTTAGACTCTTCACAGTTTGGACCTGAGCTTT	1800
DB	1741	CTTCTATGAATCCTTCAGGCGAGTTCATATTTAGACTCTTCACAGTTTGGACCTGAGCTTT	1800
QY	1801	TGGCCAGAAATGAAGTGCATTTAGTTTGTGGCTGATGGATGACTTAAATATTAGACA	1860
DB	1801	TGGCCAGAAATGAAGTGCATTTAGTTTGTGGCTGATGGATGACTTAAATATTAGACA	1860
QY	1861	TGGTGTAGGCTGTGATTCCTACTCTGTCTTTTTTTTTTGGCCCTCCAGTGTTTGGGT	1920
DB	1861	TGGTGTAGGCTGTGATTCCTACTCTGTCTTTTTTTTTTGGCCCTCCAGTGTTTGGGT	1920
QY	1921	AGTTTGTCTCCCTACAGCCAAAGCAACAGAGAAGTTGGAGTCTCGAGTGGCTACAT	1980
DB	1921	AGTTTGTCTCCCTACAGCCAAAGCAACAGAGAAGTTGGAGTCTCGAGTGGCTACAT	1980
QY	1981	AATTTTACAGACTTGCATTTCTGTGCTGCACCTTCACAAATGTATACAACTAAATACAA	2040
DB	1981	AATTTTACAGACTTGCATTTCTGTGCTGCACCTTCACAAATGTATACAACTAAATACAA	2040
QY	2041	GTCTGTGTGTTTATCACAGGAGGCTGATCAATATATGAATTAAGAAATTAAGAGGGCTGCT	2100
DB	2041	GTCTGTGTGTTTATCACAGGAGGCTGATCAATATATGAATTAAGAAATTAAGAGGGCTGCT	2100
QY	2101	CAATATTGTCTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	2160
DB	2101	CAATATTGTCTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	2160
QY	2161	TGCTTCTCTCAATATPATGAGAGAGAGCTAGATGTTCTCTCGGCTCCCTCAGGGA	2220
DB	2161	TGCTTCTCTCAATATPATGAGAGAGAGCTAGATGTTCTCTCGGCTCCCTCAGGGA	2220
QY	2221	CTTGGGAGTTCAGGCTGGGAATCTCCAGGCAAGTAGTGGCTATCAAAAATCAAAATC	2280
DB	2221	CTTGGGAGGCTCAGGCTGGGAATCTCCAGGCAAGTAGTGGCTATCAAAAATCAAAATC	2280
QY	2281	CAGTTTGTGGGGGAAAACAAAGAGAGCCCATTACCCAGAGGACTGTCCGCTTCCCT	2340
DB	2281	CAGTTTGTGGGGGAAAACAAAGAGAGCCCATTACCCAGAGGACTGTCCGCTTCCCT	2340
QY	2341	CACCCAGCTTAGGCTTTTGAAGGAAATCAAAAGACAAGCAAAAATGATGGGCTCTGA	2400
DB	2341	CACCCAGCTTAGGCTTTTGAAGGAAATCAAAAGACAAGCAAAAATGATGGGCTCTGA	2400
QY	2401	GGGAGATTCAAGCTTAGAGCTCTCTCTCCCCCAATCCCTCCCTCGGCTGAGAACTAAC	2460
DB	2401	GGGAGATTCAAGCTTAGAGCTCTCTCTCCCCCAATCCCTCCCTCGGCTGAGAACTAAC	2460
QY	2461	AAAGGAAAAAAATTCGGGAAACAGGATTTTAGAGGAAGCAAAATCCACTGGTCCCTT	2520
DB	2461	AAAGGAAAAAAATTCGGGAAACAGGATTTTAGAGGAAGCAAAATCCACTGGTCCCTT	2520
QY	2521	GGCTGGCGGAAAGCTGGAGCTAGAGAGTCTGGCGGCGAGCCGAGCCAGCGCTTCCGCG	2580

QY 1421 GACTCCAGAAATTCCTTGGCTGGCTCCACATGACATTCAGAGGCGCTGCTGGGCGCTC 1380
DB 1421 GACTCCAGAAATTCCTTGGCTGGCTCCACATGACATTCAGAGGCGCTGCTGGGCGCTC 1380
QY 1381 TTCTATCGCTCTGCTGAGTGTGTATAGAACCACTGATGTAGTACCTGGGCTTTGAGGC 1440
DB 1381 TTCTATCGCTCTGCTGAGTGTGTATAGAACCACTGATGTAGTACCTGGGCTTTGAGGC 1440
QY 1441 GTGGCGCTGGAGATTCCTGTTGACTGTAGCATGGAGGCGCTTGTGAGCTGAATGTCGCA 1500
DB 1441 GTGGCGCTGGAGATTCCTGTTGACTGTAGCATGGAGGCGCTTGTGAGCTGAATGTCGCA 1500
QY 1501 TGCAGTGGTGGAGTCTGGAATATGATGGAGCTGGAGTGGAGAGAGAGAGAGTGG 1560
DB 1501 TGCAGTGGTGGAGTCTGGAATATGATGGAGCTGGAGTGGAGAGAGAGAGAGTGG 1560
QY 1561 GGGCAGCTCTCTCATGCCACTCATTTCGGCAAAACICAGGTCAAGCTGAAGAGTCT 1620
DB 1561 GGGCAGCTCTCTCATGCCACTCATTTCGGCAAAACICAGGTCAAGCTGAAGAGTCT 1620
QY 1621 AAAATGTAATTCGCCCTTCAAGTGGCTACAAAGTATCTTTGTAAGGTAGCAGACT 1680
DB 1621 AAAATGTAATTCGCCCTTCAAGTGGCTACAAAGTATCTTTGTAAGGTAGCAGACT 1680
QY 1681 GTGGCTCCAGCTGCACTTCCAGGGCTGCTTGGGCTCTCTTACGGCTCTGCTGAGT 1740
DB 1681 GTGGCTCCAGCTGCACTTCCAGGGCTGCTTGGGCTCTCTTACGGCTCTGCTGAGT 1740
QY 1741 CTTCTATGAATTCCTCAGGCAGATTCATATTATGACTCTTACACTTACACTTACACT 1800
DB 1741 CTTCTATGAATTCCTCAGGCAGATTCATATTATGACTCTTACACTTACACTTACACT 1800
QY 1801 TGGCAGAAATAGGTGACATTTAGTTCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1860
DB 1801 TGGCAGAAATAGGTGACATTTAGTTCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1860
QY 1861 GGTGTGAGGCTGATTCCTACTCTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
DB 1861 GGTGTGAGGCTGATTCCTACTCTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
QY 1921 AGTTTCTCCCTTACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1980
DB 1921 AGTTTCTCCCTTACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1980
QY 1981 AATTTACAGCTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
DB 1981 AATTTACAGCTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
QY 2041 GTCGTGCTTTTATCAGGAGGCTGATCAATATAAATAAATAAATAAATAAATAAATAA 2100
DB 2041 GTCGTGCTTTTATCAGGAGGCTGATCAATATAAATAAATAAATAAATAAATAAATAA 2100
QY 2101 CATATTCTGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2160
DB 2101 CATATTCTGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2160
QY 2161 TCTTCTCTCAATTTATGAGAGAGCAGTAAATGTTTCTGCTGCTGCTGCTGCTGCTGCTG 2220
DB 2161 TCTTCTCTCAATTTATGAGAGAGCAGTAAATGTTTCTGCTGCTGCTGCTGCTGCTGCTG 2220
QY 2221 CTTGGGAGCTCAGGCTGGAATCTCTAAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTG 2280
DB 2221 CTTGGGAGCTCAGGCTGGAATCTCTAAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTG 2280
QY 2281 CAGGTTTGTGGGGGAAACAAAGCAGCTTATACCAAGCAGCTGCTGCTGCTGCTGCTGCT 2340
DB 2281 CAGGTTTGTGGGGGAAACAAAGCAGCTTATACCAAGCAGCTGCTGCTGCTGCTGCTGCT 2340
QY 2341 CACCCAGCTTAGGCTTTTCAAGGAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2400
DB 2341 CACCCAGCTTAGGCTTTTCAAGGAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2400

QY 2401 GGGAGATTCAGCTAGAGCTCTCTCTCCCAATTCCTCCCTCCCTCCCTCCCTCCCTCCCT 2460
DB 2401 GGGAGATTCAGCTAGAGCTCTCTCTCCCAATTCCTCCCTCCCTCCCTCCCTCCCTCCCT 2460
QY 2461 AAAGGAAAGAAATTCGGGAAAGCAGGATTTAGAGGAAGCAATTTCCACTGGTGCCTT 2520
DB 2461 AAAGGAAAGAAATTCGGGAAAGCAGGATTTAGAGGAAGCAATTTCCACTGGTGCCTT 2520
QY 2521 GGTTCGGGGAAGTGTGACTAGAGAGTCTCGGCGGAGCGCCCGAGCGCTTCCCGC 2580
DB 2521 GGTTCGGGGAAGTGTGACTAGAGAGTCTCGGCGGAGCGCCCGAGCGCTTCCCGC 2580
QY 2581 GCGTCTTATAGCGGCG 2640
DB 2581 GCGTCTTATAGCGGCG 2640
QY 2641 CTTCTGCTTACCTCCACACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC 2700
DB 2641 CTTCTGCTTACCTCCACACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC 2700
QY 2701 TCGTGGCGGCTGAACGTGCGCGCTTTAAGGGCGGCGCGCGCGCGCGCGCGCGCGCG 2760
DB 2701 TCGTGGCGGCTGAACGTGCGCGCTTTAAGGGCGGCGCGCGCGCGCGCGCGCGCGCG 2760
QY 2761 TGAGTGACTGAACATACATTAACAGAGCGCGGGAAGGGCGGGGAGGAGGAGCAG 2820
DB 2761 TGAGTGACTGAACATACATTAACAGAGCGCGGGAAGGGCGGGGAGGAGGAGCAG 2820
QY 2821 GCTTGGAGCATAGTAACTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
DB 2821 GCTTGGAGCATAGTAACTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
QY 2881 GGGCAAAACCCC 2893
DB 2881 GGGCAAAACCCC 2893

RESULT 13

US-09-984-827-146
: Sequence 146, Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFFLE, PATRICE
: APPLICANT: ROSIER-MONJUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: PRIOR FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 146
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-984-827-146

Query Match 89.5% Score 2891.4; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAGGGCATGCTGGCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
DB 1 ACAGGGCATGCTGGCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 61 GCTTCAGATTCGACCATTTGCACTCCAGCTGGGCAACAAAAGGTGAACATCTCATTT 120

! PRIOR FILING DATE: 2000-10-31
! NUMBER OF SEQ ID NOS: 161
! SOFTWARE: PatentIn Ver. 2.1
! SEQ ID NO 149
! LENGTH: 2893
! TYPE: DNA
! ORGANISM: Homo sapiens
US-09-984-827-149

Query Match 89.5% Score 2891.4; DB 9; length: 2893.
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 2; Gaps 0

QY 1 ACAGGCGATCGTGGCAGGTGCTGTAATCICAGTTACTGCGAGGTGCGAGTGTGATGA 60
DB 1 ACAGGCGATCGTGGCAGGTGCTGTAATCICAGTTACTGCGAGGTGCGAGTGTGATGA 60
QY 61 GGCAGATCGCCACCATTCACATCCAGGCCGCGGCAACAAAGGTCGAAATTCATGCAAT 120
DB 61 GGCAGATCGCCACCATTCACATCCAGGCCGCGGCAACAAAGGTCGAAATTCATGCAAT 120
QY 121 AAAAAAAGAAATGATTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180
DB 121 AAAAAAAGAAATGATTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180
QY 181 AGATGGAGGTGAGGAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
DB 181 AGATGGAGGTGAGGAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
QY 241 TTATAAGACTCTCTGCTTTTAAATCAATTCGCAAGGAGTCAAGGTTTCAACA 300
DB 241 TTATAAGACTCTCTGCTTTTAAATCAATTCGCAAGGAGTCAAGGTTTCAACA 300
QY 301 AAGTTCACCTTCAGAAAACCCCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 AAGTTCACCTTCAGAAAACCCCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 AAGATGAGAAAACAGCGCGGCGACAAATGGCTAATGCCGTAA1GCCAGGAGTGTGGAGG 420
DB 361 AAGATGAGAAAACAGCGCGGCGACAAATGGCTAATGCCGTGTATGCCAGGAGTGTGGAGG 420
QY 421 CTGAGGCGAGAGGATCGCTTGAGCTCCAGAGTTTGAGAGAGTGGCTGGAATGGAATG 480
DB 421 CTGAGGCGAGAGGATCGCTTGAGCTCCAGAGTTTGAGAGAGTGGCTGGAATGGAATG 480
QY 481 AGCTGTCTCTACAAAAAATACAAAATAGATGGCTGGTGGTGGTGGTGGTGGTGGTGG 540
DB 481 AGCTGTCTCTACAAAAAATACAAAATAGATGGCTGGTGGTGGTGGTGGTGGTGGTGG 540
QY 541 CCAGCTACTTGGGAGGTAAAGTGGGAGGATGGTGGGAGGATGGTGGGAGGATGGTGG 600
DB 541 CCAGCTACTTGGGAGGTAAAGTGGGAGGATGGTGGGAGGATGGTGGGAGGATGGTGG 600
QY 601 CTGAGGCGATGTTGGATCACTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCT 660
DB 601 CTGAGGCGATGTTGGATCACTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCT 660
QY 661 AAAAAAGAAATGAAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 AAAAAAGAAATGAAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 721 GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 GATGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 GATGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 CCCCCAAACCCAAATTTATGACCAAGGTTATCTTGTGAGGAGGAGGAGGAGGAGGAG 900
DB 841 CCCCCAAACCCAAATTTATGACCAAGGTTATCTTGTGAGGAGGAGGAGGAGGAGGAG 900

QY 901 CCTGGGCGTTGGCGTTTAGAAAAGCTCATCTCTGGCCTTTCTGAGATCCATCCCTTTCT 960
DB 901 CCTGGGCGTTGGCGTTTAGAAAAGCTCATCTCTGGCCTTTCTGAGATCCATCCCTTTCT 960
QY 961 TTATTTTCTGTGACAGGAGCTTGTCTCTCACTCAGGCTGAGGTGAGTGCAGTGCATGATC 1020
DB 961 TTATTTTCTGTGACAGGAGCTTGTCTCTCACTCAGGCTGAGGTGAGTGCAGTGCATGATC 1020
QY 1021 TCGACTCAGCTGTAACCTCTCCCTCCCGGGTTCAAGGAGTTCCTCCTCCAGCTCCCTCA 1080
DB 1021 TCGACTCAGCTGTAACCTCTCCCTCCCGGGTTCAAGGAGTTCCTCCTCCAGCTCCCTCA 1080
QY 1081 GATAACAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
DB 1081 GATAACAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
QY 1141 TCATCATGTTGGGCGAGGTTGTTTGGAACTCCTGAGCTGAGGTGAGTGCAGCTCCAGCTTGGC 1200
DB 1141 TCATCATGTTGGGCGAGGTTGTTTGGAACTCCTGAGCTGAGGTGAGTGCAGCTCCAGCTTGGC 1200
QY 1201 CTCCCAAGTGTCTGGGATFACAGGCGATGAGCCACTGGGCCAGCTCAGATCCATCCCTTT 1260
DB 1201 CTCCCAAGTGTCTGGGATFACAGGCGATGAGCCACTGGGCCAGCTCAGATCCATCCCTTT 1260
QY 1261 CTAGGCGCAACAGCTCCATGTCGAAGGGGCGCATGCCACCCAGAGTTATGAGTACCTG 1320
DB 1261 CTAGGCGCAACAGCTCCATGTCGAAGGGGCGCATGCCACCCAGAGTTATGAGTACCTG 1320
QY 1321 GACTCCAGAAATTCCTTGGCTGGCTCCACATGCACTTCCAGGCGCTGCTTGGCGCTC 1380
DB 1321 GACTCCAGAAATTCCTTGGCTGGCTCCACATGCACTTCCAGGCGCTGCTTGGCGCTC 1380
QY 1381 TTCTATCCGTTCTGCTGTGAGTGTGATAGAACCACTGATGTGAGTACCTGGGCTTGGCG 1440
DB 1381 TTCTATCCGTTCTGCTGTGAGTGTGATAGAACCACTGATGTGAGTACCTGGGCTTGGCG 1440
QY 1441 GTGGCTGGAGATCTCTTCACTGTAGCATGGAGGGGCTTGTGCACTGCAATGTCTGCA 1500
DB 1441 GTGGCTGGAGATCTCTTCACTGTAGCATGGAGGGGCTTGTGCACTGCAATGTCTGCA 1500
QY 1501 TGCAGTGGTGGGAGTTCCTGGAATATGATGAGCTGGAGGTGGGAGAGAAATAGGCTTG 1560
DB 1501 TGCAGTGGTGGGAGTTCCTGGAATATGATGAGCTGGAGGTGGGAGAGAAATAGGCTTG 1560
QY 1561 GGGCAGCTCTGTCATGCCACCTCATCTGCCAAAACCTCAGTGCAGAGTCTGAGAGTCT 1620
DB 1561 GGGCAGCTCTGTCATGCCACCTCATCTGCCAAAACCTCAGTGCAGAGTCTGAGAGTCT 1620
QY 1621 AAATGTGAAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTGTCAAGGTAGGAGACCTT 1680
DB 1621 AAATGTGAAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTGTCAAGGTAGGAGACCTT 1680
QY 1681 GTGGCCTCCAGCTGCTTGGGCGCTCTTGGGCGCTCTTCTACGGGTCTGTCTGAGT 1740
DB 1681 GTGGCCTCCAGCTGCTTGGGCGCTCTTGGGCGCTCTTCTACGGGTCTGTCTGAGT 1740
QY 1741 CTCTATCAATCTTCAGGCGAGATTCATATTTAGACTCTTCACTGTTGACCTGAGCTT 1800
DB 1741 CTCTATCAATCTTCAGGCGAGATTCATATTTAGACTCTTCACTGTTGACCTGAGCTT 1800
QY 1801 TGCCCAAGATTAAGTGCATATTTAGTGTGGCTTGTGAGTGCATGATGAGTAAATATTAGACA 1860
DB 1801 TGCCCAAGATTAAGTGCATATTTAGTGTGGCTTGTGAGTGCATGATGAGTAAATATTAGACA 1860
QY 1861 TGTGTGTAGGCTGCTTCT 1920
DB 1861 TGTGTGTAGGCTGCTTCT 1920
QY 1921 AGTTTGTCTCCCTACAGGCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
DB 1921 AGTTTGTCTCCCTACAGGCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
QY 1981 AATTTACAGGAGTGGAAATCTCTGGCTGCACTTCACAAATGTATACAAATAAATAACAA 2040


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1981 AATTTCACGACTGCAATTCCTGGCTGGACTTCACAAATGTATACAAATCAATACAA 2040
QY 2041 GTCTGTGCTTTTATCAGAGGAGGCTGATCAATATAATGAAATIAAAAGGGGCTGGTC 2100
DB 2041 GTCTGTGCTTTTATCAGAGGAGGCTGATCAATATAATGAAATIAAAAGGGGCTGGTC 2100
QY 2101 CATATGTTCTGCTGTTTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG 2160
DB 2101 CATATGTTCTGCTGTTTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG 2160
QY 2161 TCCTTCTCTCAATTTATGAGAGAGACAGTAAGATGTTCTCTCGGGTCTCTGAGGGA 2220
DB 2161 TCCTTCTCTCAATTTATGAGAGAGACAGTAAGATGTTCTCTCGGGTCTCTGAGGGA 2220
QY 2221 CCTGGGAGCTCAGGCTGGGAATCCCAAGGACAGTGTGCTGCTATCAAAATCAAGTC 2280
DB 2221 CCTGGGAGCTCAGGCTGGGAATCCCAAGGACAGTGTGCTGCTATCAAAATCAAGTC 2280
QY 2281 CAGCTTTGTGGGGGAAACAAAGACAGCCATTACGAGAGGACTGTCCGGCTTCGCT 2340
DB 2281 CAGGTTTGTGGGGGAAACAAAGACAGCCATTACGAGAGGACTGTCCGGCTTCGCT 2340
QY 2341 CACCCAGCCTTAGCCCTTGAAGGAACAAAGACAGACAAATGATTCGGGCTCTGA 2400
DB 2341 CACCCAGCCTTAGCCCTTGAAGGAACAAAGACAGACAAATGATTCGGGCTCTGA 2400
QY 2401 GGGAGATTACGCTAGAGCTGTCTGCTGCTCAATCCGCTGCTGCTGCTGCTGCTGCT 2460
DB 2401 GGGAGATTACGCTAGAGCTGTCTGCTGCTCAATCCGCTGCTGCTGCTGCTGCTGCT 2460
QY 2461 AAAGGAAAAAATTCGGGAACAGAGATTTAGAGAAACAAATTCGAGTGTGCTGCT 2520
DB 2461 AAAGGAAAAAATTCGGGAACAGAGATTTAGAGAAACAAATTCGAGTGTGCTGCT 2520
QY 2521 GGTGCTGGGAGCTGGACTAGAGATCTGGGTCAGCGCGGAGCGGAGCTTCGCT 2580
DB 2521 GGTGCTGGGAGCTGGACTAGAGATCTGGGTCAGCGCGGAGCGGAGCTTCGCT 2580
QY 2581 GGTGCTTAGCGCGGCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
DB 2581 GGTGCTTAGCGCGGCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
QY 2641 GGTGCTTAGCGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 2700
DB 2641 GGTGCTTAGCGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 2700
QY 2701 TGGTGGGCGGCTGAACCTGCGCCGCTTTAAGGGGAGGAGGAGGAGGAGGAGGAGGAG 2760
DB 2701 TGGTGGGCGGCTGAACCTGCGCCGCTTTAAGGGGAGGAGGAGGAGGAGGAGGAGGAG 2760
QY 2761 TGAGTGACTGAACCTACATTAACAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820
DB 2761 TGAGTGACTGAACCTACATTAACAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820
QY 2821 GCTTTACCGGATGATTAACCTGCGCTGCGGTAAGGAGGAGGAGGAGGAGGAGGAGGAG 2880
DB 2821 GCTTTACCGGATGATTAACCTGCGCTGCGGTAAGGAGGAGGAGGAGGAGGAGGAGGAG 2880
QY 2881 GGGGAAAAACCC 2893
DB 2881 GGGGAAAAACCC 2893

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Mon May 12 08:12:12 2003

us-09-846-456-2.ini

Page 5

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: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: PCI/JP93/01293
:   FILING DATE: 10-Sep-93
:   APPLICATION NUMBER: JP 5-87195
:   FILING DATE: 14-Apr-93
:   APPLICATION NUMBER: 07/945,289
:   FILING DATE: 10-Sep-92
: ATTORNEY/AGENT INFORMATION:
:   NAME: Jane Massey Licata
:   REGISTRATION NUMBER: 32,257
:   REFERENCE/DOCKET NUMBER: ISPH-0031
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (609) 779-8488
:   TELEFAX: (609) 779-2400
: INFORMATION FOR SEQ ID NO: 25:
:   LENGTH: 686
:   TYPE: nucleic acid
:   STRANDEDNESS: Single
:   TOPOLOGY: Linear
:   ANTI-SENSE: NO
:   SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-397-2208-25

Query Match      8.4%  Score 30; DB 4; Length 686;
Best Local Similarity 46.3%  Pred. No. 3.9;
Matches 99; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 111 CCACGGGCGTCTGCTCAGCTCTGCGCGTGGCCCTTCAAGGCTTCGAGGACAAGC 170
DB 558 CCTCGGGCGCGGAGCCCTTGGGATAGGCTGTGCGCTTCCACGGGCTGAGATCGCTCGG 499
QY 171 TGGCGGCTGCTGGCTGAGGGAACATGGCATGTGGCTTCAGCTGAGTCTGCTGCTGGGAA 230
DB 498 AAGTCTTCTGATCGCGGACACCCCAACCTGGGGCCCTGCGCGGCAACAGTAAACTC 439
QY 231 GAACCTCACTTTCAGAGAACAAACAGTAAGCTTGGGTTTTCAGCAGCGGGGGGTTTC 290
DB 438 CACCACAGCATGACACCGCGCGGACCTGACCTCTCTGTGGCGGGGTTGTGTTGTTAC 379
QY 291 TCTCAATTTTCTTCTGCTGTTTGGTTTGGTGGAT 324
DB 378 GTTGTGTTTCTTTCAGATTTAGGATTCGTCT 345

RESULT 9
US-08-650-093C-25/C
: Sequence 25; Application US/08650093C
: Patent No. 6391542
: GENERAL INFORMATION:
:   APPLICANT: Kevin P. Anderson et al.
:   TITLE OF INVENTION: Compositions And Methods For Treatment Of
:   Hepatitis C Virus-Associated Diseases
:   NUMBER OF SEQUENCES: 118
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: LICATA & TYRRELL P.C.
:     STREET: 66 E. Main Street
:     CITY: Marlton
:     STATE: NJ
:     COUNTRY: USA
:     ZIP: 08053
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
:   COMPUTER: IBM Compatible
:   OPERATING SYSTEM: Windows 95
:   SOFTWARE: WORDPERFECT 6.1 for Windows
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/650-093C
:   FILING DATE: 17-May-1996
:   CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 08/452,841
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: FILING DATE: May 30, 1995
: APPLICATION NUMBER: 08/397,220
: FILING DATE: March 9, 1995
: APPLICATION NUMBER: 07/945,289
: FILING DATE: September 10, 1992
: ATTORNEY/AGENT INFORMATION:
:   NAME: Jane Massey Licata
:   REGISTRATION NUMBER: 32,257
:   REFERENCE/DOCKET NUMBER: ISPH-
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (609) 779-2400
:   TELEFAX: (609) 779-8488
: INFORMATION FOR SEQ ID NO: 25:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 686
:     TYPE: Nucleic Acid
:     STRANDEDNESS: Single
:     TOPOLOGY: Linear
:     ANTI-SENSE: NO
:     SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-650-093C-25

Query Match      8.4%  Score 30; DB 4; Length 686;
Best Local Similarity 46.3%  Pred. No. 3.9;
Matches 99; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 111 CCACGGGCGTCTGCTCAGCTCTGCGCGTGGCCCTTCCAGGCTCCCGAGGCACACGC 170
DB 558 CCTCGGGCGCGGAGCCCTTGGGATAGGCTGTGCGCTTCCACGGGTTTCCGACGCTCGG 499
QY 171 TGGCGGCTGCTGGCTGAGGGAACATGGCATGTGGCTTCAGCTGAGTCTGCTGCTGGGAA 230
DB 498 AAGTCTTCTGATCGCGGACACCCCAACCTGGGGCCCTGCGCGGCAACAGTAAACTC 439
QY 231 GAACCTCACTTTCAGAGAACAAACAGTAAGCTTGGGTTTTCAGCAGCGGGGGGTTTC 290
DB 438 CACCACAGCATGACACCGCGCGGACCTGACCTCTCTGTGGCGGGGTTGTGTTGTTAC 379
QY 291 TCTCAATTTTCTTCTGCTGTTTGGTTTGGTGGAT 324
DB 378 GTTGTGTTTCTTTCAGATTTAGGATTCGTCT 345

RESULT 10
US-08-866-650-2
: Sequence 2; Application US/0866650
: Patent No. 5919321
: GENERAL INFORMATION:
:   APPLICANT: Greenstein, Daniel S
:   APPLICANT: Takahara, Kazuhiko
:   APPLICANT: Hoffman, Guy G
:   TITLE OF INVENTION: Mammalian Tolloid-Like Protein
:   NUMBER OF SEQUENCES: 13
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Quarles & Brady
:     STREET: 1 South Pinckney Street
:     CITY: Madison
:     STATE: WI
:     COUNTRY: US
:     ZIP: 53703
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/866,650
:   FILING DATE:
:   CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
:   NAME: Brisson, Bennett J
:   REGISTRATION NUMBER: 47094
:   REFERENCE/DOCKET NUMBER: 960296,93839
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Best local Similarity 52.4%; Pred. No. 11;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 102 AATGACGAGGCGGCTCCCTGCTGTCAGCTCTGAGCGCTGCGCTTGAAGGCTGCGCA 161
DB 141 ATTATCTTCCCGGAGCAGCGCGGTGGGAGCGGGGCGGAGGAGGTGACAGTGGT 200
QY 162 GGCACAGGCTGGCGCTGCTGGGTGAGGAAATGATGCTGGCTGACGCTGAGGTTCY 241
DB 201 TGGCTGGCGGCTCTGACAGCGCGGAGCGGCTGGAGAGGAGGCTGGATGCA 260
QY 222 GCTGTG 227
DB 261 GCTGAG 266

RESULT 14
US-08-574-043A-7/c
: Sequence 7, Application US/08574043A
: Patent No. 5807692
: GENERAL INFORMATION:
: APPLICANT: Kinzler, Kenneth W.
: APPLICANT: El-Deiry, Wafik
: APPLICANT: Vogelstein, Bert
: TITLE OF INVENTION: p21WAF1 Derivatives and Diagnostic
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Allegretti, LTD
: STREET: 1001 G Street, NW suite 1100
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20001
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/574,043A
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Kadan, Sarah A.
: REGISTRATION NUMBER: 32,141
: REFERENCE/POCKET NUMBER: 01107.4998
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202.508.9100
: INFORMATION FOR SEQ ID NO: 7:
: LENGTH: 5143 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL LINE: GM
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT: 6p21.2
US-08-574-043A-7

Query Match 8.4%; Score 30; DB 1; Length 5143;
Best local Similarity 50.7%; Pred. No. 11;
Matches 72; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 135 CTGGCCGCTTCCAGGCTCCCGAGCCACACGCTGGCGTGTGAGGCAACAT 194
DB 4420 CTGGCCGAGTTCACAGCAGCCGCGGTCCCGGACCTCGGTGCTCAGAGGCACT 4361
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QY 195 GGCATGTTGGCTCAGCTAGGTTGCTGCTGGAAGAACTCCTCCTTTCAGAGGAACA 254
DB 4360 CCCTCTCCCGCAGCTCCCTGCTGCTGCTGGCTGGACACATTTCCCGCAGGAAGCA 4301
QY 255 AACAGTAAGCTGGTTTTTCA 276
DB 4300 GGCACAAATGCTTTTITA 4279

RESULT 14
US-08-795-015-7/c
: Sequence 7, Application US/08795015
: Patent No. 5871968
: GENERAL INFORMATION:
: APPLICANT: Kinzler, Kenneth W.
: APPLICANT: El-Deiry, Wafik
: APPLICANT: Vogelstein, Bert
: TITLE OF INVENTION: p21WAF1 Derivatives and Diagnostic
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Allegretti, LTD
: STREET: 1001 G Street, NW suite 1100
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20001
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/795,015
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/574,043
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kadan, Sarah A.
: REGISTRATION NUMBER: 32,141
: REFERENCE/POCKET NUMBER: 01107.49698
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202.508.9100
: TELEFAX: 202.508.9299
: INFORMATION FOR SEQ ID NO: 7:
: LENGTH: 5143 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL LINE: GM
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT: 6p21.2
US-08-795-015-7

Query Match 8.4%; Score 30; DB 2; Length 5143;
Best local Similarity 50.7%; Pred. No. 11;
Matches 72; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 135 CTGGCCGCTTCCAGGCTCCCGAGCCACACGCTGGCGTGTGAGGCAACAT 194
DB 4420 CTGGCCGAGTTCACAGCAGCCGCGGTCCCGGACCTCGGTGCTCAGAGGCACT 4361
QY 195 GGCATGTTGGCTCAGCTAGGTTGCTGCTGGAAGAACTCCTCCTTTCAGAGGAACA 254
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 12:47:56 ; Search time 599.179 Seconds
(without alignments)
9649.520 Million cell bpd

Title: US-09-846-456-2

perfect score:

Sequence: 1 TGGAGGTCTCAGCTGAGAGG.....GAGGGGAGGAGGCTATGTTG 357

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapexl 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308173

Maximum DH seq length: 0

	maximum	DB seq	length:
Maximum DB seq length:	200000000		

Post-processing: Minimum Match 0%

Local Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3:	em_estin:*
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5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hic:*
9:	gb_estl:*
10:	qb_estl:*
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15:	em_estun:*
16:	em_estom:*
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18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pln:*
21:	em_gss_fur:*
22:	em_gss_vir:*
23:	em_gss_mad:*
24:	em_gss_mus:*
25:	em_gss_oth:*
26:	em_gss_prc:*
27:	em_gss_ror:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Query			ID	Description
			Match	Length	DB		
1	154.4	44.6	547	9	AL698654	AL698654 DWF2686N	
2	144.2	40.4	736	9	AU135588	AU135588 AU135588	
3	75.8	21.2	619	10	B8657864	B8657864 HR657864	
4	73.8	20.7	292	14	Z44377	Z44377 HNT28681.n	
5	71.2	19.9	535	12	BG384217	BG384217 AY3216.MA	
c 5	42.4	11.9	982	17	CNS02D01	AY3216.MA AY3216.MA	

C	7	39.6	11.1	910	17	CNS0060N	AL064629	Drosophila
	8	39.4	11.0	562	14	BQ609447	BQ609447	BRY_5377
C	9	38.2	10.7	503	10	AV818336	AV818336	AV818336
	10	37.4	10.5	926	17	A2542175	A2542175	ENTGPR66TF
C	11	37	10.4	440	9	AA914462	AA914462	vz01f08.r
	12	37	10.4	520	10	AV955395	AV955395	AV955395
C	13	37	10.4	533	10	AB845237	AB845237	AV845237
	14	36.8	10.3	689	14	BQ868959	BQ868959	QGD4d10.y
C	15	36.4	10.2	571	10	AB864011	AB864011	AV864011
	16	36.4	10.2	579	10	AV892280	AV892280	AV892280
C	17	36	10.1	322	9	AU056364	AU056364	AU056364
	18	36	10.1	393	9	AU162694	AU162694	AU162694
C	19	36	10.1	571	10	AV862022	AV862022	AV862022
	20	36	10.1	872	17	CNS027E7	AL184552	Tetraodon
C	21	35.8	10.0	344	13	BM149133	BM149133	TCAAP2E63
	22	35.8	10.0	785	17	AF010859	AF010859	AF010859
C	23	35.8	10.0	939	17	CNS00CNG	AL059400	Drosophila
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C	27	35.4	9.9	390	10	BH841907	BH841907	BH841907
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C	31	35.4	9.9	565	10	AV972118	AV972118	AV972118
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C	33	35.4	9.9	937	17	CNS0065T	AL064580	Drosophila
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C	35	35.2	9.9	972	12	BF733920	BF733920	601569314
	36	35.2	9.9	1201	17	CNS0162E	AL106208	Drosophila
C	37	35	9.8	963	14	HQ444735	HQ444735	AGFNCOURT
	38	34.8	9.7	301	10	AW751638	AW751638	KC5-CT007
C	39	34.8	9.7	365	10	BH843149	BH843149	BH843149
	40	34.8	9.7	516	12	BF484412	BF484412	WHE2323.B
C	41	34.8	9.7	530	10	BE471178	BE471178	WHE0285_G
	42	34.8	9.7	1068	12	BE748387	BE748387	601571806
C	43	34.8	9.7	1068	17	CNS00ETV	AL069846	Drosophila
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C	45	34.6	9.7	884	17	CNS006U0	AL064923	Drosophila


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/db_xref="taxon:9823"
/clone_lib="MARC lPig"
/tissue_type="mucled"
/lab_host="DH10B"
/notes="vector: pCMV SPORT6; Site_1: Not; Site_2: Salt;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT      121 a   159 c   136 g   119 t
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Best Local Similarity 75.9%; Pred.No. 3.5e-09;
Matches 132; Conservative 0; Mismatches 28; Indels 14; Gaps 33;

QY    97 CAGTAAATGACCACGCCAGCGCTCCCTGGCTGCAGCTGTGGCGGCTGGCTTCATCAGAGCAT 156
DB     ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB    178 CAGTTAATGACCACGCCACAG--CGCCCCCTGCITAGAGCTCTGCGCACCTTCCTCAACGCGGC 235
QY    157 CCC-----GAGCCACACGGTGG-----GGCGTCTGCTGAGGAGAACATGACAAGTGG 204
DB     || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB    236 TCCGAGCGGAGGCACACGCGAGGTGGTGTGGTCCGACCTGAGGTAACTGCCATTATGG 295
QY    205 CTCAGCTGAGTGTGCTGCTGTGAAGAACCTCACTTCACAAAGACACAACA 258
DB     |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB    296 ACTCAACTGAGGTACTGCTGTGGAAGAACCTCACTTCACAAAGACACAACA 343

RESULT 6
CNSU2XWJ/C
LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence PCR end of clone
260P19 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL192682
VERSION ALL192682.1 GI:7830786
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Clariata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 982)
AUTHORS Roest-Crollius,H., Jaillon,O., Bastiva,C., Boumeau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Broiliet,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
tetraodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 982)
AUTHORS Roest-Crollius,H., Jaillon,O., Bastiva,C., Fizames,C., Fisher,C.,
Boumeau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the complete genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
3 (bases 1 to 982)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
Location/Qualifiers
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:9988"
/clone="260P19"

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F1		/product= "ABCL polypeptide"	
XX			
FN	W020007+971.AZ.		
XX			
FC	Z8-DEC-2000.		
XX			
FF	16-JUN-2000; 2000WO-US16591.		
XX			
PR	18-JUN-1999; 990S-0140264.		
PR	14-SEP-1999; 990S-0153872.		
PR	19-MAY-1999; 990S-0166573.		
XX			
PA	(CVTII-) CV THERAPEUTICS INC.		
PA	(UNITW) UNIV WASHINGTON.		
XX			
P1	Lawn RM, Wade D, Gram JF, Garvin M;		
XX			
DR	WP1; 2001137811/14.		
XX	P PSDB: AAB31465.		
P1	Adenosine triphosphate (ATP) binding cassette protein (ABC) 1		
P1	polynucleotides and polypeptides, useful for treatment of heart disease		
P1	and other disorders associated with hypercholesterolemia and		
P1	atherosclerosis .		

990S-0140264.
18 JUN-1999;
990S-0153872.
14-SEP-1999;
990S-0166574.
19-NOV-1999;

990S-0140264.
18 JUN-1999;
990S-0153872.
14-SEP-1999;
990S-0166574.
19-NOV-1999;

PA	(CVTH-) CV THERAPEUTICS INC.
XX	Lawn RM, Wade D, Garvin M;
PI	WP1; 2001-137812/14.
XX	
XX	
XX	Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PI	useful for the development of agents for the treatment of heart disease
PI	and other disorders associated with hypercholesterolemia and
PI	atherosclerosis -
XX	
XX	Disclosure; Page 148-154; 215pp; English.
PS	
XX	The present sequence encodes a human adenosine triphosphate (ATP)
CC	binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC	a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC	ATP hydrolysis to transport a wide variety of substrates across the
CC	plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC	mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC	Tangier disease, a genetic disorder characterised by abnormal
CC	HDL cholesterol metabolism. The ABC1 gene is localised to chromosome
CC	9q22-q31. The ABC1 genes and proteins are useful for developing
CC	pharmaceutical agents for the treatment of heart disease and other
CC	disorders associated with hypercholesterolemia and atherosclerosis. The
CC	genes are useful for developing screening assays to screen for compounds
CC	that regulate the expression of genes associated with cholesterol
CC	transport. The genes and proteins are also useful for are also useful
CC	as diagnostic indicators of cardiovascular disease and other disorders
XX	associated with hypercholesterolemia.
XX	
SQ	Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
	Query Match 44.6%; Score 159.4; DB 22; Length 10474;
	Best Local Similarity 81.8%; Pred. No. 1.2e-38;
	Matches 184; Conservative 0; Mismatches 41; Indels 0; Gaps 0
QY	97 CASTTAATGACAGCAGCGGGGCCCTGTGTCGAGCTCTGGCGGCTGCCTTCCAGAGGCT 156
DB
DB	227 CAGTTAA TGACAGCAGCGGGGCCCTGTGTCGAGCTCTGGCGGCTGCCTTCCAGAGGCT 296
QY	151 CCNAGKCCACAGCGCTGGCGCTGCTGGCTGAGGAACAAGCATCTTGACTGTCAGCTGAGG 216
DB
DB	287 ACCGAGCACAGCTGGGGGCTGCTGAGGAACAGCACTGCTGCTGCTGAGCTGAGG 346
QY	217 TTGCTGCTGTGGAAGAAGCTCAGTTTCAGAGAAGAACAGTAAGTACCTTTCGCTTTC 276
DB
DB	347 TTGCTGCTGTGGAAGAAGCTCAGTTTCAGAGAAGAACAGTAAGTACCTTTCGCTTTC 406
QY	277 GCAGCGGCGGGTCTCTCATTTTTCCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 521
DB
DB	407 GTGGCTGCTGCTCTATTATCTTCTCTGATTCGCTGCTGCTGCTGCTGCTGCTGCT 473
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AAF24686	
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XX	
XX	AAF24686;
XX	
DI	20 APR 2001 (first entry)
XX	
XX	Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
DE	
DE	
KW	Human: adenosine triphosphate binding cassette protein 1; ABC1;
KW	apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW	chromosome 9q22-q31; heart disease; hypercholesterolemia;
KW	atherosclerosis; cholesterol transport; ss.
XX	
QS	Homo sapiens.
XX	
XX	
FH	Key Location/Qualifiers
FT	CDS 323..7108
FT	/tag_ a

FT		/product= "defective ABC1 polypeptide"
XX	W0200078972-A2.	
XX	28-DEC-2000.	
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PD		
XX	16-JUN-2000; 2000UO-US16765.	
PF		
XX	18-JUN-1999; 990US-0140264.	
PR	14-SEP-1999; 990US-0153872.	
PR	19-NOV-1999; 990US-G166573.	
XX	(CVTH-) CV THERAPEUTICS INC.	
PA	Lawn RM, Wade D, Garvin M;	
XX	UPI; 2001-137812/14.	
DR		
XX	Adenosine triphosphate (ATP) binding cassette (ABC) polypeptides are useful for the development of agents for the treatment of lipid metabolism disorders associated with hypercholesterolemia and other disorders associated with hypercholesterolemia and atherosclerosis -	
PT		
PT		
PT		
PT		
PT		
XX	Disclosure; Page 170-176; 215pp; English.	
XX	The present sequence encodes a human adenosine triphospho-	
CC	binding cassette protein (ABC) 1 polypeptide, and is a	
CC	Tangier disease patient. ABC1 resides in cell membrane	
CC	ATP hydrolysis to transport a wide variety of substrates	
CC	plasma membrane. ABC1 is a pivotal protein in the ApoB	
CC	mobilisation of intracellular cholesterol stores. The ABC1	
CC	Tangier disease, a genetic disorder characterised by a	
CC	HDL-cholesterol metabolism. The ABC1 gene is localised	
CC	9q22-q31. The ABC1 genes and proteins are useful for	
CC	pharmaceutical agents for the treatment of heart disease	
CC	disorders associated with hypercholesterolemia and ath-	
CC	genes are useful for developing screening assays to select	
CC	that regulate the expression of genes associated with	
CC	transport. The genes and proteins are also useful for	
CC	as diagnostic indicators of cardiovascular disease and	
CC	associated with hypercholesterolemia.	
XX		
XX	Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 o	
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	Query Match 44.6%; Score 159.4; DB 22; Lenn	
	Best Local Similarity 81.8%; Pred. No. 1.2e-38;	
	Matches 184; Conservative 0; Mismatches 41; Indels	
QY	97 CAGTTAAATGATCAGTACCGGGGTCCCTGCTGTTCAGCTGTGCCCTGG	
Dd		
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QY		
Dd	157 CCGAGCCACACAGCTTGGGCGTGCTGGCTGAGGGAACATGGCATGTGGCG	
Dd	287 CCGAGCCACACGCCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTGGCG	
QY		
Dd	217 TTGCTGCTGTGGAAGAACCTCACTTTTCAGAAGGAACAACACAGTAGCT	
Dd	347 TTGCTGCTGTGGAAGAACCTCACTTTTCAGAAGGAACAACACATGTCA	
QY		
Dd	277 GCAGCGGGGGGTCTCTCATTTTCTTTCGTTTGGTTTGGTTGGG 321	
Dd	407 GTGGCTGGCTCTTAATTATCTTCTCTATCTCTATCTCTGTTCGG 451	
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XX	AAF24707;	
AC		
XX		
DT	20-APR-2001 (first entry)	
XX		

[illegible]

DE	Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.		
XX	Human; adenosine triphosphate binding cassette protein 1; ABC1;		
XX	apolipoprotein-mediated mobilisation; cholestero.; Tangier; disease;		
KW	chromosome 9q22-q31; heart disease; hypercholesterolemia;		
XX	atherosclerosis; cholesterol transport; ss.		
XX			
OS	Homo sapiens.		
XX			
FF	Key	Location/Qualifiers	
FF	323..7108		
FT	/*tag- a		
FT	/product- "defective ABC1 polypeptide"		
FT			
XX	W020007897; A2.		
XX	28 DEC-2000.		
XX	16-JUN-2000; 2000WO-US16591.		
XX	18-JUN-1999; 990S-0140264.		
XX	14-SEP-1999; 990S-0153872.		
XX	19-NOV-1999; 990S-0166573.		
XX			
XX	{(VTH-)} CV THERAPEUTICS INC.		
XX	(UNIV) UNIV WASHINGTON.		
XX			
XX	LAWO RM, Wade D, Oram JF, Garvin M;		
XX	WPI; 2001 137811/14.		
XX	P-PSDB; AAB31366.		
XX			
XX	Adenosine triphosphate (ATP) binding cassette protein (ABC) 1		
PT	polynucleotides and polypeptides, useful for treatment of heart disease		
PT	and other disorders associated with hypercholesterolemia and		
PT	atherosclerosis -		
XX			
XX	Claim 27: Page 144-150; 21pp; English.		
XX			
XX	The present sequence encodes a human adenosine triphosphate (ATP)		
XX	binding cassette protein (ABC) 1 polypeptide, and is isolated from		
CC	a Tangier disease patient. ABC1 resides in cell membranes and utilises		
CC	ATP hydrolysis to transport a wide variety of substrates across the		
CC	plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated		
CC	mobilisation of intracellular cholesterol stores. ABC1 is defective in		
CC	Tangier disease, a genetic disorder characterised by abnormal		
CC	HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome		
CC	9q22-q31. The ABC1 genes and proteins are useful for developing		
CC	pharmaceutical agents for the treatment of heart disease and other		
CC	disorders associated with hypercholesterolemia and atherosclerosis. The		
CC	genes are useful for developing screening assays to select for compounds		
CC	that regulate the expression of genes associated with cholesterol		
CC	transport. The genes and proteins are also useful for also useful		
CC	as diagnostic indicators of cardiovascular disease and other disorders		
XX	associated with hypercholesterolemia.		
XX			
XX	Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;		
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XX	Query Match	44.6%;	Score 159.4; DB 22; Length 10474;
XX	Best local Similarity	81.8%;	Pred. No. 1 2e-38;
XX	Matches 104; Conservative	0;	Mismatches 41; Indels 3; Gaps 9;
QY	97	CAGTTAATGACGACGACGGGGCTCCCTGCTGTCAGCTCTGGGCGCTGCTGAGGCT	156
DB	227	CAGTTAATGACGACGACGGGGCTCCCTGCTGTCAGCTCTGGGCGCTGCTGAGGCT	286
QY	157	CTGAGACCCACACGCTGGGCTGCTGGCTGACGGGAACAAGATGCTGGCTGAGGCTGAGG	276
DB	287	CTGAGACCCACACGCTGGGCTGCTGGCTGACGGGAACAAGATGCTGGCTGAGGCTGAGG	446
QY	217	TGCTGCTGTGGAAGAACTCAGCTTCAGAGCAACAGCAACAGCTTCAGCTTCAGCTTC	276
DB	347	TGCTGCTGTGGAAGAACTCAGCTTCAGAGCAACAGCAACAGCTTCAGCTTCAGCTTC	406

QY	277	GCAGCGGGGTTCTCCTCATITTCITCTTGATGGTTCAGTTGGG	321
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XX	AAPF24708:		
XX			
DT	20-APR-2001 (first entry)		
XX			
DE	Nucleotide sequence of ABCI polypeptide from Tangier d		
XX			
KW	Human; adenosine triphosphate binding cassette protein;		
KW	apolipoprotein-mediated mobilisation; cholesterol; Tangier		
KW	chromosome 9q22-q31; heart disease; hypercholesterolemia		
KW	atherosclerosis; cholesterol transport; ss.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	323..7108	
FT		/**tag= d	
FT		/product= "defective ABCI polypeptide"	
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PN	WO200078971-A2.		
PD	28-DEC-2000.		
XX			
PF	16-JUN-2000; 2006WO-US16591.		
PR	18-JUN-1999; 99US-0140264.		
PR	14-SEP-1999; 99US-0153872.		
PR	19-NOV-1999; 99US-0166573.		
XX	(CVTH-) CV THERAPEUTICS INC.		
PA	(UNITH-) UNIV WASHINGTON.		
XX			
PI	Lawn RM, Wade D, Oram JF, Garvin M;		
XX			
DR	WPI; 2001-137811/14.		
DR	P-PSDB: AAR31367.		
XX			
PT	Adenosine triphosphate (ATP) binding cassette protein		
PT	polynucleotides and polypeptides, useful for treatment		
PT	and other disorders associated with hypercholesterolem		
PT	atherosclerosis .		
XX			
PS	Claim 30; Page 165-172; 21lpp; English.		
XX			
CC	The present sequence encodes a human adenosine triphosph		
CC	binding cassette protein (ABC) l polypeptide, and is a		
CC	Tangier disease patient. ABCI resides in cell membr		
CC	ATP hydrolysis to transport a wide variety of substrat		
CC	plasma membrane. ABCI is a pivotal protein in the apol		
CC	mobilisation of intracellular cholesterol stores. ABCI		
CC	Tangier disease, a genetic disorder characterised by a		
CC	HDL-cholesterol metabolism. The ABCI gene is localise		
CC	9q22-q31. The ABCI genes and proteins are useful for		
CC	pharmaceutical agents for the treatment of heart diseas		
CC	disorders associated with hypercholesterolemia and ath		
CC	genes are useful for developing screening assays to sc		
CC	that regulate the expression of genes associated with		
CC	transport. The genes and proteins are also useful for		
CC	as diagnostic indicators of cardiovascular disease and		
CC	associated with hypercholesterolemia.		
XX			
SQ	Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 o		

Query Match 44.6% Score 159.4; DB 22; Length 451

[illegible]

CC The present sequence is human ABCI gene exon 1B DNA.

XX

SQ Sequence 159 BP; 32 A; 47 C; 48 G; 32 T; 0 other;

Query Match 44.5%; Score 159; DB 24; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.5e-39;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 100 TTATGACCACTACAGGGGTGTCCTTGTCAGACTTGGCGCTGCCTTCAGAGCTCCC 159
| | | | |
Db 1 TTATGAACAACAGAGGGTGGCTGCTGTCAGCTTGGCGCTGCCTTCAGAGCTCCC 50

Gy 160 GAGCACAACATGTGGAGGTGTGGTGTGAGGAAACATGCATGCTTGGCTTCAGGTTC 219
| | | | |
Db 61 GAGCACACGCTGAGGGCTGTGGCTGTGAGGAAACATGCATGCTTGGCTTCAGGTTC 120

Gy 220 CTGCTGTGGAGAAGCTTCACCTTCAGAGAAGACAAACA 258
| | | | |
Db 121 CTGCTGTGGAGAAGCTTCACCTTCAGAGAAGACAAACA 159

RESULT 11

AAS04035

ID AAS04035 standard; cDNA; 446 bp.

XX AC AAS04035;

XX AC

DT 12-SEP-2001 (first entry)

XX AC

DE Partial human ABCI cDNA sequence.

XX AC

KW Human; ABCI gene; atherosclerosis; reverse transport; cholesterol;
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW lecithin:cholesterol acetyltransferase; malaria; diabetes; ss.
XX AC

OS Homo sapiens.

XX AC

FH Key Location/Qualifiers

FT CDS 145..458

FT /start 1

FT /product= "Human ABCI protein, amino acids 1 to 60"

XX AC

PX W0200130848 A2.

XX AC

PX 01-MAY-2001.

XX AC

PX 25 OCT-2000; 2000W EPI0886.

XX AC

PR 26-OCT-1999; 1999P 402446.

PR 01-MAR-2000; 2000S 3186250.

XX AC

PA (AVET) AVENTIS PHARMA SA.

XX AC

PI benefie P, Rostet-Nourus M, Arnould-Requigne I, Prades C, Naudin L;
PI Lumine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
PI Dean M;

XX AC

DR WPI; 2001-316327/33.

DB P-PSUH; AA002175.

XX AC

XX New human ABCI nucleic acids and polypeptides for treating
atherosclerosis, malaria and diabetes .

PT

PI

PS Example 2; Page 167; 368pp; English.

XX AC

CC The sequence represents the partial coding sequence of human ABCI,
CC which encodes amino acids 1-60 of the human ABCI protein. The nucleic
CC acid sequence, primers and probes derived from the ABCI sequence, and
CC polypeptides and vectors are useful for the prevention of
CC atherosclerosis, in a subject affected by a dysfunction in the reverse
CC transport of cholesterol. The polypeptide encoded by the ABCI gene is
CC useful for serving for an active ingredient for the prevention or
CC treatment of a disease resulting from dysfunction in the reverse

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 11:17:01 : Search time 1066.03 seconds
(without alignments)
9746.207 Million cell updates/sec

Title: US-09-846-456-2

Perfect score: 357

Sequence: 1 tggaggtctcagctgagagg.....gagagaaggaatgtatttg 357

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109250

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_pro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

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15: em_ba:*

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18: em_in:*

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20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_pi:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rtd:*

36: em_htg_sam:*

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39: em_htgo_hum:*

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41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	357	100.0	357	6	AX351030 Sequence
2	353.8	99.1	149034	9	AF275948 Homo sapi
3	351.2	98.4	183993	6	AX092589 Sequence
4	340.2	95.3	480	9	HA252277 Homo sapi
5	340.2	95.3	124608	9	AL353685 Human DNA
6	340.2	95.3	175064	2	AC012230 Homo sapi
7	340.2	95.3	201144	9	AF287262 Homo sapi
8	251.2	70.4	90698	2	AC021345 Homo sapi
9	184.2	51.6	200	9	AF258624 Homo sapi
10	159.4	44.6	10442	6	AX060713 Sequence
11	159.4	44.6	10442	6	AX060892 Sequence
12	159.4	44.6	10442	9	AF285167 Homo sapi
13	159.4	44.6	10474	6	AX060719 Sequence
14	159.4	44.6	10474	6	AX060721 Sequence
15	159.4	44.6	10474	6	AX060898 Sequence
16	159.4	44.6	10474	6	AX060900 Sequence
17	159	44.5	159	6	AX351033 Sequence
18	147	41.2	647	9	AF258627 Homo sapi
19	145.8	40.8	446	6	AX127764 Sequence
20	145.8	40.8	446	6	AX139751 Sequence
21	145.8	40.8	7260	6	AX253452 Sequence
22	145.8	40.8	9741	6	AX127830 Sequence
23	145.8	40.8	9741	6	AX139817 Sequence
24	145.8	40.8	9741	6	AX351038 Sequence
25	145.8	40.8	9854	6	AX127831 Sequence
26	145.8	40.8	9854	6	AX139818 Sequence
27	144.2	40.4	1556	9	AB017924 Homo sapi
28	136.8	38.3	298	9	AB037924 Sequence
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30	135.8	38.0	7862	6	AX135712 Sequence
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40	42.6	11.9	22881	10	AF287142 Mus muscu
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ALIGNMENTS

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AX351030

LOCUS

DEFINITION

AX351030

ACCESSION

AX351030.1

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

1

REFERENCE

AUTHORS

TITLE

AX351030 Sequence 2 from Patent WO0183746. 357 bp DNA linear PAI 06-FEB-2002

Pred. No. is the number of results predicted by chance to have a

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JOURNAL Patent: WO 0183746-A 2 08-NOV-2001;
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/organism="Homo sapiens"
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BASE COUNT 64 a 78 c 116 g 59 t
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Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Homo sapiens ABCAL (ABCAL) gene, complete cds.
DEFINITION AF275948
ACCESSION AF275948
VERSION AF275948.1 GI:9247085
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCES 1 (bases 1 to 149034)
Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.,
Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Bandreschield,C.,
Prades,C., Chimini,G., Blackmon,E., Francoise,T., Duveitger,N.,
Rubin,E.M., Rosier,M., Deneffe,P., Fredrickson,F.S. and Brewer,H.B.,
Jr.
Complete genomic sequence of the human ABCAL gene: analysis of the
human and mouse ATP-binding cassette A promoter
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7587-7592 (2000)
20345099
PUBMED 10884428
REFERENCE 2 (bases 1 to 149034)
Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
Remaley,A.T., Yang,X.-P., Bandreschild,C.C., Blackmon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
Direct Submission
Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Health, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
TITLE Location/Qualifiers
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DEFINITION Sequence 1 from Patent W00115676.
ACCESSION AX092589
VERSION AX092589.1 G1:13444647
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 18499)
AUTHORS Hayden,M.R., Brooks-Willson,A.R., Pimstone,S.N. and Chao,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and
triglyceride levels
JOURNAL Patent: W0 0115676-A 1 08-MAR-2001;
FEATURES
source University of British Columbia (CA) : Xenon Genetics Inc. (CA)
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1 (bases 1 to 201144)
 Qiu, Y., Cavellier, L., Chiu, S., Yang, X., Rubin, E., and Cheng, J. F.
 Human and mouse ABCA1 comparative sequencing and transgenesis
 studies revealing novel regulatory sequences
 Genomics 73 (1), 66-76 (2001)
 21251004
 11352567

2 (bases 1 to 201144)
 Qiu, Y., Cavellier, L., Chiu, S., Rubin, E., and Cheng, J. F.
 Direct Submission
 Submitted (13-JUL-2000) Genome Science Department, Lawrence
 Berkeley National Laboratory, 1 Cyclotron Rd. MS 84-171, Berkeley,
 CA 94720, USA

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REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
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 TITLE
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FEATURES
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70.4% Score 251.2; DB 2; Length 96698;

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VERSION AF285167.1 GI:9755158
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Hominidae;
Schwartz, K., Lawn, R.M. and Wade, D.P.
ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
regulated by LXR
Unpublished
JOURNAL
REFERENCE 1 (bases 1 to 10442)
Lawn, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
Direct Submission
Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter drive, Palo Alto, CA 94304, USA
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 10474)
Lawn, R.M., Wade, D. and Garvin, M.
AUTHORS Regulation with binding cassette transporter protein abc1
TITLE Patent: WO 0078972-A 7 28-DEC-2000;
JOURNAL CV THERAPEUTICS, INC. (US)
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ACCESSION AX060721
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn, R.M., Wade, D., and Garvin, M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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ACCESSION AX060898
VERSION AX060898.1 GI:12406275
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE ATP binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
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Title: us-09-846-456-2

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Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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43	145.8	40.8	9870	9	US-09-846-827-125	Sequence 125, App
44	145.8	40.8	9870	9	US-09-846-827-126	Sequence 126, App
45	99	27.7	99	10	US-09-846-456-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-846-827-4
: Sequence 4, Application US/0984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFLER, PATRICE
: APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN AB2A1 GENE, THEIR USES,
: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: CURRENT FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 90/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 357
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-846-827-4

Query Match 100.0%; Score 357; DB 9; Length 357;

Best Local Similarity 100.0%; Pred No. 1.6e-108;

Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGGAGGCTCAGCTGAGAGGGCTGGATTAGCAGTCTCATTTGGTGTATGGCTTTTCAGCA 60

|||||

Db 1 TGGAGGCTCAGCTGAGAGGGCTGGATTAGCAGTCTCATTTGGTGTATGGCTTTTCAGCA 60

Oy 61 ATAATCATGCTGCTTCCCTCCTCTTATCTTTTACGTTAATGACCAAGCCAGCGGCT 120

|||||

Db 61 ATAATCATGCTGCTTCCCTCCTCTTATCTTTTACGTTAATGACCAAGCCAGCGGCT 120

Oy 121 CCCTGCTGTCAGCTCTGGCGGCTGCCCTCCAGGGCTCCGAGCCAGCAGCTGGGCTGCT 180

|||||

Db 121 CCCTGCTGTCAGCTCTGGCGGCTGCCCTCCAGGGCTCCGAGCCAGCAGCTGGGCTGCT 180

GenCore version 5.1.5
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OM nucleic - nucleic search, using SW model

Run on: May 9, 2003, 16:10:46 : Search time 939.59 seconds
(without alignments)
12013.236 Million cell updates/sec

Title: US-09-846-456-1

Perfect score: 3231
Sequence: 1 acaggcagtggtgcaggtg.....gccccatccgacacactt 3231

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searchcd: 2054640 seqs, 14551402878 residues

Word size : 30 *or more*

Total number of hits satisfying chosen parameters: 90357

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	3231	100.0	3231	6	AX351029 Sequence
2	2893	89.5	2893	6	AX351031 Sequence
3	1749	54.1	201144	9	AF287262 Homo sapi
4	1487	46.0	149034	9	AF275948 Homo sapi
5	891	27.6	96717	9	AL359182 Human DNA
6	814	25.2	183959	6	AX092589 Sequence
7	686	21.2	175064	2	AC012230 Homo sapi
8	589	18.2	1167	9	AF258623 Homo sapi
9	589	18.2	1167	9	AF258623S1 Homo sapi
10	541	16.7	1643	6	AX060715 Sequence
11	541	16.7	1643	6	AX060894 Sequence
12	348	10.8	69570	2	AC021246 Homo sapi
13	344	10.6	175064	2	AC012230 Homo sapi
14	336	10.4	1750	9	AK022254 Homo sapi
15	303	9.4	697	9	AF258627 Homo sapi
16	282	8.7	90698	2	AC021345 Homo sapi
17	228	7.1	7260	6	AX253452 Sequence
18	221	6.8	221	6	AX351032 Sequence
19	217	6.7	1556	9	AK024328 Homo sapi
20	205	6.3	9854	6	AX127831 Sequence
21	205	6.3	9854	6	AX139818 Sequence
22	197	6.1	10442	6	AX060713 Sequence
23	197	6.1	10442	6	AX060892 Sequence
24	197	6.1	10442	9	AF285167 Homo sapi
25	188	5.8	10474	6	AX060719 Sequence
26	188	5.8	10474	6	AX060721 Sequence
27	188	5.8	10474	6	AX060898 Sequence
28	188	5.8	10474	6	AX060900 Sequence
29	152	4.7	90698	2	AC021345 Homo sapi
30	117	3.6	117	6	AX351034 Sequence
31	92	2.8	446	6	AX127764 Sequence
32	92	2.8	446	6	AX139751 Sequence
33	92	2.8	9741	6	AX127830 Sequence
34	92	2.8	9741	6	AX139817 Sequence
35	92	2.8	9741	6	AX351038 Sequence
36	65	2.0	126295	9	AC004139 Homo sapi
37	61	1.9	186889	2	AL807243 Mus muscu
38	61	1.9	256966	9	AC021850 Homo sapi
39	61	1.9	276572	10	AF287263 Mus muscu
40	59	1.8	44897	2	AC103824 Homo sapi
41	58	1.8	57662	2	AC107969 Homo sapi
42	58	1.8	81874	9	HS931E15 Human DNA
43	58	1.8	98360	9	HS0247C2 Human DNA
44	58	1.8	141273	9	AL611933 Human DNA
45	58	1.8	145264	9	AC107939 Homo sapi
46	58	1.8	146312	2	AC015494 Homo sapi
47	58	1.8	155982	2	AC015495 Homo sapi
48	58	1.8	158071	2	AC018988 Homo sapi
49	58	1.8	158450	2	AC068082 Homo sapi
50	58	1.8	162419	2	AC093737 Homo sapi
51	58	1.8	166011	2	AC019307 Homo sapi
52	58	1.8	177533	2	AC069120 Homo sapi
53	58	1.8	188820	2	AC013281 Homo sapi
54	58	1.8	192396	9	AC012668 Homo sapi
55	58	1.8	193314	2	AC087478 Homo sapi
56	58	1.8	194433	9	HSBA425W5 Human DNA
57	58	1.8	195386	2	AL805961 Homo sapi
58	58	1.8	196520	2	AC083830 Homo sapi
59	58	1.8	201197	2	HS424J12 Homo sapi
60	58	1.8	292703	2	AC027176 Homo sapi
61	57	1.8	2532	9	AK094822 Homo sapi
62	57	1.8	4261	9	AB037785 Homo sapi
63	57	1.8	58958	9	AC091813 Homo sapi
64	57	1.8	91907	9	AC131566 Homo sapi
65	57	1.8	104906	9	AC069314 Homo sapi

c 66	1.8 116148	9	AC026423	AC026423 Homo sapi	c 139	55	1.7 135405	9	AC000025	AC000025 Homo sapi
c 67	1.8 116650	9	AC004003	AC004003 Homo sapi	140	55	1.7 136098	9	AC006970	AC006970 Homo sapi
c 68	1.8 117026	9	HS329A5	257832 Human DNA s	141	55	1.7 136646	9	AL138726	AL138726 Homo sapi
c 69	1.8 118603	2	AL1360017	AP060017 Homo sapi	c 142	55	1.7 138532	2	AL139222	AL139222 Homo sapi
c 70	1.8 121600	9	AP003555	AP003555 Homo sapi	c 143	55	1.7 140934	2	AC007460	AC007460 Homo sapi
c 71	1.8 125146	9	AL512770	AL512770 Human DNA	c 144	55	1.7 141456	9	AL355300	AL355300 Homo sapi
c 72	1.8 134036	9	AC007845	AC007845 Homo sapi	c 145	55	1.7 143583	9	HS467016	HS467016 Human DNA
c 73	1.8 140020	2	AC046162	AC046162 Homo sapi	c 146	55	1.7 145173	9	AC005599	AC005599 Homo sapi
c 74	1.8 152558	2	AC013487	AC013487 Homo sapi	c 147	55	1.7 147594	9	AC013829	AC013829 Homo sapi
c 75	1.8 154130	9	HS657E11	AL055413 Human DNA	c 148	55	1.7 148750	9	AC002326	AC002326 Genomic s
c 76	1.8 155691	9	AC016868	AC016868 Homo sapi	c 149	55	1.7 148975	2	AC012145	AC012145 Homo sapi
c 77	1.8 163437	9	AC082606	AC082606 Homo sapi	c 150	55	1.7 149308	9	AC005527	AC005527 Homo sapi
c 78	1.8 174711	9	AC026639	AC026639 Homo sapi	c 151	55	1.7 154772	9	AL138764	AL138764 Human DNA
c 79	1.8 175594	2	AC011134	AC011134 Homo sapi	c 152	55	1.7 155138	9	AL139260	AL139260 Human DNA
c 80	1.8 176212	2	AC084015	AC084015 Homo sapi	c 153	55	1.7 156619	2	AC013363	AC013363 Homo sapi
c 81	1.8 177303	2	AC026576	AC026576 Homo sapi	c 154	55	1.7 157566	9	AC022517	AC022517 Homo sapi
c 82	1.8 179641	9	AC058591	AC058591 Homo sapi	c 155	55	1.7 158193	2	AC010828	AC010828 Homo sapi
c 83	1.8 182427	2	AC061492	AC061492 Homo sapi	c 156	55	1.7 160450	2	AC087388	AC087388 Homo sapi
c 84	1.8 184444	9	AL359091	AL359091 Human DNA	c 157	55	1.7 161054	9	AC104444	AC104444 Homo sapi
c 85	1.8 185979	9	AC091296	AC091296 Pan trogl	c 158	55	1.7 161355	2	AC011154	AC011154 Homo sapi
c 86	1.8 187587	9	AC016026	AC016026 Homo sapi	c 159	55	1.7 162746	9	AC006050	AC006050 Homo sapi
c 87	1.8 189927	30	AC037439	AC037439 Homo sapi	c 160	55	1.7 163825	2	AC016669	AC016669 Homo sapi
c 88	1.8 190628	30	AC017012	AC017012 Homo sapi	c 161	55	1.7 163904	9	AP003070	AP003070 Homo sapi
c 89	1.8 196622	9	AC125238	AL145238 Homo sapi	c 162	55	1.7 169418	9	AC104163	AC104163 Homo sapi
c 90	1.8 196784	2	AC016543	AC016543 Homo sapi	c 163	55	1.7 169649	9	HS86286	HS86286 Homo sapi
c 91	1.8 199496	2	AF235096	AF235096 Homo sapi	c 164	55	1.7 171140	9	AC090685	AC090685 Homo sapi
c 92	1.8 203003	9	AL731556	AL731556 Human DNA	c 165	55	1.7 171966	2	AC092516	AC092516 Papio cyn
c 93	1.8 206835	9	AC093539	AC093539 Pan trogl	c 166	55	1.7 172449	2	AC124068	AC124068 Homo sapi
c 94	1.8 217981	9	AC074051	AC074051 Homo sapi	c 167	55	1.7 173016	2	AC019123	AC019123 Homo sapi
c 95	1.8 259685	2	AC063928	AC063928 Homo sapi	c 168	55	1.7 173785	9	AP000355	AP000355 Homo sapi
c 96	1.8 280140	2	AC055751	AC055751 Homo sapi	c 169	55	1.7 173864	9	AL365364	AL365364 Human DNA
c 97	1.8 303717	2	AC063530	AC063530 Homo sapi	c 170	55	1.7 175986	2	AC023071	AC023071 Homo sapi
c 98	1.7 48522	2	AC105112	AC105112 Homo sapi	c 171	55	1.7 176946	9	AC009078	AC009078 Homo sapi
c 99	1.7 51815	2	AC068454	AC068454 Homo sapi	c 172	55	1.7 177402	9	AC007406	AC007406 Homo sapi
c 100	1.7 139737	9	HS228H13	AL330955 Human DNA	c 173	55	1.7 177947	2	AC021467	AC021467 Homo sapi
c 101	1.7 144627	9	AC015710	AC015710 Homo sapi	c 174	55	1.7 180760	2	AC130435	AC130435 Homo sapi
c 102	1.7 150812	9	AC004765	AC004765 Homo sapi	c 175	55	1.7 181683	2	AC021618	AC021618 Homo sapi
c 103	1.7 155125	9	AC004561	AC004561 Homo sapi	c 176	55	1.7 182374	2	AP003968	AP003968 Homo sapi
c 104	1.7 157871	9	AC104365	AC104365 Homo sapi	c 177	55	1.7 182839	2	AC022619	AC022619 Homo sapi
c 105	1.7 165036	9	AC0100835	AC0100835 Homo sapi	c 178	55	1.7 184515	9	AC010653	AC010653 Homo sapi
c 106	1.7 166279	9	CNS01DRQ	AL117694 Human chr	c 179	55	1.7 186012	2	AC073083	AC073083 Homo sapi
c 107	1.7 171296	9	CNS06CR6	AL141262 Human chr	c 180	55	1.7 186981	9	AC006459	AC006459 Homo sapi
c 108	1.7 173354	2	AC027554	AC027554 Homo sapi	c 181	55	1.7 194211	2	AL442633	AL442633 Homo sapi
c 109	1.7 173692	2	AC025994	AC025994 Homo sapi	c 182	55	1.7 194955	9	AC084198	AC084198 Homo sapi
c 110	1.7 176850	2	AC103736	AC103736 Homo sapi	c 183	55	1.7 201134	9	AC021077	AC021077 Homo sapi
c 111	1.7 178035	2	AC058663	AC058663 Homo sapi	c 184	55	1.7 211001	9	AC018695	AC018695 Homo sapi
c 112	1.7 181637	9	AC011741	AC011741 Homo sapi	c 185	55	1.7 215617	9	AP000936	AP000936 Homo sapi
c 113	1.7 183083	9	AC007650	AC007650 Homo sapi	c 186	55	1.7 246240	6	AR036572	AR036572 Sequence
c 114	1.7 184396	9	AC010853	AC010853 Homo sapi	c 187	55	1.7 246240	6	AR036573	AR036573 Sequence
c 115	1.7 194198	2	AC013298	AC013298 Homo sapi	c 188	55	1.7 246240	6	AR036574	AR036574 Sequence
c 116	1.7 194627	9	AC096996	AC096996 Homo sapi	c 189	55	1.7 246242	9	HS091328	HS091328 Human heret
c 117	1.7 195840	9	CNS03000	AL249664 Human chr	c 190	55	1.7 318488	9	AC005529	AC005529 Homo sapi
c 118	1.7 201861	9	AC067796	AC067796 Homo sapi	c 191	55	1.7 328439	2	AL590137	AL590137 Homo sapi
c 119	1.7 216902	2	AC018475	AC018475 Homo sapi	c 192	54	1.7 82156	9	AP001617	AP001617 Homo sapi
c 120	1.7 227008	2	AP001771	AP001771 Homo sapi	c 193	54	1.7 23599	9	AP001504	AP001504 Homo sapi
c 121	1.7 227430	2	AC091590	AC091590 Homo sapi	c 194	54	1.7 43147	9	AP002955	AP002955 Homo sapi
c 122	1.7 279308	2	AC091918	AC091918 Homo sapi	c 195	54	1.7 44663	9	AC093518	AC093518 Homo sapi
c 123	1.7 13646	9	HUMBRPA	14219 Homo sapien	c 196	54	1.7 44913	9	AC005786	AC005786 Homo sapi
c 124	1.7 39915	9	AC010512	AC010512 Homo sapi	c 197	54	1.7 50334	9	HS995312	HS995312 Human DNA
c 125	1.7 51891	2	AC047403	AC047403 Homo sapi	c 198	54	1.7 69537	2	AC107379	AC107379 Homo sapi
c 126	1.7 55627	9	AL589951	AL589951 Human DNA	c 199	54	1.7 88738	9	AL513343	AL513343 Human DNA
c 127	1.7 64360	2	AC104349	AC104349 Homo sapi	c 200	54	1.7 94343	9	AC005255	AC005255 Homo sapi
c 128	1.7 81971	9	AC018753	AC018753 Homo sapi	c 201	54	1.7 95930	9	AC106033	AC106033 Homo sapi
c 129	1.7 84841	9	AL391813	AL391813 Human DNA	c 202	54	1.7 96075	9	AL590639	AL590639 Human DNA
c 130	1.7 85500	9	HS199H16	AL022320 Human DNA	c 203	54	1.7 102349	9	AL161671	AL161671 Human DNA
c 131	1.7 87925	9	AC065318	AC065318 Homo sapi	c 204	54	1.7 142116	9	AC034215	AC034215 Homo sapi
c 132	1.7 88238	9	AL353780	AL353780 Human DNA	c 205	54	1.7 145933	2	AC125837	AC125837 Rattus no
c 133	1.7 94882	2	AC002317	AC002317 Homo sapi	c 206	54	1.7 147345	9	AL158824	AL158824 Human DNA
c 134	1.7 110000	2	AL135900_1	Centromeric (2 ot	c 207	54	1.7 152867	9	AC027671	AC027671 Homo sapi
c 135	1.7 119082	9	AP000903	AP000903 Homo sapi	c 208	54	1.7 153716	9	AL590631	AL590631 Human DNA
c 136	1.7 125886	9	HS503G16	294020 Human s	c 209	54	1.7 155699	9	AL360176	AL360176 Human DNA
c 137	1.7 127145	9	HS1119A7	AL022413 Human DNA	c 210	54	1.7 157361	9	AC007606	AC007606 Homo sapi
c 138	1.7 127286	2	AC025286	AC025286 Homo sapi	c 211	54	1.7 160059	2	AC064867	AC064867 Homo sapi

c 358	52	1.6 108907	9	AL135911	431	52	1.6 171978	2	AC009669	AC009669 Homo sapi
c 359	52	1.6 110000	2	AC112773_0	c 432	52	1.6 172853	9	AC084361	AC084361 Homo sapi
c 360	52	1.6 111998	9	AC011509	c 433	52	1.6 172964	9	AC069413	AC069413 Homo sapi
c 361	52	1.6 112748	9	AC007242	c 434	52	1.6 173117	2	AL157885	AL157885 Homo sapi
c 362	52	1.6 123004	9	AC007384	c 435	52	1.6 173677	2	AC084768	AC084768 Homo sapi
c 363	52	1.6 126368	9	HS1043E3	c 436	52	1.6 173728	2	AC018507	AC018507 Homo sapi
c 364	52	1.6 126543	2	AC026154	c 437	52	1.6 174144	2	AC091765	AC091765 Homo sapi
c 365	52	1.6 129435	9	AL139114	c 438	52	1.6 174311	2	AL1365319	AL1365319 Homo sapi
c 366	52	1.6 131345	9	AC069023	c 439	52	1.6 174527	2	AC092859	AC092859 Pan trogl
c 367	52	1.6 133236	2	AC091026	c 440	52	1.6 174741	9	AC040977	AC040977 Homo sapi
c 368	52	1.6 133258	9	AC004944	c 441	52	1.6 175162	9	AL1590103	AL1590103 Human DNA
c 369	52	1.6 133614	2	AC025433	c 442	52	1.6 176153	9	AC006287	AC006287 Homo sapi
c 370	52	1.6 133690	9	AL158074	c 443	52	1.6 176967	2	AC022742	AC022742 Homo sapi
c 371	52	1.6 134308	9	AC011488	c 444	52	1.6 178494	2	AC009819	AC009819 Homo sapi
c 372	52	1.6 135964	9	AC005914	c 445	52	1.6 178710	2	AC106766	AC106766 Homo sapi
c 373	52	1.6 137473	2	AC015944	c 446	52	1.6 179655	2	AC018940	AC018940 Homo sapi
c 374	52	1.6 137718	9	AL137066	c 447	52	1.6 179969	9	AC016643	AC016643 Homo sapi
c 375	52	1.6 137945	2	AL133508	c 448	52	1.6 180531	9	AC008745	AC008745 Homo sapi
c 376	52	1.6 138063	9	AC092473	c 449	52	1.6 180533	2	AC119427	AC119427 Homo sapi
c 377	52	1.6 138839	9	HUAC002400	c 450	52	1.6 181636	2	AC025108	AC025108 Homo sapi
c 378	52	1.6 140179	2	AC084688	c 451	52	1.6 184519	9	AC007339	AC007339 Homo sapi
c 379	52	1.6 140919	9	AC110747	c 452	52	1.6 185316	9	AP002797	AP002797 Homo sapi
c 380	52	1.6 143423	9	AL161932	c 453	52	1.6 185367	2	AC092977	AC092977 Homo sapi
c 381	52	1.6 144620	9	ACC23787	c 454	52	1.6 186109	2	AP001890	AP001890 Homo sapi
c 382	52	1.6 145242	9	AC008610	c 455	52	1.6 186524	2	AC024465	AC024465 Homo sapi
c 383	52	1.6 145579	2	AC015737	c 456	52	1.6 186920	9	AP000824	AP000824 Homo sapi
c 384	52	1.6 145616	9	HS108K11	c 457	52	1.6 189174	9	AC092687	AC092687 Homo sapi
c 385	52	1.6 147461	9	AC027348	c 458	52	1.6 189219	9	AC092982	AC092982 Homo sapi
c 386	52	1.6 147565	2	AC080146	c 459	52	1.6 189355	2	AC053539	AC053539 Homo sapi
c 387	52	1.6 148278	9	AC006101	c 460	52	1.6 190253	2	AC090500	AC090500 Homo sapi
c 388	52	1.6 148507	9	AC008784	c 461	52	1.6 191717	2	AC104115	AC104115 Homo sapi
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TITLE Qiu, Y., Caveller, L., Chiu, S., Yang, X., Rubin, E. and Cheng, J. F.
Human and mouse ABCA1 comparative sequencing and transgenesis
studies revealing novel regulatory sequences
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JOURNAL 2 (bases 1 to 201144)
MEDLINE Qiu, Y., Caveller, L., Chiu, S., Rubin, E. and Cheng, J. F.
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Prades, C., Chimini, G., Blackmon, E., Francois, I., Duvetger, N.,
Rubio, E.M., Rosier, M., Deneffe, P., Fredrickson, D.S. and Brewer, H.B.
Jr.

TITLE Complete genomic sequence of the human ABCA1 gene: analysis of the
human and mouse ATP-binding cassette A Promoter

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)

MEDLINE 20345099

PUBMED 1068428

REFERENCE 2 (bases 1 to 149034)

AUTHORS Santamarina-Fojo, S., Peterson, K.M., Knapper, C.L., Freeman, L.A.,
Remaley, A.T., Yang, X.-P., Haudenschild, C.C., Blackmon, E.E.,
Francois, T.L. and Brewer, H.B. Jr.

TITLE Direct Submission

JOURNAL Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Health, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA

FEATURES Location/Qualifiers

source

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 Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Apr 22, 2000 this sequence version replaced g1:6454034.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: 12510

Center clone name: 1_M10

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.9607s

Consensus quality: 117571 bases at least Q40

Consensus quality: 145749 bases at least Q40

Consensus quality: 160940 bases at least Q40

Insert size: 185000; agarose-tp

Quality coverage: 2.9 in Q20 bases; agarose-tp

Quality coverage: 3.2 in Q20 bases; sum-cl-coverage

----- NOTE: This is a 'working draft' sequence. It currently
 * consists of 39 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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location/Qualifiers

FEATURES

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QY 2956

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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be genetically and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
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Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A.

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BASE COUNT 2498 a 2498 g 2835 t 4 others
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 DB 1 GCGCAGACCGCAGCGAGCGAGCGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 61

QY 2976 GCGCAGACCGCAGCGAGCGGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 3057
 DB 61 GCGCAGACCGCAGCGAGCGGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 129

QY 3048 GTCTCTTTTCTCCCTCTCCGAGAGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 3097
 DB 121 GTCTCTTTTCTCCCTCTCCGAGAGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 3097

QY 3098 ACAAAGTSGAAACAG 3114
 DB 181 ACAAAGTSGAAACAG 197

RESULT 25
 LOCUS AX060719 10474 bp DNA linear PAT 22-JAN-2001
 DEFINITION Sequence 7 from patent W0078972.
 ACCESSION AX060719
 VERSION AX060719.1 GI:12406108
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 1 (bases 1 to 10474)
 AUTHORS Lawn, R.M., Wade, D. and Garvin, M.
 TITLE Regulation with binding cassette transporter protein and
 JOURNAL Patent: W0 0078972-A 7 28 Dec 2000;
 CV THERAPEUTICS, INC. (US)
 FEATURES
 Location/Qualifiers
 Source 1..10474
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 2906 a 2305 c 2416 g 2844 t 4 others
 ORIGIN

Query Match 5.8%; Score 188; DB 6; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 9.6e-96;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2927 GCGCAGACCGCAGCGAGCGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 2986
 DB 42 GCGCAGACCGCAGCGAGCGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 101

QY 2987 GCGCAGACCGCAGCGAGCGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 3046
 DB 102 GCGCAGACCGCAGCGAGCGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 161

QY 3047 TCTCCCTTCTCCGGAGAGCTTCTCAAGGGGTAGAGAAAGAGACGCAACACAAAAGTG 3106
 DB 162 TCTCCCTTCTCCGGAGAGCTTCTCAAGGGGTAGAGAAAGAGACGCAACACAAAAGTG 221

QY 3107 GAAAACAG 3114
 DB 222 GAAAACAG 229

RESULT 27
 LOCUS AX060898 10474 bp DNA linear PAT 22-JAN-2001
 DEFINITION Sequence 9 from patent W0078972.
 ACCESSION AX060721
 VERSION AX060721.1 GI:12406109
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 1 (bases 1 to 10474)
 AUTHORS Lawn, R.M., Wade, D. and Garvin, M.
 TITLE Regulation with binding cassette transporter protein and
 JOURNAL Patent: W0 0078972-A 9 28 Dec 2000;
 CV THERAPEUTICS, INC. (US)
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 Location/Qualifiers
 Source 1..10474
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
 ORIGIN

Query Match 5.8%; Score 188; DB 6; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 9.6e-96;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2927 GCGCAGACCGCAGCGAGCGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 2986
 DB 42 GCGCAGACCGCAGCGAGCGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 101

QY 2987 GCGCAGACCGCAGCGAGCGCTTCTCTCCGGGCTGCGGCGAGCGCGGAGCTCCG 3046
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QY 3107 GAAAACAG 3114
 DB 222 GAAAACAG 229

RESULT 27
 LOCUS AX060898 10474 bp DNA linear PAT 22-JAN-2001
 DEFINITION Sequence 9 from patent W0078972.
 ACCESSION AX060898
 VERSION AX060898.1 GI:12406109

KEYWORDS

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10474)

AUTHORS Lawo, K.M., Wade, D., Oram, J.F. and Garvin, M.

TITLE ATP binding cassette transporter protein abci polypeptides

JOURNAL Patent: WO 0078971-A 9 28-DEC-2000

CV THERAPEUTICS, INC. (US)

FEATURES Location/Qualifiers

source 1..10474

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others

ORIGIN

Query Match 5.88; Score 188; DB 6; Length 10474;

Best Local Similarity 100.0%; Pred. No. 9,6e-96;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2927 CCAGAGCGGAGCGGACCTTCTCTCCGGGCTGCGGAGGCGGAGCGGAGCTCG 2986

Db 42 CCGAGAGCGGAGCGGACCTTCTCTCCGGGCTGCGGAGGCGGAGCGGAGCTCG 101

QY 2987 CGACCAACAGCGGCTTCTCAGGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCT 3045

Db 102 CGACCAACAGCGGCTTCTCAGGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCT 161

QY 4047 TCTCCCTTCTCCGAGGCTTGTCAAGGCTAGGAGAGAGAGAGAGAGAGAGAGAG 3106

Db 162 TCTCCCTTCTCCGAGGCTTGTCAAGGCTAGGAGAGAGAGAGAGAGAGAGAGAG 221

QY 3107 GAAACAG 3114

Db 222 GAAACAG 229

RESULT 29

AX060900

DEFINITION Sequence 9 from Patent WO0078971.

ACCESSION AX060900

VERSION AX060900.1 GI:12406276

KEYWORDS

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10474)

AUTHORS Lawo, K.M., Wade, D., Oram, J.F. and Garvin, M.

TITLE ATP binding cassette transporter protein abci polypeptides

JOURNAL Patent: WO 0078971-A 9 28-DEC-2000

CV THERAPEUTICS, INC. (US)

FEATURES Location/Qualifiers

source 1..10474

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others

ORIGIN

Query Match 5.88; Score 188; DB 6; Length 10474;

Best Local Similarity 100.0%; Pred. No. 9,6e-96;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2927 CCAGAGCGGAGCGGACCTTCTCTCCGGGCTGCGGAGGCGGAGCGGAGCTCG 2986

Db 42 CCGAGAGCGGAGCGGACCTTCTCTCCGGGCTGCGGAGGCGGAGCGGAGCTCG 101

QY 2987 CGACCAACAGCGGCTTCTCAGGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCT 3045

Db 102 CGACCAACAGCGGCTTCTCAGGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCT 161

QY 3107 GAAACAG 3114

Db 222 GAAACAG 229

RESULT 29

AX060900

DEFINITION Sequence 9 from Patent WO0078971.

ACCESSION AX060900

VERSION AX060900.1 GI:12406276

KEYWORDS

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10474)

AUTHORS Lawo, K.M., Wade, D., Oram, J.F. and Garvin, M.

TITLE ATP binding cassette transporter protein abci polypeptides

JOURNAL Patent: WO 0078971-A 9 28-DEC-2000

CV THERAPEUTICS, INC. (US)

FEATURES Location/Qualifiers

source 1..10474

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/db_xref="taxon:9606"

BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others

ORIGIN

QY 3047 TCTCCCTTCTCCGAGGCTTGTCAAGGCTAGGAGAGAGAGAGAGAGAGAGAGAG 3106

Db 162 TCTCCCTTCTCCGAGGCTTGTCAAGGCTAGGAGAGAGAGAGAGAGAGAGAGAG 221

QY 3107 GAAACAG 3114

Db 222 GAAACAG 229

RESULT 29

AC021345

DEFINITION Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.

ACCESSION AC021345

VERSION AC021345.2 GI:9130845

KEYWORDS HTG; HTGS_PHASE0.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 90698)

AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 90698)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavsky, L., Boukhvalter, B., Brown, A., Burkert, G., Castle, A., Choquel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P., DeRellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyua, S., Grant, C., Hago, B., Heaford, A., Horton, L., Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, J., Lehorzky, J., Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrum, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, N., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

JOURNAL Direct Submission

REFERENCE 3 (bases 1 to 90698)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavsky, L., Boukhvalter, B., Brown, A., Burkert, G., Castle, A., Choquel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P., DeRellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyua, S., Grant, C., Hago, B., Heaford, A., Horton, L., Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, J., Lehorzky, J., Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrum, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, N., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

JOURNAL Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIGR

Web site: http://www.seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: 14483

Center clone name: 24_J_9

NOTE: This record contains 92 individual

sequencing reads that have not been assembled into

contigs. Runs of N are used to separate the reads

and the order in which they appear is completely

arbitrary. Low-pass sequence sampling is useful for

identifying clones that may be gene-rich and allows

overlap relationships among clones to be deduced.

However, it should not be assumed that this clone

will be sequenced to completion. In the event that

the record is updated, the accession number will

be preserved.

1 910: contig of 910 bp in length

911 1010: gap of 100 bp

1011 1874: contig of 863 bp in length

1874 1973: gap of 100 bp

1974 2824: contig of 851 bp in length
2825 2924: gap of 100 bp
2925 3802: contig of 878 bp in length
3803 3902: gap of 100 bp
3903 4816: contig of 914 bp in length
4817 4916: gap of 100 bp
4917 5759: contig of 843 bp in length
5760 5859: gap of 100 bp
5860 6764: contig of 905 bp in length
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6865 7747: contig of 883 bp in length
7748 7847: gap of 100 bp
7848 8755: contig of 938 bp in length
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9854 10757: contig of 904 bp in length
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11833 12739: contig of 907 bp in length
12740 12839: gap of 100 bp
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33448 33547: gap of 100 bp
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36541 37422: contig of 882 bp in length
37423 37522: gap of 100 bp
37523 38402: contig of 880 bp in length

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61168 62051: contig of 884 bp in length
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62152 63022: contig of 871 bp in length
63023 63122: gap of 100 bp
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69911 70010: gap of 100 bp

Query Match: 4.78; Score 152; DB 2; Length 90698;
Best Local Similarity 99.28; Pred. No. 5.8e-75;
Matches 252; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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EB 10177 TACTCGAGGTTGGAGTTGGCAATGACGCCAGATCGGCACCTCCAGCTCGGCA 10236

Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G. H.,
 Remaley, A., Brewer, H. B. and Dean, M.
 Nucleic acids of the human abcl gene and their therapeutic and
 diagnostic application
 Patent: WO 0130848-A 69 03-MAY-2001;
 Aventis Pharma S.A. (FR)
 Location/Qualifiers
 1. 9741
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 2650 a 2180 c 2290 g 2620 t 1 others
 ORIGIN
 Query Match 2.8%; Score 92; DB 6; Length 9741;
 Best Local Similarity 100.0%; Pred. No. 1.5e-40;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3023 CTGTGTTTCCCGGGTCTGTTTCTCCCTCTCCGGAAGGCTTGTCAAGGGGTAGGA 3082
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 DB 61 GAAAGACGCGCAACACAAAAGTGGAAAACAG 92
 RESULT 34
 AX139817 9741 bp DNA linear PAT 30-MAY-2001
 LOCUS
 DEFINITION Sequence 69 from Patent EP1096012.
 ACCESSION AX139817
 VERSION AX139817.1 GI:14275399
 KEYWORDS
 SOURCE human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 9741)
 Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G. H.,
 Remaley, A., Brewer, H. B. and Dean, M.
 Nucleic acids of the human abcl gene and their therapeutic and
 diagnostic application
 Patent: EP 1096012-A 69 02-MAY-2001;
 Aventis Pharma S.A. (FR)
 Location/Qualifiers
 1. 9741
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 2650 a 2180 c 2290 g 2620 t 1 others
 ORIGIN
 Query Match 2.8%; Score 92; DB 6; Length 9741;
 Best Local Similarity 100.0%; Pred. No. 1.5e-40;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3023 CTGTGTTTCCCGGGTCTGTTTCTCCCTCTCCGGAAGGCTTGTCAAGGGGTAGGA 3082
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 RESULT 35
 AX351038 9741 bp DNA linear PAT 06-FEB-2002
 LOCUS
 DEFINITION Sequence 10 from Patent WO0183746.
 ACCESSION AX351038
 VERSION AX351038.1 GI:18616393
 KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Rosier, Montus, M. F., Prades, C., Lemoine, C., Naudin, L., Denelle, P.,
 Brewer, H., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
 Regulatory nucleic acid sequences of the abcl gene
 Patent: WO 0183746-A 10 08-NOV-2001;
 Aventis Pharma S.A. (FR)
 Location/Qualifiers
 1. 9741
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 2650 a 2180 c 2290 g 2620 t 1 others
 ORIGIN
 Query Match 2.8%; Score 92; DB 6; Length 9741;
 Best Local Similarity 100.0%; Pred. No. 1.5e-40;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3023 CTGTGTTTCCCGGGTCTGTTTCTCCCTCTCCGGAAGGCTTGTCAAGGGGTAGGA 3082
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 QY 3083 GAAAGACGCGCAACACAAAAGTGGAAAACAG 3114
 DB 61 GAAAGACGCGCAACACAAAAGTGGAAAACAG 92
 RESULT 36
 AC004139 126295 bp DNA linear PRI 02-SEP-1998
 LOCUS
 DEFINITION Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.
 ACCESSION AC004139
 VERSION AC004139.1 GI:3513309
 KEYWORDS
 SOURCE HTG.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 126295)
 Birren, R., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome 17, clone HRPC843B9
 Unpublished
 2 (bases 1 to 126295)
 Birren, B., Fasmann, K., McKernan, K., Nusbaum, C., Richardson, P.,
 Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckery, R.,
 Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P.,
 Daly, M., J., Depayre, E., Devon, K., Dewar, K., Donelan, L., Durette, B.,
 Etmadi, S., Ferreira, P., Forrest, C., Funke, R., Gage, D., Gardyna, S.,
 Gensheimer, S., Geraghty, K., Gilmartin, T., Gray, D., Hagos, H.,
 Harris, K., Horton, L., Howland, J. C., Hul, L., Jacotot, L., Linton, L.,
 McKernan, K., Marquis, N., McEwan, P., McGurk, A., Meidrum, J.,
 Molla, M., Morris, W., Morrow, J., Nachman, A., Naylor, J., O'Connor, T.,
 Pavlin, B., Peterson, K., Ranganath, S., Riley, R., Roberts, D.,
 Rollins, G., Rossello, R., Roy, A., Shyam, R., Soohoo, S.,
 Stange-Thomann, N., Stillwell, J., Stone, C., Strickland, C., Sydney, K.,
 Tang, L., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y.,
 Ye, W. J., Zemseval, I., Zhao, J. and Zody, M.
 Direct Submission
 Submitted (13-FEB-1998) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 126295)
 Birren, B., Fasmann, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
 Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckery, R., Benn, J.,
 Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M.,
 Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E.,
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 Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P.,
 Stange-Thomann, N., Stillwell, J., Stojanovic, N., Store, C.,
 Subramanian, A., Testave, S., Tichovolsky, N., Torruella-Miller, I.,
 Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D.,
 Ye, W. J., Zhao, J. and Zody, M.
 Direct Submission
 Submitted (02-SEP-1998) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Sep 2, 1998 this sequence version replaced qi:3451370.
 All repeats were identified using RepeatMasker: Smit, A.F.A. &
 Green, P. (1996-1997)
<http://ftp.genome.washington.edu/HW/RepeatMasker.html>.

TITLE JOURNAL

COMMENT

FEATURES

Source

Location/Qualifiers
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36204..36516
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Query Match      2.0%  Score 65;  DB 9;  Length 25295;
Best local Similarity 100.0%;  Pred. No. 6.1e-25;
Matches 65;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1017 GATCTCGACTGACTGACCTGCTCCCTCCGGGTTCAAGGATTCCTGCTGAGCTC 1076
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Db 31115 GATCTCGACTGACTGACCTGACCTGCTCCGGGTTCAAGGATTCCTGCTGAGCTC 31174

QY 1077 CTGAG 1081
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Db 31175 CTGAG 31179

RESULT 37
AL807243/1 186889 bp DNA linear HIG 30-JUN-2002
LOCUS MUS MUSCULUS CHROMOSOME 4 CLONE RP23-25D17. *** SEQUENCING IN
DEFINITION PROGRESS ***, 24 unordered pieces.
ACCESSION AL807243
VERSION AL807243.5 Gi:21668234
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT;
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE 1 (bases 1 to 186889)
JOURNAL Direct Submission
Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonereq@sanger.ac.uk
On Jul 2, 2002 this sequence version replaced at 21668136.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BW25D17
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% G; reads
Consensus quality: 175959 bases at least Q40
Consensus quality: 179463 bases at least Q30
Consensus quality: 182069 bases at least Q20
Insert size: 184589; sum-of-ctrls
Insert size: 189466; 5.5% error; average-tp
Quality coverage: 4.72x in Q20 bases; sum-of-ctrls Quality
coverage: 4.82x in Q20 bases; average-tp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 4849: contig of 4849 bp in length
* 4850 4949: gap of 100 bp

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* 22721 29963: contig of 7243 bp in length
* 29964 30063: gap of 100 bp
* 30064 40087: contig of 10024 bp in length
* 40088 40187: gap of 100 bp
* 40188 44438: contig of 4251 bp in length
* 44439 44538: gap of 100 bp
* 44539 48960: contig of 4422 bp in length
* 48961 49060: gap of 100 bp
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* 56008 56107: gap of 100 bp
* 56108 58284: contig of 2177 bp in length
* 58285 58384: gap of 100 bp
* 58385 60786: contig of 2402 bp in length
* 60787 60886: gap of 100 bp
* 60887 66707: contig of 5821 bp in length
* 66708 66807: gap of 100 bp
* 66808 92102: contig of 25295 bp in length
* 92103 92202: gap of 100 bp
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* 99910 100009: gap of 100 bp
* 100010 103760: contig of 3751 bp in length
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* 110766 110865: gap of 100 bp
* 110866 114785: gap of 100 bp
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* 126060 128749: contig of 2690 bp in length
* 128750 128849: gap of 100 bp
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* 134931 135030: gap of 100 bp
* 135031 139301: contig of 4271 bp in length
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Raymond, C., Retta, R., Kieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triplio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (29-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 4897)

REFERENCE
AUTHORS

Barna, N., Bastien, V., Bloom, T., Boguski, L., Boeckmann, H., Camarata, J., Chang, J., Chazaro, B., Choe, Y., Collymore, A., Cook, A., Cooke, P., DeRubeis, R., Dewar, R., Diaz, J., Dodge, S., Fato, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardina, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Landers, J., Levine, R., Lischke, T., K., Liv, G., MacLean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneses, J., Minova, T., Miodini, V., Murphy, J., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., O'Connor, J., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 30, 2002 this sequence version replaced a:1714709.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: submissions@genome.wi.mit.edu
Project information
Center project name: 121814
Center Clone name: 2319_014

NOTE: This record contains 54 individual:
• sequencing reads that have not been assembled into
• contigs. Runs of N are used to separate the reads
• and the order in which they appear is completely
• arbitrary. Low-pass sequence sampling is useful for
• identifying clones that may be over-represented and allows
• overlap relationships among clones to be deduced.
• However, it should not be assumed that this clone
• will be sequenced to completion. In the event that
• the record is updated, the accession number will
• be preserved.

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6628 6727: gap of 100 bp
6728 7449: contig of 722 bp in length

7450 7549: gap of 100 bp
7550 8322: contig of 773 bp in length
8323 8422: gap of 100 bp
8423 9126: contig of 704 bp in length
9127 9226: gap of 100 bp
9227 9973: contig of 747 bp in length
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* 50585 51288: contig of 704 bp in length
* 51289 51388: gap of 100 bp
* 51389 52107: contig of 719 bp in length
* 52108 52207: gap of 100 bp
* 52208 52909: contig of 702 bp in length
* 52910 53009: gap of 100 bp
* 53010 53665: contig of 656 bp in length
* 53666 53765: gap of 100 bp
* 53766 54444: contig of 679 bp in length

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Best Local Similarity 100.0%; Pred. No. 6e-21;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGAGCCACTGCGCCAGC 1244

DB 39017 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGAGCCACTGCGCCAGC 38960

RESULT 42

HS931E15/C

LOCUS HS931E15 81874 bp DNA linear PRI 23-NOV-1999

DEFINITION Human DNA sequence from clone 931E15 on chromosome Xq25. Contains

STSS, GSSs and genomic marker DXS8098, complete sequence.

ACCESSION AL023575

VERSION AL023575.1 GI:3618163

KEYWORDS HTG; DXS8098.

SOURCE Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 81874)

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (24-SEP-1998) Sanger Centre, Hinxton, Cambridgeshire.

CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On Sep 18, 1998 this sequence version replaced gi:3550203.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

annotated human repeat sequence elements (e.g. Alu). Where the

sequence is ambiguous, there is an annotation using the 'unsure'

feature key.

This sequence was generated from part of bacterial clone contigs of

human chromosome X, constructed by the Sanger Centre Chromosome X

Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/ChrX

931E15 is from the library RPC15 constructed at the Roswell Park

Cancer Institute by the group of Pieter de Jong. For further

details see http://bacpac.med.buffalo.edu/VECTOR: prYPAC2

IMPORTANT: This sequence is not the entire insert of clone 931E15.

It may be shorter because we only sequence overlapping sections

once, or longer because we arrange for a small overlap between

neighbouring submissions.

The true left end of 424312 (282207) is at 36643 in this sequence.

The true right end of 50662 (282213) is at 37431.

Location/Qualifiers

i. 81874


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complement(32381..33599)
/Note="MLT2-internal repeat: matches 4572..3316 of
consensus"
repeat_region 33603..33906
/Note="AluJo repeat: matches 1..302 of consensus"
34020..34321
/Note="AluJb repeat: matches 1..301 of consensus"
complement(34388..34933)

Query Match 1.8% Score 58; DB 9; Length 81874;
Best Local Similarity 100.0%; Pred. No. 6.2e-21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 GTGCCACCTGGCTCCCAAGTCTGGATTACAGCATGAGCTACTTCGTCGACG 1244
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Db 19890 GTGCCACCTGGCTCCCAAGTCTGGATTACAGCATGAGCTACTTCGTCGACG 19893

RESULT 43
HSDJ247C2/c 98360 bp DNA linear PRI 03-AUG-2001
LOCUS Human DNA sequence from clone RPI-247C2 on chromosome 11p13
DEFINITION Contains STSS and GSSs, complete sequence.
ACCESSION AL049713.20 GI:103334639
VERSION AL049713.20
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 98360)
Wallis, J.
Direct Submission
Submitted (02-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 27, 2000 this sequence version replaced at1606528.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi, EMBL; Swi, SWISSPROT; Trn, TrEMBL; Wp, WormPeP; information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/H_sapiens/wormpep/IMPORTANT: this
sequence is not the entire insert of clone RPI-247C2. It may be
shorter because we sequence overlapping sections only once, except
for a 100 base overlap.
The true left end of clone RPI-247C2 is at 1 in this sequence. The
true left end of clone RPI-879J18 is at 98261 in this sequence. The
true right end of clone RPI-85M6 is at 4631 in this sequence. This
sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RPI-247C2 is from the
library RPI-1 constructed by the group of Pieter de Jong. For
further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
Location/Qualifiers
1..98360
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="p13"

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```

/clone="RPI-247C2"
/clone_lib="BPC1-1"
complement(627..983)
/Note="match: STS: Em:HS198YB10"
804..829
/Note="13 copies 2 mer gt 100% conserved"
3773..3810
/Note="L1PA11 repeat: matches 2154..2191 of consensus"
4956..3992
/Note="L1PA11 repeat: matches 2180..2215 of consensus"
4265..5286
/Note="L1PA11 repeat: matches 2215..3216 of consensus"
5586..8453
/Note="L1PA11 repeat: matches 3216..6162 of consensus"
10697..10906
/Note="L1MEC repeat: matches 2142..1979 of consensus"
12202..11493
/Note="L1MEC repeat: matches 1978..2279 of consensus"
13794..113857
/Note="32 copies 2 mer cc 68% conserved"
14618..115078
/Note="L1R2 repeat: matches 1..449 of consensus"
complement(14642..15322)
/Note="match: GSS: Em:B04935"
15910..15911
/Note="Single clone region. Assembly confirmed by
restriction digest data."
/Note="13 copies 2 mer tg 92% conserved"
16984..17077
/Note="MLT1A2 repeat: matches 1..92 of consensus"
17380..17654
/Note="MLT1A2 repeat: matches 92..374 of consensus"
complement(17710..18372)
/Note="match: GSS: Em:AQ485260"
18444..18750
/Note="match: GSS: Em:AQ545989"
complement(20477..21170)
/Note="match: GSS: Em:AQ488664"
complement(20761..21177)
/Note="match: GSS: Em:AQ669825"
complement(23626..26158)
/Note="match: GSS: Em:AQ505438"
25991..26104
/Note="match: GSS: Em:AZ393320"
26106..26561
/Note="match: GSS: Em:AZ393320"
24550..24636
/Note="L1MAB repeat: matches 6175..6268 of consensus"
33434..33473
/Note="L1R29 repeat: matches 56..98 of consensus"
complement(34597..34987)
/Note="match: GSS: Em:AQ877394"
35999..36384
/Note="L1PH3 repeat: matches 5743..6147 of consensus"
37497..37542
/Note="23 copies 2 mer tg 100% conserved"
38577..38776
/Note="match: STS: Em:G45608"
38617..38781
/Note="match: STS: Em:AU048503"
38620..38772
/Note="match: STS: Em:AU046429"
complement(38660..38777)
/Note="match: GSS: Em:AZ398168"
38685..38746
/Note="31 copies 2 mer gt 91% conserved"
38956..39215
/Note="Charliela repeat: matches 28..281 of consensus"
40351..40840
/Note="Charliela repeat: matches 277..769 of consensus"
42053..42372
/Note="Charliela repeat: matches 778..1137 of consensus"

```

FEATURES
Source

misc_feature 44071..44491
 /note="match: GSS: Em:AQ112832"
 /complement(45407..45624)
 /note="match: GSS: Em:A1247033"
 53815..53904
 /note="Charlie2 repeat: matches 3272..3470 of consensus"
 54009..54235
 /note="Charlie2 repeat: matches 2889..3117 of consensus"
 56236..57009
 /note="LIP2 repeat: matches 1..376 of consensus"
 57005..58248
 /note="LIP2 repeat: matches 900..6144 of consensus"
 63508..63541
 /note="17 copies 2 mer aa 82% conserved"
 63586..63668
 /note="LIP2 repeat: matches 738..819 of consensus"
 63917..64021
 /note="LIP2 repeat: matches 984..1089 of consensus"
 /complement(64074..64343)
 /note="match: GSS: Em:AQ885350"
 /complement(66096..66577)
 /note="match: GSS: Em:AQ611651"
 69990..70342
 /note="match: STS: Em:G21603"
 /complement(76094..76635)
 /note="match: GSS: Em:AQ277578"
 /complement(76184..76636)
 /note="match: GSS: Em:AQ8:2553"
 /complement(76460..76628)
 /note="match: GSS: Em:AQ140871"
 /complement(80581..89052)
 /note="match: GSS: Em:AQ201907"
 89057..89594
 /note="match: GSS: Em:AQ543464"
 91625..91990
 /note="THE1C repeat: matches 1..337 of consensus"
 92079..92237
 /note="LIP2 repeat: matches 5949..6125 of consensus"
 BASE COUNT 32991 a 18802 c 18896 g 27671 t
 ORIGIN

Query Match 1.8%; Score 58; DB 9; Length 44491;
 Best Local Similarity 100.0%; Pred. No. 6.5e-21;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1187 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGCATGAGCAGTCCGCTCCAGC 1244
 BB 18635 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGCATGAGCAGTCCGCTCCAGC 18578

RESULT 44
 AC107939/c
 LOCUS Human DNA sequence from clone RP11-374C13 on chromosome 1, complete
 DEFINITION sequence.
 ACCESSION AL611933
 VERSION AL611933.30 GI:21425229
 KEYWORDS HTG.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 141273)
 TITLE Direct Submission
 JOURNAL Submitted (11-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Jun 13, 2002 this sequence version replaced GI:21263916.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WormPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep/
 was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/WGP/Chr1/>
 RP11-374C13 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACE3.6.

FEATURES
 Location/Qualifiers
 source 1..141273
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 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="RP11-374C13"
 /clone_lib="RP11-11.2"
 BASE COUNT 35351 a 32122 c 33734 g 40066 t
 ORIGIN
 Query Match 1.8%; Score 58; DB 9; Length 141273;
 Best Local Similarity 100.0%; Pred. No. 6.5e-21;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1187 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGCATGAGCAGTCCGCTCCAGC 1244
 BB 4256 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGCATGAGCAGTCCGCTCCAGC 4199

RESULT 45
 AC107939/c
 LOCUS Homo sapiens chromosome 11, clone RP11-4809, complete sequence.
 DEFINITION
 ACCESSION AC107939
 VERSION AC107939.5 GI:19849381
 KEYWORDS HTG.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 145264)
 TITLE
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 JOURNAL
 REFERENCE
 AUTHORS

2 (bases 1 to 145264)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Glade, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Haqos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., LaRocque, K., Lamazares, R., Landers, T., Lehorzky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Melrim, J., Meneus, L., Milhova, T., Mienda, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, L., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, K., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,

Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trifunovic, J., Vassiliev, B., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J. Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

TITLE JOURNAL REFERENCE AUTHORS

Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 145264)

Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Bonafant-Luk, L., Boukhalter, B., Brown, A., Camarata, J., Camparino, A., Chang, J., Chazaro, B., Choepel, Y., Colanquinto, M., Collins, S., Collamore, A., Cook, A., Cooke, P., DeArelano, K., Dewar, K., Di, J. S., Dodge, S., Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Gallardo, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hayes, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamet, A., Karakas, A., Kells, C., Labèque, K., Lazarides, R., Landers, T., Lehocsky, J., Levine, K., Lindblad-Toh, K., Lin, J., MacDonald, C., MacDonald, P., Major, J., Marquis, N., Matthews, G., McCarthy, M., McEwan, P., McKernan, K., Melnick, J., Mendenhall, T., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, K., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pitaru, V., Raymond, C., Retta, R., Rieback, M., Riley, K., Ris, E., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trifunovic, J., Vassiliev, B., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J. Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 145264)

Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Bonafant-Luk, L., Boukhalter, B., Brown, A., Camarata, J., Camparino, A., Chang, J., Chazaro, B., Choepel, Y., Colanquinto, M., Collins, S., Collamore, A., Cook, A., Cooke, P., DeArelano, K., Dewar, K., Di, J. S., Dodge, S., Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Gallardo, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hayes, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamet, A., Karakas, A., Kells, C., Labèque, K., Lazarides, R., Landers, T., Lehocsky, J., Levine, K., Lindblad-Toh, K., Lin, J., MacDonald, C., MacDonald, P., Major, J., Marquis, N., Matthews, G., McCarthy, M., McEwan, P., McKernan, K., Melnick, J., Mendenhall, T., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, K., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pitaru, V., Raymond, C., Retta, R., Rieback, M., Riley, K., Ris, E., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trifunovic, J., Vassiliev, B., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J. Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (31-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 31, 2002 this sequence version replaced at 14526475.

All repeats were identified using RepeatMasker.

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/SW/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
 Web site: <http://www.seq.w.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L24318
 Center clone name: 48_0_9

FEATURES	Location/Qualifiers
source	1..145264 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="11" /map="11"
repeat_region	/clone="rpl1-4809" /clone_lib="RPL1-11 Human Male BAC"
repeat_region	803..904 /rpt_family="FLAM_C"
repeat_region	405..1010 /rpt_family="L1MC4"
repeat_region	1129..1151 /rpt_family="AT-rich"
repeat_region	1200..1507 /rpt_family="AluSx"
repeat_region	2953..3126 /rpt_family="AluSg/x"
repeat_region	3285..3573 /rpt_family="AluSx"
repeat_region	3585..3886 /rpt_family="AluSg"
repeat_region	3996..4372 /rpt_family="ML11"
repeat_region	4436..4618 /rpt_family="MER104"
repeat_region	5800..5866 /rpt_family="AluJo"
repeat_region	6046..6122 /rpt_family="L2"
repeat_region	6264..6550 /rpt_family="AluSx"
repeat_region	complement(6560..6680) /rpt_family="MER5A"
repeat_region	complement(6681..6986) /rpt_family="AluJb"
repeat_region	complement(6987..7057) /rpt_family="MER5A"
repeat_region	complement(7446..7635) /rpt_family="L1PA13"
repeat_region	7636..7923 /rpt_family="L1M4"
repeat_region	8453..8962 /rpt_family="AluJo/FLAM"
repeat_region	8056..8160 /rpt_family="AluSg/x"
repeat_region	8189..8244 /rpt_family="L1M4"
repeat_region	8245..8517 /rpt_family="AluJ"
repeat_region	8518..8584 /rpt_family="L1M4"
repeat_region	8585..8877 /rpt_family="AluJb"
repeat_region	8878..9031 /rpt_family="L1M4"
repeat_region	complement(9033..9150) /rpt_family="FLAM_A"
repeat_region	9410..10353 /rpt_family="L1M5"
repeat_region	complement(10428..10725) /rpt_family="AluSg"
repeat_region	10855..10920 /rpt_family="MIR"
repeat_region	11386..11510 /rpt_family="FLAM_A"
repeat_region	11900..12026 /rpt_family="L2"
repeat_region	complement(12466..12754) /rpt_family="AluSg"
repeat_region	13442..13925 /rpt_family="L1PA14"

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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L3990
Center clone name: 2L.E12
----- Summary Statistics -----
Sequencing vector: M13; M77815; 38 of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 142529 bases at least Q4C
Consensus quality: 144014 bases at least Q30
Consensus quality: 144580 bases at least Q20
Insert size: 128000; agarose-fp
Insert size: 145212; sum-of-contigs
Quality coverage: 9.4 in Q20 bases; agarose-fp
Quality coverage: 8.3 in Q20 bas.
* NOTE: this is a working draft sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1732: contig of 1732 bp in length
* 1733 1832: gap of 100 bp
* 1833 2945: contig of 1113 bp in length
* 2946 3045: gap of 100 bp
* 3046 4116: contig of 1071 bp in length
* 4117 4216: gap of 100 bp
* 4217 5757: contig of 1541 bp in length
* 5758 5857: gap of 100 bp
* 5858 7545: contig of 1688 bp in length
* 7546 7645: gap of 100 bp
* 7646 11527: contig of 3882 bp in length
* 11528 11627: gap of 100 bp
* 11628 55477: contig of 43850 bp in length
* 55478 55577: gap of 100 bp
* 55578 66767: contig of 11190 bp in length
* 66768 66867: gap of 100 bp
* 66868 83973: contig of 17106 bp in length
* 83974 84073: gap of 100 bp
* 84074 107174: contig of 23101 bp in length
* 107175 107274: gap of 100 bp
* 107275 137395: contig of 30121 bp in length
* 137396 137495: gap of 100 bp
* 137496 146312: contig of 8817 bp in length.
* Location/Qualifiers
* 1. 146312
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /clone="RP11-2LE12"
* /clone_lib="RPC1-11 Human Male BAC"
* 1. 1732
* /note="assembly_fragment
clone_end:SP6
vector_side:left"
1833..2945
/note="assembly_fragment"
3046..4116
/note="assembly_fragment"
4217..5757
/note="assembly_fragment"
5858..7545
/note="assembly_fragment"
7646..11527
/note="assembly_fragment"
11628..55477
/note="assembly_fragment"
55578..66767

```


misc_feature 154110..155982
/note=assembly_fragment
clone_end:17
vector_side:right
49795 a 29360 c 29340 g 46582 t 1205 others

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0% Pred. No. 6.6e-21; Length 155982;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACTTGGCTCCCAAGTCTGGATTACAGCATGACGACCTGCGGTACG 1244
|||||
DB 9997 CTGCCACTTGGCTCCCAAGTCTGGATTACAGCATGACGACCTGCGGTACG 10054

RESULT 48
AC0618988

LOCUS
AC0618988 Homo sapiens chromosome 15 clone RP11-233C13 map 15, *** SEQUENCING
IN PROGRESS ***, 2 ordered pieces.

ACCESSION
AC0618988 GI:21307395

VERSION
HTG: HTGS_PHASE2; HTGS_FULLJOB; HTGS_ACTIVEFIN.

KEYWORDS
human

SOURCE
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 158071)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-233C13
unpublished

TITLE
2 (bases 1 to 158071)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckert,A., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepl,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Foster,J.,
Freireira,P., FitzHugh,W., Forrest,C., Gage,D., Galadon,J.,
Gardyna,S., Grant,G., Hagoes,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kaul,R., Karatas,A., Klein,J.,
Lander,T., Lehoczy,J., Levine,K., Liu,Q., Lindblad-Toh,K.,
Macdonald,P., Marquis,L., McEwan,P., McElrath,K.A., McKernan,K.,
McLirim,J., Meneus,N., Morrow,J., Naylor,J., Norman,C.H.,
O'Connor,T., O'Donnell,P., Olivat,T.M., Peterson,K., Pierrin,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,P., Rothman,D., Roy,A.,
Santos,R., Severy,P., Spencer,B., Stange-Therand,N., Stojanovic,N.,
Sutermanian,A., Talamas,J., Testave,S., Theodor,J., Trifilio,A.,
Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Yee,W.J., Zimm,J.A.
and Zody,M.

Direct Submission
Submitted (25-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 158071)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarato,J., Campotano,A., Chang,J.,
Chazaro,B., Choepl,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodde,S.,
Farooq,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Gorette,R., Graham,L.,
Grand-Pierre,N., Hagoes,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,
Lamazares,R., Lander,T., Lehoczy,J., Levine,K., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McLirim,J.,
Meneus,N., Mihova,T., Meneus,V., Murphy,T., Naylor,S., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phuchang,P., Pierrin,N.,
Pollara,V., Raymond,C., Retta,K., Ribback,M., Riley,K., Rise,B.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Therand,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testave,S.,
Theodor,J., Trifilio,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Yee,W.J., Zimm,J.A.
and Zody,M.

TITLE
JOURNAL
AUTHORS
REFERENCE

Theodore,J., Topham,K., Travers,M., Travis,N., Trifilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Yee,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 1, 2002 this sequence version replaced gi:20331004.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/MIT Center for Genome Research
Center code: W1BR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L5451
Center clone name: 233-C_13

* NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
been provided by the submitter.
* This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
* 1 41244: contig of 41244 bp in length
* 41245 41344: gap of 100 bp
* 41345 158071: contig of 116727 bp in length.

FEATURES
Source
1 158071
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/map="15"
/clone="RP11-233C13"
/clone_lib="RP11-11 Human Male BAC"
BASE COUNT 41814 a 38724 c 38609 g 38824 t 100 others
ORIGIN

Query Match 1.8%; Score 58; DB 2; Length 158071;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACTTGGCTCCCAAGTCTGGATTACAGCATGACGACCTGCGGTACG 1244
|||||
DB 144019 CTGCCACTTGGCTCCCAAGTCTGGATTACAGCATGACGACCTGCGGTACG 144076

RESULT 49
AC068082/c

LOCUS
AC068082/c Homo sapiens chromosome 2 clone RP11-21M2 map 2, WORKING DRAFT
SEQUENCE, 23 unordered pieces.

ACCESSION
AC068082

VERSION
AC068082.2 GI:8247823

KEYWORDS
HTG: HTGS_PHASE1; HTGS_DRAFT.

SOURCE
Homo sapiens

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158450)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 2, clone RP11-21M2
unpublished

2 (bases 1 to 158450)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campotano,A., Castle,A., Choepl,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodd,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Gorette,R., Graham,L.,
Grand-Pierre,N., Hagoes,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,
Lamazares,R., Lander,T., Lehoczy,J., Levine,K., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McLirim,J.,
Meneus,N., Mihova,T., Meneus,V., Murphy,T., Naylor,S., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phuchang,P., Pierrin,N.,
Pollara,V., Raymond,C., Retta,K., Ribback,M., Riley,K., Rise,B.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Therand,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testave,S.,
Theodor,J., Trifilio,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Yee,W.J., Zimm,J.A.
and Zody,M.

TITLE
JOURNAL
AUTHORS
REFERENCE

Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Haqos, R., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kama, L., Karatas, A., Klein, J., LaRoque, K., Lamazares, K., Landers, J., Lebeckzy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Mphahlele, R., Meldrum, J., Menelus, L., Mihova, T., Miranda, C., Miñana, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisanic, C., Pollard, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, H., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Triolillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wymann, D., Ye, M. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (28-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 4, 2000 this sequence version replaced qi:7658356.
All repeats were identified using RepeatMasker:
Snit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.htm>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information:
Center project name: L10095
Center Clone name: 21_M_2

Summary Statistics

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.9607.1
Consensus quality: 146955 bases at least Q40
Consensus quality: 153080 bases at least Q40
Consensus quality: 155308 bases at least Q20
Insert size: 163000; agarose-gel
Insert size: 156250; sum-of-coverage
Quality coverage: 3.6 in Q20 bases; agarose-gel
Quality coverage: 3.8 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1749: contig of 1749 bp in length
1750 1849: gap of 100 bp
1850 3169: contig of 1320 bp in length
3170 3269: gap of 100 bp
3270 4573: contig of 1304 bp in length
4574 4673: gap of 100 bp
4674 7997: contig of 3424 bp in length
7998 8097: gap of 100 bp
8098 13045: contig of 4948 bp in length
13046 13145: gap of 100 bp
13146 16766: contig of 3621 bp in length
16767 16866: gap of 100 bp
16867 20859: contig of 3943 bp in length
20860 20959: gap of 100 bp
20960 23743: contig of 2784 bp in length
23744 23843: gap of 100 bp
23844 27652: contig of 3809 bp in length
27653 27752: gap of 100 bp
27753 31395: contig of 3643 bp in length
31396 31495: gap of 100 bp
31496 36408: contig of 4913 bp in length
36409 36508: gap of 100 bp

36509 42265: contig of 5757 bp in length
42266 42365: gap of 100 bp
42366 47307: contig of 4942 bp in length
47308 47407: gap of 100 bp
47408 52438: contig of 5031 bp in length
52439 52538: gap of 100 bp
52539 60035: contig of 7497 bp in length
60036 60135: gap of 100 bp
60136 68356: contig of 8221 bp in length
68357 68456: gap of 100 bp
68457 76898: contig of 8442 bp in length
76899 76998: gap of 100 bp
76999 85827: contig of 8829 bp in length
85828 85927: gap of 100 bp
85928 96327: contig of 10400 bp in length
96328 96427: gap of 100 bp
96428 108928: contig of 12501 bp in length
108929 109028: gap of 100 bp
109029 121274: contig of 12246 bp in length
121275 121374: gap of 100 bp
121375 141287: contig of 19913 bp in length
141288 141387: gap of 100 bp
141388 158450: contig of 17063 bp in length.

FEATURES

Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone="RP11-21M2"
/clone_lib="RPC1-11 Human Male BAC"
1..1749
/note="assembly_fragment"
1850..3169
/note="assembly_fragment"
3270..4573
/note="assembly_fragment"
4674..7997
/note="assembly_fragment"
8098..13045
/note="assembly_fragment"
13146..16766
/note="assembly_fragment"
16867..20859
/note="assembly_fragment"
20960..23743
/note="assembly_fragment"
clone_end:SP6
vector_side:left
23844..27652
/note="assembly_fragment"
clone_end:7
vector_side:left
27753..31395
/note="assembly_fragment"
31496..36408
/note="assembly_fragment"
36509..42265
/note="assembly_fragment"
42366..47307
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47408..52438
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52539..60035
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60136..68356
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68457..76898
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76999..85827
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85928..96327
/note="assembly_fragment"

misc_feature

misc_feature

misc_feature

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misc_feature

misc_feature

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misc_feature 96428..108928
  /note="assembly_fragment"
misc_feature 109029..121274
  /note="assembly_fragment"
misc_feature 121375..141287
  /note="assembly_fragment"
misc_feature 141388..158450
  /note="assembly_fragment"
BASE COUNT 48293 a 29527 c 30211 g 48215 t 2204 others
ORIGIN
Query Match 1.8%; Score 58; DB 2: Length 15845;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACGACGACG 1244
DB 64666 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACGACGACG 54009

RESULT 50
AC093737 162419 bp DNA linear REG 10-SEP-2001
LOCUS Homo sapiens chromosome 2 clone RP11-21M2, WORKING DRAFT SEQUENCE.
DEFINITION 2 unordered pieces.
AC093737
VERSION AC093737.1 GI:15529775
KEYWORDS HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 162419)
  Waterston, R.H.
  The sequence of Homo sapiens clone
  Unpublished
  2 (bases 1 to 162419)
  Waterston, R.H.
  Direct Submission
  Submitted (10-SEP-2001) Genome Sequencing Center, Washington
  University School of Medicine, 4444 Forest Park Parkway, St. Louis,
  MO 63108, USA

COMMENT
  ----- Genome Center -----
  Center: Washington University Genome Sequencing Center
  Center code: WUGSC
  Web site: http://genome.wustl.edu/usrc/index.shtml
  ----- Project Information -----
  Center project name: H_NIH021M2
  -----
  Drafting center: QC_Core
  -----
  ----- Summary Statistics -----
  Sequencing vector: M13; 36%
  Sequencing vector: plasmid; 64%
  Chemistry: Dye-primer ET; 0% of reads
  Assembly: Dye-terminator H10; 100% of reads
  Assembly program: Phrap; version 0.950319
  Consensus quality: 162064 bases at least Q40
  Consensus quality: 162155 bases at least Q40
  Consensus quality: 162211 bases at least Q40
  NOTE: This is a 'working draft' sequence. It currently
  * consists of 2 contigs. The true order of the pieces
  * is not known and their order in this sequence record is
  * arbitrary. Gaps between the contigs are represented as
  * runs of N, but the exact sizes of the gaps are unknown.
  * This record will be updated with the finished sequence
  * as soon as it is available and the accession number will
  * be preserved.
  * 1 70250: contig of 70250 bp in length
  * 70251 70350: gap of unknown length
  * 70351 162419: contig of 92069 bp in length.

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FEATURES
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    Location/Qualifiers
      i..162419
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="2"
      /clone="RP11-21M2"
      1..70250
      /note="assembly_name:Contig13"
      clone_end:T7
      vector_side:right
      70451..162419
      /note="assembly_name:Contig14"
      clone_end:SP6
      vector_side:right
  misc_feature
    BASE COUNT 50019 a 30933 c 30950 g 50417 t 100 others
  misc_feature
    ORIGIN
      Query Match 1.8%; Score 58; DB 2: Length 162419;
      Best Local Similarity 100.0%; Pred. No. 6.6e-21;
      Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACGACG 1244
      DB 52046 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACGACG 52103
      Search completed: May 10, 2003, 00:31:40
      Job time : 13938.7 secs

```

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 17:55:06 : Search time 141.721 seconds

(without alignment's)
6260.245 Million cell updates/sec

Title: US-09-846-456-3
Perfect score: 2893
Sequence: 1 acagggcaggtggcaggagggg.....ctadtcctgggaaacacccc 2893

Scoring table: Oligo_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 30

Total number of hits satisfying chosen parameters: 753

Minimum DH seq length: 0

Maximum LB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by Chancer to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	55	1.9	246240	2	US-08-724-394A-20	Sequence 20, App.
C 2	55	1.9	246240	2	US-08-724-394A-21	Sequence 21, App.
C 3	55	1.9	246240	2	US-08-724-394A-22	Sequence 22, App.
C 4	51	1.8	162450	4	US-09-345-692-1	Sequence 1, App.
C 5	50	1.7	162450	4	US-09-345-692-1	Sequence 1, App.
C 6	49	1.7	8866	4	US-09-257-179-11	Sequence 1, App.
C 7	49	1.7	21234	4	US-09-810-671-3	Sequence 3, App.
C 8	49	1.7	36159	4	US-09-749-588-3	Sequence 1, App.
C 9	48	1.7	31571	1	US-08-323-443B-1	Sequence 1, App.
C 10	48	1.7	36651	4	US-09-738-894A-3	Sequence 3, App.
C 11	48	1.7	53526	3	US-08-658-136-2	Sequence 2, App.
C 12	48	1.7	53577	3	US-08-658-136-2	Sequence 1, App.
C 13	47	1.6	13158	2	US-08-667-080-105	Sequence 105, App
C 14	45	1.6	153	2	US-08-849-761-2	Sequence 2, App.
C 15	45	1.6	891	4	US-09-247-155-141	Sequence 141, App
C 16	45	1.6	1040	4	US-09-288-143-16	Sequence 16, App
C 17	45	1.6	1701	4	US-09-078-294-9	Sequence 9, App.
C 18	45	1.6	3267	2	US-08-257-463B-12	Sequence 12, App.
C 19	45	1.6	3267	4	US-08-367-841A-12	Sequence 12, App.
C 20	45	1.6	3267	5	PCT-US95-07201-12	Sequence 12, App.
C 21	45	1.6	3663	4	US-09-499-872A-11	Sequence 11, App.
C 22	45	1.6	3844	4	US-09-689-423-1	Sequence 1, App.
C 23	45	1.6	5262	4	US-08-520-373B-5	Sequence 5, App.
C 24	45	1.6	5581	4	US-08-973-544-1	Sequence 1, App.
C 25	45	1.6	8396	4	US-09-328-174A-1	Sequence 1, App.
C 26	45	1.6	8409	4	US-09-167-681-37	Sequence 37, App
C 27	45	1.6	22481	4	US-08-367-841A-43	Sequence 43, App

28	45	1.6	22481	5	PCT-US95-07201-43	Sequence 43, Appl
29	45	1.6	22484	4	US-09-875-223-2	Sequence 2, Appl
30	45	1.6	84495	4	US-09-797-906-3	Sequence 3, Appl
31	45	1.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
32	45	1.6	246240	2	US-08-724-394A-21	Sequence 21, Appl
33	45	1.6	246240	2	US-08-724-394A-22	Sequence 22, Appl
C 34	44	1.5	6792	4	US-09-374-454-20	Sequence 20, Appl
C 35	44	1.5	112132	4	US-09-741-150-3	Sequence 3, Appl
C 36	44	1.5	176373	3	US-09-128-155-17	Sequence 17, Appl
C 37	43	1.5	2310	1	US-08-471-570-9	Sequence 9, Appl
C 38	43	1.5	2676	1	US-08-471-570-7	Sequence 7, Appl
C 39	43	1.5	14796	4	US-08-975-080-35	Sequence 35, Appl
C 40	43	1.5	14796	4	US-09-630-706-10	Sequence 10, Appl
C 41	43	1.5	14796	4	US-09-496-694B-3	Sequence 3, Appl
C 42	43	1.5	28720	4	US-09-341-587-7	Sequence 7, Appl
C 43	43	1.5	40030	4	US-09-780-049-18	Sequence 18, Appl
C 44	43	1.5	70000	4	US-09-851-896-3	Sequence 3, Appl
C 45	43	1.5	72604	4	US-09-268-992-7	Sequence 7, Appl
C 46	43	1.5	72604	4	US-09-657-474-7	Sequence 7, Appl
C 47	43	1.5	81001	4	US-09-750-580-1	Sequence 1, Appl
C 48	43	1.5	98844	4	US-09-791-211-10	Sequence 10, Appl
C 49	43	1.5	99500	4	US-09-798-096-10	Sequence 10, Appl
50	42	1.5	1613	2	US-08-812-204-1	Sequence 1, Appl
51	42	1.5	1656	1	US-08-324-465-2	Sequence 2, Appl
52	42	1.5	1656	2	US-08-465-981-2	Sequence 2, Appl
53	42	1.5	1656	5	PCT-US93-11915-2	Sequence 2, Appl
54	42	1.5	1725	1	US-08-324-465-5	Sequence 5, Appl
55	42	1.5	1725	2	US-08-465-981-5	Sequence 5, Appl
56	42	1.5	1725	5	PCT-US93-11915-5	Sequence 5, Appl
57	42	1.5	2086	2	US-08-655-640-5	Sequence 5, Appl
58	42	1.5	5590	4	US-09-050-159-129	Sequence 129, App
C 59	42	1.5	62804	4	US-09-800-960-3	Sequence 3, Appl
60	41	1.4	198	2	US-08-967-101-107	Sequence 107, App
61	41	1.4	198	2	US-08-967-541-107	Sequence 107, App
62	41	1.4	198	3	US-09-124-698-107	Sequence 107, App
63	41	1.4	198	4	US-09-127-480-107	Sequence 107, App
64	41	1.4	198	4	US-08-496-841C-107	Sequence 107, App
65	41	1.4	198	4	US-09-124-523-103	Sequence 103, App
66	41	1.4	386	2	US-08-967-101-103	Sequence 103, App
67	41	1.4	386	2	US-08-592-541-103	Sequence 103, App
68	41	1.4	386	3	US-09-124-698-103	Sequence 103, App
69	41	1.4	386	4	US-09-127-480-103	Sequence 103, App
70	41	1.4	386	4	US-08-496-841C-103	Sequence 103, App
71	41	1.4	386	4	US-09-124-523-103	Sequence 103, App
C 72	41	1.4	719	4	US-09-227-357-74	Sequence 74, Appl
73	41	1.4	893	2	US-08-967-101-13	Sequence 13, Appl
74	41	1.4	893	2	US-08-592-541-13	Sequence 13, Appl
75	41	1.4	893	3	US-09-124-698-13	Sequence 13, Appl
76	41	1.4	893	4	US-09-127-480-13	Sequence 13, Appl
77	41	1.4	893	4	US-08-496-841C-13	Sequence 13, Appl
78	41	1.4	893	4	US-09-124-523-13	Sequence 13, Appl
C 79	41	1.4	896	4	US-08-943-731-31	Sequence 31, Appl
80	41	1.4	1117	2	US-08-967-101-156	Sequence 156, App
81	41	1.4	1117	2	US-08-592-541-156	Sequence 156, App
82	41	1.4	1117	3	US-08-888-077A-6	Sequence 6, Appl
83	41	1.4	1117	3	US-09-124-698-156	Sequence 156, App
84	41	1.4	1117	4	US-09-127-480-156	Sequence 156, App
85	41	1.4	1117	4	US-08-496-841C-156	Sequence 156, App
86	41	1.4	1117	4	US-09-124-523-156	Sequence 156, App
87	41	1.4	1624	2	US-08-852-807-10	Sequence 10, Appl
C 88	41	1.4	2559	2	US-08-886-152-4	Sequence 4, Appl
C 89	41	1.4	2559	4	US-09-196-222-4	Sequence 4, Appl
C 90	41	1.4	11811	4	US-09-078-294-7	Sequence 7, Appl
C 91	41	1.4	13674	2	US-08-852-807-1	Sequence 1, Appl
C 92	41	1.4	18609	4	US-08-943-731-1	Sequence 1, Appl
C 93	41	1.4	19311	1	US-08-310-356-36	Sequence 36, Appl
C 94	41	1.4	19557	5	PCT-US92-06300-1	Sequence 1, Appl
C 95	41	1.4	35060	3	US-08-814-095-7	Sequence 7, Appl
C 96	41	1.4	38564	4	US-09-734-673-3	Sequence 3, Appl
C 97	41	1.4	98844	4	US-09-791-211-10	Sequence 10, Appl
C 98	41	1.4	99500	4	US-09-798-096-10	Sequence 10, Appl
C 99	41	1.4	168575	4	US-09-426-290-1	Sequence 1, Appl
C 100	40	1.4	295	2	US-08-849-701-8	Sequence 8, Appl

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c 101	40	1-4	577	4	US-09-227-357-92	Sequence 92, App:	174	37	1-3	657	4	US-09-385-982-335	Sequence 335, App
c 102	40	1-4	1804	1	US-08-306-691B-40	Sequence 40, App:	175	37	1-3	668	4	US-09-347-114A-93	Sequence 93, Appl
c 103	40	1-4	1804	4	US-09-167-122-14	Sequence 14, Appl	176	37	1-3	680	4	US-09-056-285A-2	Sequence 2, Appl
c 104	40	1-4	1804	5	PCT-US93-06251-82	Sequence 82, Appl	c 177	37	1-3	819	4	US-09-337-171-13	Sequence 13, Appl
c 105	40	1-4	2896	2	US-08-709-923-1	Sequence 1, Appl	178	37	1-3	926	4	US-08-938-669A-4	Sequence 4, Appl
c 106	40	1-4	38844	4	US-09-734-675-3	Sequence 3, Appl	179	37	1-3	1000	4	US-09-018-584A-30	Sequence 30, Appl
c 107	40	1-4	80246	4	US-09-078-294-4	Sequence 4, Appl	180	37	1-3	1000	4	US-09-018-584A-31	Sequence 31, Appl
c 108	40	1-4	80595	4	US-09-078-294-3	Sequence 3, Appl	c 181	37	1-3	1145	4	US-09-078-294-17	Sequence 17, Appl
c 109	40	1-4	87350	3	US-08-781-891-79	Sequence 79, Appl	c 182	37	1-3	1460	4	US-09-257-179-23	Sequence 23, Appl
c 110	40	1-4	87543	4	US-09-791-211-3	Sequence 7, Appl	183	37	1-3	2372	1	US-07-503-103-1	Sequence 1, Appl
c 111	39	1-3	885	4	US-09-288-143-55	Sequence 55, Appl	184	37	1-3	2372	1	US-08-044-619A-1	Sequence 1, Appl
c 112	39	1-3	1164	3	US-08-755-587-32	Sequence 32, Appl	185	37	1-3	2372	1	US-08-283-911-1	Sequence 1, Appl
c 113	39	1-3	2834	4	US-09-305-384-6	Sequence 6, Appl	186	37	1-3	2372	1	US-08-245-500A-2	Sequence 2, Appl
c 114	39	1-3	3507	1	US-08-842-683-67	Sequence 67, Appl	187	37	1-3	2372	1	US-08-390-546-2	Sequence 2, Appl
c 115	39	1-3	3507	2	US-08-842-677-67	Sequence 67, Appl	188	37	1-3	2372	1	US-08-390-546-2	Sequence 2, Appl
c 116	39	1-3	6235	4	US-09-305-384-5	Sequence 5, Appl	189	37	1-3	2372	1	US-08-557-393-2	Sequence 2, Appl
c 117	39	1-3	6679	4	US-09-305-384-1	Sequence 1, Appl	190	37	1-3	2372	1	US-08-390-516C-2	Sequence 2, Appl
c 118	39	1-3	8835	3	US-08-884-324-10	Sequence 10, App:	191	37	1-3	2372	1	US-08-390-517A-2	Sequence 2, Appl
c 119	39	1-3	10684	3	US-08-618-100B-3	Sequence 3, Appl	192	37	1-3	2372	1	US-08-390-515A-2	Sequence 2, Appl
c 120	39	1-3	19736	4	US-09-740-045-3	Sequence 3, Appl	193	37	1-3	2372	2	US-08-801-718-2	Sequence 2, Appl
c 121	39	1-3	20598	4	US-09-593-995-10	Sequence 10, Appl	194	37	1-3	2372	3	US-09-073-567-1	Sequence 1, Appl
c 122	39	1-3	28994	3	US-08-884-324-14	Sequence 14, Appl	195	37	1-3	2372	4	US-09-280-805-1	Sequence 1, Appl
c 123	39	1-3	35100	1	US-08-306-691B-19	Sequence 19, Appl	196	37	1-3	2372	4	US-09-048-810-1	Sequence 1, Appl
c 124	39	1-3	35100	5	PCT-US93-06251-15	Sequence 15, Appl	197	37	1-3	2372	4	US-09-170-159A-2	Sequence 2, Appl
c 125	39	1-3	112132	4	US-09-741-150-3	Sequence 3, Appl	198	37	1-3	2372	4	US-09-480-718-43	Sequence 43, Appl
c 126	39	1-3	152331	3	US-09-128-155-16	Sequence 16, App:	199	37	1-4	2455	4	US-08-406-030A-4	Sequence 4, Appl
c 127	39	1-3	152331	3	US-09-128-155-16	Sequence 16, App:	c 200	37	1-3	2713	2	US-08-916-901-6	Sequence 6, Appl
c 128	38	1-3	152331	4	US-09-060-024A-2	Sequence 4, Appl	c 201	37	1-3	2713	4	US-09-154-602-6	Sequence 6, Appl
c 129	38	1-3	257	2	US-08-849-701-4	Sequence 4, Appl	c 202	37	1-3	2839	3	US-08-468-856B-5	Sequence 5, Appl
c 130	38	1-3	579	4	US-09-128-111-741	Sequence 741, App	c 203	37	1-3	2839	3	US-08-468-859A-5	Sequence 5, Appl
c 131	38	1-3	646	4	US-09-345-982-614	Sequence 614, App	c 204	37	1-3	2839	4	US-09-061-702-1	Sequence 1, Appl
c 132	38	1-3	776	4	US-09-545-008-43	Sequence 43, App	c 205	37	1-3	3117	4	US-09-146-580-6	Sequence 6, Appl
c 133	38	1-3	1037	4	US-09-257-279-16	Sequence 16, App	c 206	37	1-3	4233	4	US-09-056-105-27	Sequence 27, Appl
c 134	38	1-3	1363	1	US-08-776-088-21	Sequence 21, App	207	37	1-3	4823	2	US-08-457-254-5	Sequence 5, Appl
c 135	38	1-3	1363	5	PCT-US95-09149A-21	Sequence 21, App	208	37	1-3	4823	3	US-08-484-257-20	Sequence 20, Appl
c 136	38	1-3	1381	2	US-08-454-557C-49	Sequence 49, Appl	209	37	1-3	4823	3	US-08-999-927-5	Sequence 5, Appl
c 137	38	1-3	1381	2	US-08-340-420C-49	Sequence 49, Appl	210	37	1-3	4823	5	US-08-461-819-5	Sequence 5, Appl
c 138	38	1-3	1381	2	US-08-450-674C-49	Sequence 49, Appl	211	37	1-3	4823	5	PCT-US94-08806-28	Sequence 28, Appl
c 139	38	1-3	1381	5	PCT-US95-17111A-49	Sequence 49, App:	212	37	1-3	4823	5	PCT-US95-01829-5	Sequence 5, Appl
c 140	38	1-3	1418	5	PCT-US95-17111A-120	Sequence 120, App	213	37	1-3	4823	5	PCT-US95-16626-5	Sequence 5, Appl
c 141	49	1-3	1442	2	US-08-454-557C-120	Sequence 120, App	214	37	1-3	4922	2	US-08-330-272-5	Sequence 5, Appl
c 142	38	1-3	1442	2	US-08-340-420C-120	Sequence 120, App	215	37	1-3	4922	5	PCT-US95-13663-5	Sequence 5, Appl
c 143	38	1-3	1442	2	US-08-450-674C-120	Sequence 120, App	c 216	37	1-3	5375	3	US-08-757-223-7	Sequence 7, Appl
c 144	38	1-3	5035	2	US-08-610-492C-4	Sequence 4, Appl	c 217	37	1-3	5543	2	US-08-687-080-101	Sequence 101, App
c 145	38	1-3	5789	4	US-09-242-248-4	Sequence 4, Appl	218	37	1-3	7210	2	US-08-257-963B-10	Sequence 10, Appl
c 146	38	1-3	7680	4	US-09-250-748A-4	Sequence 4, Appl	219	37	1-3	7210	4	US-08-367-841A-10	Sequence 10, Appl
c 147	38	1-3	40352	3	US-08-646-113B-15	Sequence 15, Appl	220	37	1-3	7210	5	PCT-US95-07201-10	Sequence 10, Appl
c 148	38	1-3	40352	4	US-09-443-677-15	Sequence 15, Appl	221	37	1-3	9365	4	US-09-608-285A-8	Sequence 8, Appl
c 149	38	1-3	45546	4	US-09-146-014-5	Sequence 6, Appl	222	37	1-3	9365	4	US-09-350-836B-8	Sequence 8, Appl
c 150	38	1-3	80246	4	US-09-078-294-4	Sequence 4, Appl	223	37	1-3	9365	4	US-09-370-265-8	Sequence 8, Appl
c 151	38	1-3	80595	4	US-09-078-294-3	Sequence 3, Appl	224	37	1-3	9734	4	US-09-347-114A-80	Sequence 80, Appl
c 152	38	1-3	168575	4	US-09-426-290-1	Sequence 1, Appl	225	37	1-3	11811	4	US-09-078-294-7	Sequence 7, Appl
c 153	37	1-3	184	2	US-08-454-557C-47	Sequence 47, Appl	226	37	1-3	14581	4	US-08-520-373D-4	Sequence 4, Appl
c 154	37	1-3	184	2	US-08-340-420C-47	Sequence 47, App:	227	37	1-3	14747	4	US-09-608-285A-42	Sequence 42, Appl
c 155	37	1-3	184	2	US-08-450-674C-47	Sequence 47, Appl	228	37	1-3	15777	4	US-09-608-285A-59	Sequence 59, Appl
c 156	37	1-3	184	5	PCT-US95-17111A-47	Sequence 47, App:	229	37	1-3	17327	1	US-07-906-871-15	Sequence 15, Appl
c 157	37	1-3	245	2	US-08-454-557C-46	Sequence 46, App:	c 230	37	1-3	17327	1	US-07-906-871-15	Sequence 15, Appl
c 158	37	1-3	245	2	US-08-440-420C-46	Sequence 46, App:	231	37	1-3	20674	4	US-09-641-638-651	Sequence 651, App
c 159	37	1-3	245	2	US-08-450-674C-46	Sequence 46, App:	c 232	37	1-3	36741	4	US-09-301-665-3	Sequence 3, Appl
c 160	37	1-3	245	5	PCT-US95-17111A-86	Sequence 86, Appl	233	37	1-3	42571	4	US-09-810-347-3	Sequence 3, Appl
c 161	37	1-3	421	1	US-08-480-784-24	Sequence 24, Appl	234	37	1-3	43950	4	US-09-735-934A-3	Sequence 3, Appl
c 162	37	1-3	421	1	US-08-484-553-24	Sequence 24, Appl	c 235	37	1-3	43950	4	US-09-735-934A-3	Sequence 3, Appl
c 163	37	1-3	421	1	US-08-487-002-24	Sequence 24, Appl	236	37	1-3	50000	4	US-09-146-053-3	Sequence 3, Appl
c 164	37	1-3	421	1	US-08-484-554B-24	Sequence 24, Appl	c 237	37	1-3	50300	4	US-09-146-053-3	Sequence 3, Appl
c 165	37	1-3	421	1	US-08-488-011B-24	Sequence 24, Appl	c 238	37	1-3	70900	4	US-09-851-896-3	Sequence 3, Appl
c 166	37	1-3	421	4	US-08-850-727-24	Sequence 24, Appl	c 239	37	1-3	84455	4	US-09-727-906-3	Sequence 3, Appl
c 167	37	1-3	421	5	PCT-US95-10202-24	Sequence 24, Appl	240	36	1-2	685	4	US-09-227-357-100	Sequence 100, App
c 168	37	1-3	421	5	PCT-US95-10203-24	Sequence 24, App:	241	36	1-2	951	4	US-09-605-785-570	Sequence 570, App
c 169	37	1-3	421	5	PCT-US95-10204-24	Sequence 24, App:	c 242	36	1-2	1001	4	US-09-641-638-464	Sequence 464, App
c 170	37	1-3	562	4	US-09-385-962-442	Sequence 442, App:	c 243	36	1-2	1373	4	US-09-227-357-13	Sequence 13, Appl
c 171	37	1-3	606	4	US-09-385-962-442	Sequence 442, App:	c 244	36	1-2	1459	4	US-09-020-956-174	Sequence 174, App
c 172	37	1-3	632	4	US-09-385-962-177	Sequence 177, App	c 245	36	1-2	1459	4	US-09-030-607-174	Sequence 174, App
c 173	37	1-3	653	4	US-09-385-962-124	Sequence 124, App:	c 246	36	1-2	1459	4	US-09-605-785-174	Sequence 174, App

c 247	1.2	1459	4	US-09-435-313-174	Sequence 174, App	c 320	35	1.2	22481	5	PCT-US95-07201-43	Sequence 43, Appl
c 248	1.2	1459	4	US-09-452-616A-174	Sequence 174, App	c 321	35	1.2	22484	4	US-09-875-223-2	Sequence 2, Appl
c 249	1.2	1459	4	US-09-232-145A-174	Sequence 174, App	c 322	35	1.2	22674	1	US-08-370-975B-1	Sequence 1, Appl
c 250	1.2	2099	4	US-08-638-665A-5	Sequence 5, Appl	c 323	35	1.2	29629	4	US-09-729-995-3	Sequence 3, Appl
c 251	1.2	2921	3	US-08-618-70-4	Sequence 4, Appl	c 324	35	1.2	35060	3	US-08-814-095-7	Sequence 7, Appl
c 252	1.2	3350	3	US-09-110-115-2	Sequence 2, Appl	c 325	35	1.2	35100	1	US-08-306-691B-19	Sequence 19, Appl
c 253	1.2	3609	4	US-09-705-249-1	Sequence 11, Appl	c 326	35	1.2	45100	5	PCT-US93-06251-19	Sequence 19, Appl
c 254	1.2	4326	2	US-08-852-857-12	Sequence 12, Appl	c 327	35	1.2	40000	4	US-09-780-049-18	Sequence 18, Appl
c 255	1.2	4517	4	US-09-140-804-9	Sequence 9, Appl	c 328	35	1.2	40328	4	US-08-742-185-102	Sequence 102, App
c 256	1.2	5220	2	US-08-777-405A-1	Sequence 1, Appl	c 329	35	1.2	43795	4	US-08-742-185-101	Sequence 101, App
c 257	1.2	5220	2	US-08-977-871A-1	Sequence 1, Appl	c 330	35	1.2	45716	4	US-08-965-048-5	Sequence 5, Appl
c 258	1.2	5220	2	US-09-225-951-1	Sequence 1, Appl	c 331	35	1.2	45989	4	US-08-965-048-6	Sequence 6, Appl
c 259	1.2	8133	4	US-09-659-791A-10	Sequence 10, Appl	c 332	35	1.2	49065	4	US-09-813-817-3	Sequence 3, Appl
c 260	1.2	13674	2	US-08-852-807-1	Sequence 1, Appl	c 333	35	1.2	59065	4	US-09-978-197-3	Sequence 3, Appl
c 261	1.2	14636	4	US-09-173-914-6	Sequence 6, Appl	c 334	35	1.2	62804	4	US-09-800-960-3	Sequence 3, Appl
c 262	1.2	15297	4	US-09-817-180-3	Sequence 3, Appl	c 335	35	1.2	72928	3	US-09-009-913-1	Sequence 1, Appl
c 263	1.2	16063	4	US-09-801-052-3	Sequence 3, Appl	c 336	35	1.2	81001	4	US-09-750-580-1	Sequence 1, Appl
c 264	1.2	17949	4	US-09-387-465-3	Sequence 3, Appl	c 337	35	1.2	176373	3	US-09-128-155-17	Sequence 17, Appl
c 265	1.2	38564	4	US-09-734-673-3	Sequence 3, Appl	c 338	34	1.2	547	4	US-08-991-789A-158	Sequence 158, App
c 266	1.2	40328	3	US-08-742-185-102	Sequence 102, App	c 339	34	1.2	547	4	US-09-062-451-158	Sequence 158, App
c 267	1.2	43795	3	US-08-742-185-101	Sequence 101, App	c 340	34	1.2	547	4	US-09-598-326-158	Sequence 158, App
c 268	1.2	45716	4	US-08-965-048-5	Sequence 5, Appl	c 341	34	1.2	685	4	US-09-227-357-100	Sequence 100, App
c 269	1.2	5989	4	US-08-965-048-6	Sequence 6, Appl	c 342	34	1.2	728	4	US-09-404-879A-16	Sequence 16, Appl
c 270	1.2	59000	4	US-09-146-053-4	Sequence 4, Appl	c 343	34	1.2	1057	4	US-09-257-173-16	Sequence 16, Appl
c 271	1.2	59065	4	US-09-813-817-3	Sequence 3, Appl	c 344	34	1.2	1220	4	US-09-227-357-54	Sequence 54, Appl
c 272	1.2	59065	4	US-09-978-197-3	Sequence 3, Appl	c 345	34	1.2	1838	4	US-09-227-357-32	Sequence 32, Appl
c 273	1.2	72604	4	US-09-268-992-7	Sequence 7, Appl	c 346	34	1.2	2076	2	US-08-979-095-3	Sequence 3, Appl
c 274	1.2	72604	4	US-09-657-474-7	Sequence 7, Appl	c 347	34	1.2	2129	2	US-08-979-095-1	Sequence 1, Appl
c 275	1.2	577	4	US-09-328-113-302	Sequence 302, App	c 348	34	1.2	2336	1	US-08-247-946A-1	Sequence 1, Appl
c 276	1.2	729	4	US-09-641-636-116	Sequence 116, App	c 349	34	1.2	2336	5	PCT-US95-06420-1	Sequence 1, Appl
c 277	1.2	776	4	US-09-535-008-37	Sequence 37, App	c 350	34	1.2	2337	3	US-09-156-253-1	Sequence 1, Appl
c 278	1.2	1250	4	US-09-018-584A-36	Sequence 36, Appl	c 351	34	1.2	2957	2	US-08-394-152A-48	Sequence 48, Appl
c 279	1.2	12024	2	US-08-458-970A-1	Sequence 1, Appl	c 352	34	1.2	3017	2	US-08-394-152A-39	Sequence 39, Appl
c 280	1.2	2236	3	US-08-829-525-23	Sequence 23, Appl	c 353	34	1.2	3172	4	US-08-978-289-11	Sequence 11, Appl
c 281	1.2	2236	4	US-08-659-563A-25	Sequence 25, Appl	c 354	34	1.2	3198	4	US-09-601-478-3	Sequence 3, Appl
c 282	1.2	2236	4	US-08-937-496-23	Sequence 23, Appl	c 355	34	1.2	4326	2	US-08-852-807-12	Sequence 12, Appl
c 283	1.2	2236	4	US-09-310-367-23	Sequence 23, Appl	c 356	34	1.2	7210	2	US-08-257-963B-10	Sequence 10, Appl
c 284	1.2	2236	4	US-09-032-337-23	Sequence 23, Appl	c 357	34	1.2	7210	4	US-08-367-841A-10	Sequence 10, Appl
c 285	1.2	3172	4	US-08-978-249-11	Sequence 11, Appl	c 358	34	1.2	7210	5	PCT-US95-07201-10	Sequence 10, Appl
c 286	1.2	3198	4	US-09-602-478-3	Sequence 3, Appl	c 359	34	1.2	8835	3	US-08-884-324-10	Sequence 10, Appl
c 287	1.2	3609	4	US-09-705-249-11	Sequence 11, App	c 360	34	1.2	9388	4	US-08-991-789A-141	Sequence 141, App
c 288	1.2	3663	4	US-09-496-884-11	Sequence 11, App	c 361	34	1.2	9488	4	US-09-062-451-141	Sequence 141, App
c 289	1.2	3748	2	US-08-978-240-1	Sequence 1, App	c 362	34	1.2	9488	4	US-09-598-326-141	Sequence 141, App
c 290	1.2	4084	3	US-08-866-440-1	Sequence 1, Appl	c 363	34	1.2	12394	4	US-09-488-856A-10	Sequence 10, App
c 291	1.2	4084	3	US-08-856-440-1	Sequence 1, Appl	c 364	34	1.2	12394	4	US-08-520-474D-4	Sequence 4, Appl
c 292	1.2	4460	4	US-09-138-826-4	Sequence 4, Appl	c 365	34	1.2	14581	4	US-09-173-914-6	Sequence 6, Appl
c 293	1.2	4460	4	US-09-138-826-4	Sequence 4, Appl	c 366	34	1.2	14636	4	US-09-644-634-17	Sequence 17, Appl
c 294	1.2	6769	1	US-08-380-763-26	Sequence 26, App	c 367	34	1.2	15632	4	US-09-078-294-12	Sequence 12, Appl
c 295	1.2	6769	1	US-08-380-763-26	Sequence 26, App	c 368	34	1.2	18074	4	US-08-884-324-14	Sequence 14, Appl
c 296	1.2	6769	1	US-08-380-763-26	Sequence 26, App	c 369	34	1.2	28924	4	US-08-884-324-14	Sequence 14, Appl
c 297	1.2	6769	1	US-08-418-633B-20	Sequence 20, App	c 370	34	1.2	44354	4	US-09-146-053-5	Sequence 5, Appl
c 298	1.2	6769	1	US-08-418-633B-20	Sequence 20, App	c 371	34	1.2	44354	4	US-09-146-053-5	Sequence 5, Appl
c 299	1.2	6769	1	US-08-418-633B-20	Sequence 20, App	c 372	34	1.2	50000	4	US-09-146-053-4	Sequence 4, Appl
c 300	1.2	6769	5	PCT-US95-13202-20	Sequence 20, App	c 373	34	1.2	50000	4	US-08-658-136-2	Sequence 2, Appl
c 301	1.2	6769	5	PCT-US95-13202-20	Sequence 20, App	c 374	34	1.2	50000	4	US-08-658-136-1	Sequence 1, Appl
c 302	1.2	6769	5	PCT-US95-13202-20	Sequence 20, App	c 375	34	1.2	50000	4	US-09-784-316-3	Sequence 3, Appl
c 303	1.2	8174	1	US-07-914-281-5	Sequence 5, Appl	c 376	33	1.1	125	5	PCT-US95-09114-17	Sequence 17, Appl
c 304	1.2	8174	1	US-08-393-246-5	Sequence 5, Appl	c 377	33	1.1	384	2	US-08-967-101-68	Sequence 68, Appl
c 305	1.2	8174	1	US-08-525-958A-3	Sequence 3, Appl	c 378	33	1.1	384	3	US-09-124-598-68	Sequence 68, Appl
c 306	1.2	8174	2	US-08-696-731-5	Sequence 5, Appl	c 379	33	1.1	384	4	US-09-127-480-68	Sequence 68, Appl
c 307	1.2	8174	4	US-09-042-563-5	Sequence 5, Appl	c 380	33	1.1	384	4	US-08-496-841C-68	Sequence 68, Appl
c 308	1.2	8174	5	PCT-US91-06899-3	Sequence 3, Appl	c 381	33	1.1	384	4	US-09-124-523-68	Sequence 68, Appl
c 309	1.2	9704	4	US-09-814-952A-4	Sequence 4, Appl	c 382	33	1.1	446	2	US-08-332-766A-26	Sequence 26, Appl
c 310	1.2	9837	1	US-08-842-883-64	Sequence 64, App	c 383	33	1.1	446	2	US-08-332-766A-26	Sequence 26, Appl
c 311	1.2	9837	1	US-08-842-883-64	Sequence 64, App	c 384	33	1.1	457	4	US-09-643-597-306	Sequence 306, App
c 312	1.2	10504	4	US-09-423-743A-19	Sequence 19, App	c 385	33	1.1	483	5	PCT-US95-08429-14	Sequence 14, Appl
c 313	1.2	11461	3	US-08-659-563A-29	Sequence 29, App	c 386	33	1.1	483	5	US-09-058-380A-21	Sequence 21, Appl
c 314	1.2	12143	4	US-09-423-743A-19	Sequence 19, App	c 387	33	1.1	508	4	US-09-611-781-21	Sequence 21, Appl
c 315	1.2	12565	4	US-09-423-743A-19	Sequence 19, App	c 388	33	1.1	508	4	US-09-611-781-21	Sequence 21, Appl
c 316	1.2	12847	3	US-08-750-716-1	Sequence 1, Appl	c 389	33	1.1	643	4	US-09-195-982-314	Sequence 314, App
c 317	1.2	18073	4	US-09-370-274-12	Sequence 12, App	c 390	33	1.1	643	4	US-09-605-785-571	Sequence 571, App
c 318	1.2	20303	1	US-08-370-274-12	Sequence 12, App	c 391	33	1.1	643	4	US-09-605-785-571	Sequence 571, App
c 319	1.2	22481	4	US-08-367-416-4	Sequence 16, App	c 392	33	1.1	643	4	US-09-605-785-571	Sequence 571, App

c 393	33	1.1	1043	4	US-09-165-868-4	Sequence 4, Appl	466	33	1.1	16595	4	US-09-146-053-7	Sequence 7, Appl
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c 395	33	1.1	1250	4	US-09-018-584A-36	Sequence 46, Appl	c 468	33	1.1	17425	4	US-09-511-625B-5	Sequence 5, Appl
c 396	33	1.1	1289	4	US-09-247-155-148	Sequence 148, Appl	c 469	33	1.1	19736	4	US-09-740-035-3	Sequence 3, Appl
c 397	33	1.1	1381	2	US-08-454-567C-49	Sequence 49, Appl	c 470	33	1.1	41571	1	US-08-423-443B-1	Sequence 1, Appl
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c 399	33	1.1	1381	2	US-08-450-674C-49	Sequence 49, Appl	c 472	33	1.1	42571	4	US-09-810-347-3	Sequence 3, Appl
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c 403	33	1.1	1442	2	US-08-340-426D-129	Sequence 129, Appl	c 476	33	1.1	169998	4	US-09-676-610B-24	Sequence 24, Appl
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c 406	33	1.1	2048	1	US-08-261-578-11	Sequence 11, Appl	c 479	32	1.1	289	2	US-08-486-756A-63	Sequence 63, Appl
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c 408	33	1.1	2396	3	US-09-611-781-10	Sequence 10, Appl	c 481	32	1.1	289	3	US-08-787-739-63	Sequence 63, Appl
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c 410	33	1.1	3267	2	US-08-367-841A-12	Sequence 12, Appl	c 483	32	1.1	289	3	US-08-485-863A-63	Sequence 63, Appl
c 411	33	1.1	3267	5	PCT-US95-07201-12	Sequence 12, Appl	c 484	32	1.1	289	4	US-08-485-049D-63	Sequence 63, Appl
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c 415	33	1.1	3480	1	US-08-485-865-219	Sequence 219, Appl	c 488	32	1.1	615	4	US-09-385-982-30	Sequence 30, Appl
c 416	33	1.1	3480	2	US-08-477-162-219	Sequence 219, Appl	c 489	32	1.1	844	4	US-08-927-219-46	Sequence 46, Appl
c 417	33	1.1	3480	2	US-08-477-134-219	Sequence 219, Appl	c 490	32	1.1	988	4	US-08-642-274D-53	Sequence 53, Appl
c 418	33	1.1	3480	3	US-08-473-489A-219	Sequence 219, Appl	c 491	32	1.1	988	4	US-08-952-014C-53	Sequence 53, Appl
c 419	33	1.1	3480	4	US-08-485-595-219	Sequence 219, Appl	c 492	32	1.1	1001	4	US-09-641-618-396	Sequence 396, Appl
c 420	33	1.1	3480	4	US-08-018-760-219	Sequence 219, Appl	c 493	32	1.1	1002	4	US-09-641-618-581	Sequence 581, Appl
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c 422	33	1.1	4040	2	US-08-685-118-1	Sequence 1, Appl	c 495	32	1.1	1110	4	US-09-511-625B-43	Sequence 43, Appl
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c 427	33	1.1	4823	2	US-08-484-257-20	Sequence 20, Appl	c 500	32	1.1	1334	2	US-08-481-658B-44	Sequence 44, Appl
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c 430	33	1.1	4823	5	PCT-US94-08806-28	Sequence 28, Appl	c 503	32	1.1	1334	2	US-08-485-862B-44	Sequence 44, Appl
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c 432	33	1.1	4823	5	PCT-US95-16620-5	Sequence 5, Appl	c 505	32	1.1	1334	3	US-08-487-077A-44	Sequence 44, Appl
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c 436	33	1.1	5232	4	US-09-617-053A-4	Sequence 4, Appl	c 509	32	1.1	1334	4	US-09-177-776-44	Sequence 44, Appl
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c 438	33	1.1	5835	4	US-09-013-333-1	Sequence 3, Appl	c 511	32	1.1	1401	4	US-08-913-014A-5	Sequence 5, Appl
c 439	33	1.1	5835	4	US-09-614-956-2	Sequence 2, Appl	c 512	32	1.1	1554	1	US-08-370-975H-10	Sequence 10, Appl
c 440	33	1.1	5835	4	US-09-614-956-2	Sequence 2, Appl	c 513	32	1.1	1574	4	US-09-189-527-10	Sequence 10, Appl
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c 442	33	1.1	5836	3	US-08-121-690-1	Sequence 1, Appl	c 515	32	1.1	1664	1	US-07-695-472B-3	Sequence 3, Appl
c 443	33	1.1	5836	3	US-08-841-561-1	Sequence 1, Appl	c 516	32	1.1	1701	4	US-09-078-294-9	Sequence 9, Appl
c 444	33	1.1	5836	4	US-09-633-113-2	Sequence 2, Appl	c 517	32	1.1	1701	4	US-09-006-186-1	Sequence 1, Appl
c 445	33	1.1	5836	4	US-09-033-556-1	Sequence 1, Appl	c 518	32	1.1	1773	4	US-08-943-731-215	Sequence 215, Appl
c 446	33	1.1	5836	4	US-09-614-955-2	Sequence 2, Appl	c 519	32	1.1	1808	1	US-08-351-149-4	Sequence 4, Appl
c 447	33	1.1	6063	1	US-08-195-744-4	Sequence 4, Appl	c 520	32	1.1	1808	1	US-08-384-828-4	Sequence 4, Appl
c 448	33	1.1	6063	2	US-08-788-279-4	Sequence 4, Appl	c 521	32	1.1	1808	3	US-08-895-474-4	Sequence 4, Appl
c 449	33	1.1	6330	4	US-09-880-427-2	Sequence 2, Appl	c 522	32	1.1	1901	4	US-09-338-907-181	Sequence 181, Appl
c 450	33	1.1	6330	4	US-09-405-538B-2	Sequence 2, Appl	c 523	32	1.1	1901	4	US-09-218-207-181	Sequence 181, Appl
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c 452	33	1.1	7676	2	US-08-451-777A-7	Sequence 7, Appl	c 525	32	1.1	1988	2	US-08-257-963B-11	Sequence 11, Appl
c 453	33	1.1	7676	2	US-08-998-208-7	Sequence 7, Appl	c 526	32	1.1	1988	4	US-08-367-841A-11	Sequence 11, Appl
c 454	33	1.1	7676	5	PCT-US95-06743-7	Sequence 7, Appl	c 527	32	1.1	1988	5	PCT-US95-07201-11	Sequence 11, Appl
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c 458	33	1.1	8174	2	US-08-696-731-5	Sequence 5, Appl	c 531	32	1.1	2140	4	US-09-611-781-6	Sequence 6, Appl
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c 462	33	1.1	10380	4	US-09-777-154B-4	Sequence 4, Appl	c 535	32	1.1	2426	4	US-09-605-785-470	Sequence 470, Appl
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690 1 1.1 6769 5 PCT-US95-10220-20 Sequence 20, Appl
691 1 1.1 7130 4 US-09-056-105-32 Sequence 20, Appl
692 1 1.1 7152 4 US-09-167-681-29 Sequence 20, Appl
693 1 1.1 7505 4 US-09-078-294-15 Sequence 16, App
694 1 1.1 7705 2 US-08-587-080-315 Sequence 115, App
695 1 1.1 7720 4 US-09-318-448-5 Sequence 45, Appl
696 1 1.1 8453 4 US-09-167-681-45 Sequence 1, Appl
697 1 1.1 8517 3 US-08-827-268-1 Sequence 1, Appl
698 1 1.1 8517 4 US-09-500-158-1 Sequence 1, Appl
699 1 1.1 8517 4 US-09-448-809-1 Sequence 1, Appl
700 1 1.1 12047 2 US-09-022-461-1 Sequence 1, Appl
701 1 1.1 12047 4 US-09-033-556-4 Sequence 1, Appl
702 1 1.1 12597 4 US-09-705-299-12 Sequence 12, Appl
703 1 1.1 13953 4 US-09-748-884-3 Sequence 1, Appl
704 1 1.1 14753 4 US-09-821-736-3 Sequence 1, Appl
705 1 1.1 15202 3 US-08-922-635-31 Sequence 1, Appl
706 1 1.1 17410 1 US-07-841-646-3 Sequence 21, Appl
707 1 1.1 17410 1 US-08-147-023-3 Sequence 1, Appl
708 1 1.1 17410 1 US-08-447-570-3 Sequence 1, Appl
709 1 1.1 17410 2 US-08-449-730-3 Sequence 1, Appl
710 1 1.1 17410 2 US-08-449-592A-3 Sequence 1, Appl
711 1 1.1 17415 3 US-08-486-146A-1 Sequence 1, Appl
712 1 1.1 17415 5 PCT-US95-07449-1 Sequence 1, Appl
713 1 1.1 18596 4 US-09-318-448-11 Sequence 1, Appl
714 1 1.1 36741 4 US-09-301-665-7 Sequence 1, Appl
715 1 1.1 45546 4 US-09-146-053-6 Sequence 1, Appl
716 1 1.1 49136 4 US-09-422-869-1 Sequence 1, Appl
717 1 1.1 65042 4 US-09-784-336-3 Sequence 1, Appl
718 1 1.1 111282 4 US-09-754-250-3 Sequence 1, Appl
719 1 1.1 169998 4 US-09-679-610B-24 Sequence 24, Appl
720 1 1.1 84 2 US-08-454-553-91 Sequence 41, Appl
721 1 1.1 84 2 US-08-340-426B-91 Sequence 41, Appl
722 1 1.1 84 2 US-08-450-673-91 Sequence 41, Appl
723 1 1.1 84 5 PCT-US95-17111A-91 Sequence 41, Appl
724 1 1.1 151 2 US-08-454-553-91 Sequence 41, Appl
725 1 1.1 151 2 US-08-340-426B-91 Sequence 41, Appl
726 1 1.1 151 2 US-08-450-673-91 Sequence 41, Appl
727 1 1.1 151 5 PCT-US95-17111A-91 Sequence 41, Appl
728 1 1.1 240 1 US-08-222-177A-9 Sequence 41, Appl
729 1 1.1 345 4 US-09-585-082-145 Sequence 41, Appl
730 1 1.1 377 2 US-08-454-553-91 Sequence 41, Appl
731 1 1.1 377 2 US-08-340-426B-91 Sequence 41, Appl
732 1 1.1 377 5 PCT-US95-17111A-91 Sequence 41, Appl
733 1 1.1 542 4 US-09-235-037-1 Sequence 114, Appl
734 1 1.1 613 4 US-09-085-082-114 Sequence 114, Appl
735 1 1.1 651 4 US-09-257-177-12 Sequence 114, Appl
736 1 1.1 690 4 US-09-148-111-74 Sequence 114, Appl
737 1 1.1 700 4 US-08-991-789A-174 Sequence 174, Appl
738 1 1.1 700 4 US-09-062-151-174 Sequence 174, Appl
739 1 1.1 700 4 US-09-598-126-174 Sequence 174, Appl
740 1 1.1 1000 4 US-09-018-584A-42 Sequence 12, Appl
741 1 1.1 1052 4 US-09-442-143A-9 Sequence 9, Appl
742 1 1.1 1196 3 US-07-959-369-4 Sequence 4, Appl
743 1 1.1 1237 4 US-09-545-008-15 Sequence 5, Appl
744 1 1.1 1419 4 US-08-943-743-164 Sequence 164, Appl
745 1 1.1 1480 2 US-08-454-553-91 Sequence 48, Appl
746 1 1.1 1480 2 US-08-340-426B-91 Sequence 48, Appl
747 1 1.1 1480 2 US-08-450-673-91 Sequence 48, Appl
748 1 1.1 1480 5 PCT-US95-17111A-91 Sequence 48, Appl
749 1 1.1 1699 4 US-08-923-165A-6 Sequence 5, Appl
750 1 1.1 1744 4 US-09-511-625B-19 Sequence 19, Appl
751 1 1.1 2061 2 US-08-966-622-11 Sequence 1, Appl
752 1 1.1 2777 4 US-09-413-461-4 Sequence 1, Appl
753 1 1.1 2777 4 US-08-842-248A-3 Sequence 1, Appl
754 1 1.1 2790 3 US-08-985-950-20 Sequence 1, Appl
755 1 1.1 2922 4 US-09-310-461-2 Sequence 1, Appl
756 1 1.1 2922 4 US-08-842-248A-3 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-08-724-594A-20/3

Sequence 20, Application: US/08724-594A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Kronmal, Gregory S.

APPLICANT: Loner, Peter M.

APPLICANT: Roddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1

TITLE OF INVENTION: Sequences and Antibodies Thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-0844

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724-594A

FILING DATE: 01 Oct 1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

RESULT 4
US-09-345-882-1
: Sequence 1, Application US/09345882
: Patent No. 6399373
: GENERAL INFORMATION:
: APPLICANT: Bouguetelret, Lydie
: TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOLAST-MA BINDING PROTEIN (RSP-7)
: FILE REFERENCE: GENSET.031A
: CURRENT APPLICATION NUMBER: US/09/345.882
: PRIORITY FILING DATE: 1999-06-30
: PRIOR APPLICATION NUMBER: US 60/091,415
: PRIORITY FILING DATE: 1998-06-30
: PRIOR APPLICATION NUMBER: US 60/111,909
: PRIORITY FILING DATE: 1998-12-10
: NUMBER OF SEQ ID NOS: 140
: SOFTWARE: Patent.pm
: SEQ ID NO 1
: LENGTH: 162450
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: allele
: LOCATION: 72794
: OTHER INFORMATION: 5-124-273 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 88073
: OTHER INFORMATION: 5-127-261 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 90842
: OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 91714
: OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97122
: OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97152
: OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99098
: OTHER INFORMATION: 5-130-257 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99117
: OTHER INFORMATION: 5-130-276 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 103806
: OTHER INFORMATION: 5-131-395 : polymorphic base A or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106940
: OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108106
: OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108149
: OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
: FEATURE:
: NAME/KEY: allele

: LOCATION: 108308
: OTHER INFORMATION: 5-135-357 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108471
: OTHER INFORMATION: 5-136-174 : polymorphic base C or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 134134
: OTHER INFORMATION: 5-140-120 : polymorphic base C or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 144362
: OTHER INFORMATION: 5-140-148 : polymorphic base insertion of A
: FEATURE:
: NAME/KEY: allele
: LOCATION: 134374
: OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
: FEATURE:
: NAME/KEY: allele
: LOCATION: 146328
: OTHER INFORMATION: 5-143-84 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 146345
: OTHER INFORMATION: 5-143-101 : polymorphic base A or C
: FEATURE:
: NAME/KEY: allele
: LOCATION: 150129
: OTHER INFORMATION: 5-145-24 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 160031
: OTHER INFORMATION: 5-148-352 : polymorphic base G or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 72771..72817
: OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
: FEATURE:
: NAME/KEY: allele
: LOCATION: 72771..72817
: OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
: FEATURE:
: NAME/KEY: allele
: LOCATION: 88050..88096
: OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
: FEATURE:
: NAME/KEY: allele
: LOCATION: 88050..88096
: OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
: FEATURE:
: NAME/KEY: allele
: LOCATION: 90819..90865
: OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
: FEATURE:
: NAME/KEY: allele
: LOCATION: 90819..90865
: OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
: FEATURE:
: NAME/KEY: allele
: LOCATION: 93690..93736
: OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
: FEATURE:
: NAME/KEY: allele
: LOCATION: 93690..93736
: OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97099..97145
: OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97099..97145

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OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ 11671
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ 11666
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ 11666
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ 11664
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OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ 11666
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NAME/KEY: allele
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OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ 11666
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ 11666
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ 11667
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ 11667
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ 11666
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ 11666
FEATURE:
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Query Match 1.88; Score 51; DB 4; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2,ile 13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
UY 1194 CTTGGCTCCCAAGTCTGGATTACAGGATCAGGACATGCGCCAGC 1244
|||||
DB 40273 CTTGGCTCCCAAGTCTGGATTACAGGATCAGGACATGCGCCAGC 40323
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RESULT 5

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US-09-845-882-1/c
Sequence 1, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
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APPLICANT: Bouquellet, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (
FILE REFERENCE: GPNSET.031A
CURRENT APPLICATION NUMBER: US/09/845,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 152450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of G
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
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NAME/KEY: allele
LOCATION: 134134 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146345 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 150329 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817 : polymorphic fragment 5-124-273 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817 : polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096 : polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096 : polymorphic fragment 5-127-261 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865 : complement polymorphic fragment 99-142-425 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865 : complement polymorphic fragment 99-142-425 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736 : polymorphic fragment 5-128-60 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736 : polymorphic fragment 5-128-60 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145 : polymorphic fragment 99-1442-224 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145 : polymorphic fragment 99-1442-224 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177 : polymorphic fragment 5-129-144 SEQ ID60
FEATURE:
NAME/KEY: allele

LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:

Query Match 1.7%; Score 50; DB 4; Length 162450;
Best Local Similarity 100.0%; Pred. No. 6e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTGGCTCCCAAGTCTGGCAITACAGGATGAGCCACTG 1236
|||||
Db 141422 CTGCCACCTGGCTCCCAAGTCTGGCAITACAGGATGAGCCACTG 141373

RESULT 6
US-09-257-179-11/c
Sequence 11, Application US/09257179
Patent No. 6410709
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CURRENT APPLICATION NUMBER: US/09/257,179
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: PCT/US96/17709
EARLIER FILING DATE: 1998-08-27

EARLIER APPLICATION NUMBER: 60/056,270
CURRENT FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 36159
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(36159)
OTHER INFORMATION: n = A,T,C or G
US-09-749-588-3

Query Match 1.7% Score 49; DB 4; Length 36159;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTGCTCCCGGTTCAAGGCAATCTCTCCGCTACGCTCTCTGAG 108;
|||||
DB 772 AACCTGCTCCCGGTTCAAGGCAATCTCTCCGCTACGCTCTCTGAG 74

RESULT 7
US-09-810-671-3
Sequence 3; Application US/09810671
Patent No. 6455291
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEOTIDE SEQUENCES, AND USES
FILE REFERENCE: CIG00758
CURRENT APPLICATION NUMBER: US/09/810,671
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 21254
TYPE: DNA
ORGANISM: human
US-09-810-671-3

Query Match 1.7% Score 49; DB 4; Length 21254;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTGCTCCCGGTTCAAGGCAATCTCTCCGCTACGCTCTCTGAG 108;
|||||
DB 12052 AACCTGCTCCCGGTTCAAGGCAATCTCTCCGCTACGCTCTCTGAG 12100

RESULT 8
US-09-749-588-3
Sequence 3; Application US/09749588
Patent No. 6425521
GENERAL INFORMATION:
APPLICANT: CHANDRAMOULISWARAN, Ishwar et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEOTIDE SEQUENCES, AND USES
FILE REFERENCE: CIG001068
CURRENT APPLICATION NUMBER: US/09/749,588

CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 36159
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(36159)
OTHER INFORMATION: n = A,T,C or G
US-09-749-588-3

Query Match 1.7% Score 49; DB 4; Length 36159;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCAGCTTGGCTCCCAAGTGTGGGATTACAGGATGAGCCACT 1235;
|||||
DB 6516 CTGCCAGCTTGGCTCCCAAGTGTGGGATTACAGGATGAGCCACT 6564

RESULT 9
US-08-323-4438-1
Sequence 1; Application US/083234438
Patent No. 5654170
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LANDES, GREGORY M.
APPLICANT: HURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: JACKOWSKI, WILLIAM R.
APPLICANT: GERMINO, GREGORY
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,4438
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DRAWING NUMBER: 0372/0A462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PCCL-37NM1
US-08-323-4438-1

Query Match 1.7% Score 48; DB 1; Length 3162;
Best Local Similarity 100.0%; Pred. No. 4.9e-12;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGGCCAC 1234
|||||
Db 1117 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGGCCAC 1194

RESULT 10
US-09-748-894A-1/c
Sequence 3, Application US/09738894A
Patent No. 6331423
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEOT
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CLO00616
CURRENT APPLICATION NUMBER: US/09/738,894A
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 36651
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C or G
US-09-748-894A-3

Query Match 1.7% Score 48; DB 4; Length 6645;
Best Local Similarity 100.0%; Pred. No. 4.9e-12;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGGCCAC 1234
|||||
Db 1591 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGGCCAC 1644

RESULT 11
US-08-658-136-2
Sequence 2, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4 17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match 1.7% Score 48; DB 3; Length 53526;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGGCCAC 1234
|||||
Db 1712 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGGCCAC 1759

RESULT 12
US-08-658-136-1
Sequence 1, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match 1.7% Score 48; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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NAME/KEY: CDS
LOCATION: 4..447
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 4..147
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.6999980926514
OTHER INFORMATION: seq LLLFFGKILVVGG/VG
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 858..863
FEATURE:
NAME/KEY: polyA_site
LOCATION: 880..891
US-09-247-155-141

Query Match      1.68; Score 45; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 AACCTCTGCTCCCGGGTTCAGGCGATTCCTCTGCTCAGCTCT 1077
      |||||
DB 772 AACCTCTGCTCCCGGGTTCAGGCGATTCCTCTGCTCAGCTCT 728

RESULT 16
US-09-288-143 16/C
Sequence 16, Application US/09288143
Patent No. 6433139
GENERAL INFORMATION:
APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: P2018P1
CURRENT APPLICATION NUMBER: US/09/288.143
CURRENT FILING DATE: 1998-04-08
EARLIER APPLICATION NUMBER: PCT/JUS96/21142
EARLIER FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061.463
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061.529
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/071.498
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061.527
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061.546
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061.542
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 16
LENGTH: 1646
TYPE: DNA
ORGANISM: Homo sapiens
US-09-288-143-16

Query Match      1.68; Score 45; DB 4; Length 1077
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 AACCTCTGCTCCCGGGTTCAGGCGATTCCTCTGCTCAGCTCT 1077
      |||||
DB 947 AACCTCTGCTCCCGGGTTCAGGCGATTCCTCTGCTCAGCTCT 943

RESULT 17
US-09-078-294-9
Sequence 9, Application US/09078294
Patent No. 6265211
GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
```

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APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 1701
TYPE: DNA
ORGANISM: BAC P2 contig 5
US-09-078-294-9

Query Match      1.68; Score 45; DB 4; Length 1701;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTCTGCTCCCGGGTTCAGGCGATTCCTCTGCTCAGCTCT 1077
      |||||
DB 1182 AACCTCTGCTCCCGGGTTCAGGCGATTCCTCTGCTCAGCTCT 1226

RESULT 18
US-08-257-963B-12
Sequence 12, Application US/08257963B
Patent No. 5840686
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Tanigaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 145 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: WINDOWS/MS-DOS
SOFTWARE: WAREPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DACKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: J1109
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 kb PCR product
```

OTHER INFORMATION: using primers, SEQ ID No. 5849686 16 and 16
US-08-257-463B-12

Query Match: 1.6%; Score 45; DB 2; Length 4267;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 1234
|||||
DB 613 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 657

RESULT 19

US 08-467-841A-12
Sequence 12, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazurek, Krzysztof;
APPLICANT: Lomban-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF THE PIGMENT GENE
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PIGMENT GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367.841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUIH
REGISTRATION NUMBER: 46434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6840
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: JT109
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 kb PCR product
OTHER INFORMATION: using primers, SEQ ID No. 5849687 16 and 16
US-08-367-841A-12

Query Match: 1.6%; Score 45; DB 4; Length 4267;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 1234

DB 613 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 657

RESULT 20

PCT-US95-07201-12
Sequence 12, Application PC/1059507201
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF THE PIGMENT GENE
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PIGMENT GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06 JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUIH
REGISTRATION NUMBER: 46434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6840
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: JT109
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 kb PCR product
OTHER INFORMATION: using primers, SEQ ID No: 15 and 16
PCT-US95-07201-12

Query Match: 1.6%; Score 45; DB 5; Length 3267;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 1234

DB 613 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 657

RESULT 21

US-09-499-884-11/C

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; Sequence 11, Application US/09499884
; Patent No. 6265172
; GENERAL INFORMATION:
; APPLICANT: St. Clair, Daret
; APPLICANT: Urano, Muneyasu
; APPLICANT: Kasarskis, Edward
; TITLE OF INVENTION: DIAGNOSTIC TEST AND THERAPY FOR MAN-ANPSE SUPEROXIDE DISMUTASE
; FILE REFERENCE: 50229-180
; CURRENT APPLICATION NUMBER: US/09/499,884
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-499-884-11

Query Match      1.6%; Score 45; DB 4; Length 4563;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1033 AACCTGCTCCCTCCGGGTTCAAGCGATTCTCTCCCTCAGCGCTCC 1077
      |||||||
Db 1970 AACCTGCTCCCTCCGGGTTCAAGCGATTCTCTCCCTCAGCGCTCC 1926

RESULT 22
US-09-689-423-1
; Sequence 1, Application US/09689423
; Patent No. 6414131
; GENERAL INFORMATION:
; APPLICANT: Herrettini, Wade H.
; TITLE OF INVENTION: Gene and Methods for Diagnosing Neuropsychiatric
; FILE REFERENCE: PENN-0731
; CURRENT APPLICATION NUMBER: US/09/689,423
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/195,620
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/159,354
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3844
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-689-423-1

Query Match      1.6%; Score 45; DB 4; Length 644;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1033 AACCTGCTCCCTCCGGGTTCAAGCGATTCTCTCCCTCAGCGCTCC 1077
      |||||||
Db 1472 AACCTGCTCCCTCCGGGTTCAAGCGATTCTCTCCCTCAGCGCTCC 1516

RESULT 23
US-09-520-3730-5
; Sequence 5, Application US/08520373D
; Patent No. 6451763
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NERVE GROWTH FACTOR
; FILE REFERENCE: 2026-4203U51
```

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; CURRENT APPLICATION NUMBER: US/08/520,373D
; CURRENT FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5262
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: EXON 35-161; EXON 1142-1297; EXON 1984-2187;
; OTHER INFORMATION: EXON 5170-5255; INTRON 162-1141; INTRON
; OTHER INFORMATION: 1298-1983; INTRON 2188-5169; CDS 35-161; CDS
; OTHER INFORMATION: 1142-1297; CDS 1984-2187; CDS 5170-5255
; NAME/KEY: exon
; LOCATION: (35)..(160)
; NAME/KEY: exon
; LOCATION: (1142)..(1297)
; NAME/KEY: exon
; LOCATION: (1984)..(2187)
; NAME/KEY: exon
; LOCATION: (5170)..(5256)
; NAME/KEY: intron
; LOCATION: (162)..(1141)
; NAME/KEY: intron
; LOCATION: (1298)..(1983)
; NAME/KEY: intron
; LOCATION: (2188)..(5169)
; OTHER INFORMATION: n = a or g or t or c, any base
; US-08-520-3730-5

Query Match      1.6%; Score 45; DB 4; Length 5262;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1190 CCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGGCAC 1234
      |||||||
Db 2607 CCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGGCAC 2651

RESULT 24
US-08-973-544-1/c
; Sequence 1, Application US/08973544
; Patent No. 6338950
; GENERAL INFORMATION:
; APPLICANT: WEISS, Elisabeth
; TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKALDO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth St., NW, Suite 300, G St. Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,544
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCI EP 96/02663
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;; FILING DATE: 20-JUN-1996
;; PRIOR APPLICATION DATA: EP 95109511.6
;; FILING DATE: 20-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95112201.9
;; FILING DATE: 03-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kitts, Monica Chin
;; REGISTRATION NUMBER: 36,105
;; REFERENCE/DOCKET NUMBER: P8341-7073
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 638-5009
;; TELEFAX: (202) 638-4810
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5581 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 48..162
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 544..652
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 1044..1162
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 1475..1567
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 1775..1797
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 2325..2709
;;
US-09-973-544-1

Query Match 1.6% Score 45; DB 4; Length 5581;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCGCTCAGCCTCC 1077
|||||
DB 4362 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCGCTCAGCCTCC 4419

RESULT 25
US-09-328-174A-1
;; Sequence 1, Application US/09328174A
;; Patent No. 6448003
;; GENERAL INFORMATION:
;; APPLICANT: Guida, Marco
;; APPLICANT: Kurth, Janice
;; TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
;; TITLE OF INVENTION: (STP2)
;; FILE REFERENCE: 4389-6 (formerly SEQ-16P)
;; CURRENT APPLICATION NUMBER: US/09/328.174A
;; CURRENT FILING DATE: 1999-06-08
;; PRIOR APPLICATION NUMBER: 09/328.174
;; PRIOR FILING DATE: 1999-06-08
;; NUMBER OF SEQ ID NOS: 110
;; SOFTWARE: FastSEQ for Windows Version 3.0
;; SEQ ID NO 1
;; LENGTH: 8396
;; TYPE: DNA
;; ORGANISM: H. sapiens
US-09-328-174A-1

Query Match 1.6% Score 45; DB 4; Length 8396;

Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1033 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCGCTCAGCCTCC 1077
|||||
DB 701 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCGCTCAGCCTCC 745

RESULT 26
US-09-167-681-37
;; Sequence 37, Application US/09167681A
;; Patent No. 6265561
;; GENERAL INFORMATION:
;; APPLICANT: Weinshilbaum, M.D., Richard M.
;; APPLICANT: Raffoulanis, Rebecca B.
;; APPLICANT: Wood, Thomas C.
;; APPLICANT: Otterliuss, Diane M.
;; TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
;; FILE REFERENCE: 07039/118001
;; CURRENT APPLICATION NUMBER: US/09/167,681A
;; CURRENT FILING DATE: 1998-10-07
;; NUMBER OF SEQ ID NOS: 52
;; SOFTWARE: FastSEQ for Windows Version 3.0
;; SEQ ID NO 37
;; LENGTH: 8397
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (3730)...(3879)
;; NAME/KEY: CDS
;; LOCATION: (3987)...(4112)
;; NAME/KEY: CDS
;; LOCATION: (4198)...(4293)
;; NAME/KEY: CDS
;; LOCATION: (6088)...(6213)
;; NAME/KEY: CDS
;; LOCATION: (6309)...(6404)
;; NAME/KEY: CDS
;; LOCATION: (7214)...(7393)
;; NAME/KEY: CDS
;; LOCATION: (7516)...(7629)
;;
US-09-167-681-37

Query Match 1.6% Score 45; DB 4; Length 8409;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCGCTCAGCCTCC 1077
|||||
DB 701 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCGCTCAGCCTCC 745

RESULT 27
US-08-367-841A-43
;; Sequence 43, Application US/08367841A
;; Patent No. 6319687
;; GENERAL INFORMATION:
;; APPLICANT: Chader, Gerald J.; Rodriguez,
;; APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
;; APPLICANT: Tombran-Tink, Joyce
;; TITLE OF INVENTION: PIGMENT EPITHELIUM
;; TITLE OF INVENTION: DERIVED FACTOR; CHARACTERIZATION GENOMIC
;; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Morgan & Finnegan
;; STREET: 345 Park Avenue
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:

QY 1196 CACCTTGGCTCCCAAGTGGCTGGGATTAACAGGCAATGAGCGCA 124
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 17174 CCAAGCTGGCTCCCAAGTGGCTGGGATTAACAGGCAATGAGCGCA 17218

RESULT 40
US 09-797-906-3
Sequence 3, Application US/09797906
Patent No. 6329188
GENERAL INFORMATION:
APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFPANTECO, Eileen M. BEASLEY
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001151CIP
CURRENT APPLICATION NUMBER: US/09/797,906
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 84495
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match 1.6% Score 45; DB 4; Length 84495
Best Local Similarity 100.0%; Pred. No. 1e 10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1192 CACCTTGGCTCCCAAGTGGCTGGGATTAACAGGCAATGAGCGCA 124
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 24248 CACCTTGGCTCCCAAGTGGCTGGGATTAACAGGCAATGAGCGCA 24265

RESULT 41
US-08-724-394A-20
Sequence 20, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereof
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/KEY INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0400
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature

REFERENCE/KEY NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0400
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1...246240
OTHER INFORMATION: /note- "HLA-H-CONTIG"
US-08-724-394A-20

Query Match 1.6% Score 45; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTTGGCTCCCAAGTGGCTGGGATTAACAGGCAATGAGCGCTCC 1077
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 242021 AACCTTGGCTCCCAAGTGGCTGGGATTAACAGGCAATGAGCGCTCC 242065

RESULT 32
US-08-724-394A-20
Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereof
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/KEY INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0400
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature

REFERENCE/KEY NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0400
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature

LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H-CONTIG"
US-08-724-394A-21

Query Match 1.6% Score 45; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 4,6e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTGAGGCTG 1672
|||||
DB 242021 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTGAGGCTG 242021

RESULT 44

US-08-724-394A-22
Sequence 22, Application US/08724394A
Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237
TITLE OF INVENTION: Sequences and Antibodies Thereof
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS: 31
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 01-OCT-1996
CLASSIFICATION: 516
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: C17957

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
SIGNATURE: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H-CONTIG"

US-08-724-394A-22

Query Match 1.6% Score 45; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 4,6e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTGAGGCTG 1672
|||||
DB 242021 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTGAGGCTG 242021

RESULT 34

US-09-374-454-20/c
Sequence 20, Application US/093744454
Patent No. 6395548
GENERAL INFORMATION:

APPLICANT: Lee, Mu En
APPLICANT: Matsumura, Koji
APPLICANT: Hsieh, Chung-Ming
TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
FILE REFERENCE: 05435/037001
CURRENT APPLICATION NUMBER: US/09/374,454

CURRENT FILING DATE: 1999-08-13

EARLIER APPLICATION NUMBER: US 60/096,515

EARLIER FILING DATE: 1998-08-14

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 20

LENGTH: 6792

TYPE: DNA

ORGANISM: Homo sapiens

US-09-374-454-20

Query Match 1.5% Score 44; DB 4; Length 6792;

Best Local Similarity 100.0%; Pred. No. 3.1e-10;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1198 GGCTCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGGCC 1241

|||||

DB 5397 GGCTCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGGCC 5354

RESULT 35

US-09-741-150-3/c

Sequence 3, Application US/09741150

Patent No. 6436689

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,

TITLE OF INVENTION: USFS THEREOF

FILE REFERENCE: C1G00968

CURRENT APPLICATION NUMBER: US/09/741,150

CURRENT FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 112132

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)..(112132)

OTHER INFORMATION: n = A,T,C or G

US-09-741-150-3

Query Match 1.5% Score 44; DB 4; Length 112132;

Best Local Similarity 100.0%; Pred. No. 2.8e-10;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGTC 1237

|||||

DB 18454 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGTC 18411

RESULT 36

US-09-128-155-17/c

Sequence 17, Application US/09128155

Patent No. 6117654

GENERAL INFORMATION:

APPLICANT: Pao, Yung

TITLE OF INVENTION: NEW MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 09434/052-01

CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n - A.T.C or G
US-09-128-155 17

Query Match 1.5%: Score 44; DB 4; Length 176373;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1194 CTTGGCCTCCCAAGTGTGGGATTACAGGATGAGGACACTG 1237
|||||
DB 45158 CTTGGCCTCCCAAGTGTGGGATTACAGGATGAGGACACTG 15115

RESULT 47
US-08-471-570-9/c
Sequence 9, Application US/0847:570
Patent No. 5750371
GENERAL INFORMATION:
APPLICANT: IGARASHI, Koichi
APPLICANT: SENOO, Masaharu
APPLICANT: WATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.26
CURRENT APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE:

APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, Ernest V
REGISTRATION NUMBER: 29822
REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2310 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 25..1986
US-08-471-570-9

Query Match 1.5%: Score 43; DB 1; Length 2310;
Best Local Similarity 100.0%; Pred. No. 9.2e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1198 GGCTTCGCAAGTGTGGGATTACAGGATGAGGACACTGCGCC 1240
|||||
DB 2066 GGCTTCGCAAGTGTGGGATTACAGGATGAGGACACTGCGCC 2024

RESULT 38
US-08-471-570-7/c
Sequence 7, Application US/0847:1570
Patent No. 5750371
GENERAL INFORMATION:

APPLICANT: IGARASHI, Koichi
APPLICANT: SENOO, Masaharu
APPLICANT: WATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE:

APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, Ernest V
REGISTRATION NUMBER: 29822
REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 25..2331
US-08-471-570-7

Query Match 1.5%: Score 43; DB 1; Length 2676;
Best Local Similarity 100.0%; Pred. No. 9.1e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1198 GGCTTCGCAAGTGTGGGATTACAGGATGAGGACACTGCGCC 1240
|||||

Db 2417 GCGCTCCCAAGTGTGGATTACAGGCGATGAGCGACTGGCC 2475

RESULT 39

US-09-975-080-35
Sequence 35, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975-080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01 WC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 14796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-975-080-35

Query Match 1.5%: Score 43; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 CCTGTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 1077
DB 2420 CCTGTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 2462

RESULT 40

US-09-630-706-10
Sequence 10, Application US/09630706
Patent No. 6277640
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
FILE REFERENCE: RFS-0053
CURRENT APPLICATION NUMBER: US/09/630,706
CURRENT FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 10
LENGTH: 14796
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

LOCATION: (2811)...(2921)
NAME/KEY: CDS
LOCATION: (3174)...(3283)
NAME/KEY: CDS
LOCATION: (5158)...(5275)
NAME/KEY: CDS
LOCATION: (11955)...(12044)
US-09-630-706-10

Query Match 1.5%: Score 43; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 CCTGTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 1077
DB 2320 CCTGTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 2362

RESULT 41

US-09-496-694B-3
Sequence 3, Application US/09496694B
Patent No. 6335194
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric E. Swayze
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 09/163,162
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
SEQ ID NO 3
LENGTH: 14796
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2811)...(2921)
NAME/KEY: CDS
LOCATION: (3174)...(3283)
NAME/KEY: CDS
LOCATION: (5158)...(5275)
NAME/KEY: CDS
LOCATION: (11955)...(12044)
US-09-496-694B-3

Query Match 1.5%: Score 43; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 CCTGTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 1077
DB 2320 CCTGTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 2362

RESULT 42

US-09-341-587-7
Sequence 7, Application US/09341587
Patent No. 6345606
GENERAL INFORMATION:
APPLICANT: Moltenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 28720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-7

Query Match      1.5%: Score 43; DB 4; Length 28720;
Best Local Similarity 100.0%; Pred. No. 8.1e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1033 AACCTCCTCCCGGTTCAAGCGATTCTCGTGGTACGCT 1075
      |||||||
DB 19480 AACCTCCTCCCGGTTCAAGCGATTCTCGTGGTACGCT 19522

RESULT 45
US-09-268-992-7/c
; Sequence 7, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; PRIOR FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: all n positions
; OTHER INFORMATION: n-a, c, g, or t
US-09-268-992-7

Query Match      1.5%: Score 43; DB 4; Length 72604;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1199 GCCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCC 1241
      |||||||
DB 63856 GCCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCC 63814

RESULT 46
US-09-657-474-7/c
; Sequence 7, Application US/09657474
; Patent No. 6393762
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/657,474
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/288,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
;

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 28720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-7

Query Match      1.5%: Score 43; DB 4; Length 28720;
Best Local Similarity 100.0%; Pred. No. 8.1e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1033 AACCTCCTCCCGGTTCAAGCGATTCTCGTGGTACGCT 1075
      |||||||
DB 19480 AACCTCCTCCCGGTTCAAGCGATTCTCGTGGTACGCT 19522

RESULT 45
US-09-780-049-18
; Sequence 18, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-049-18

Query Match      1.5%: Score 43; DB 4; Length 40000;
Best Local Similarity 100.0%; Pred. No. 8e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTGGCCCTCCCAAGTGTGGGATTACAGGCATGAGCCACTG 1236
      |||||||
DB 16933 CTTGGCCCTCCCAAGTGTGGGATTACAGGCATGAGCCACTG 16976

RESULT 44
US-09-851-896-3/c
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Wall
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+)-INDEPENDENT
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

Query Match      1.5%: Score 43; DB 4; Length 70000;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1199 GCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCC 1241
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DB 31602 GCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCC 31563
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; LOCATION: all n positions
; OTHER INFORMATION: n-a, c, g, or t
US-09-657 474-7

Query Match      1.5%: Score 43; DB 4; Length 72604;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1199 GCGTCGCAAGTCTGGGATTACAGGCATGCGGC 1241
      |||||
DB 64856 GCGTCGCAAGTCTGGGATTACAGGCATGCGGC 64814

RESULT 47
US-09-750-580-1
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89 US2.CIP
; CURRENT APPLICATION NUMBER: US/09750580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/594,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCI/IB00/C101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCI/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10946..12946
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; NAME/KEY: misc_feature
; LOCATION: 15969..17969
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 1239
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 20-841-149.mis complement
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 77058
; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
; NAME/KEY: primer_bind
; LOCATION: 929..949
; OTHER INFORMATION: 20-828.pu
; NAME/KEY: primer_bind
; LOCATION: 1357..1377
; OTHER INFORMATION: 20-828.rp complement
; NAME/KEY: primer_bind
; LOCATION: 12029..12050
; OTHER INFORMATION: 17-42.pu
; NAME/KEY: primer_bind
; LOCATION: 12581..12603
; OTHER INFORMATION: 17-42.rp complement
; NAME/KEY: primer_bind
; LOCATION: 14992..15012
; OTHER INFORMATION: 17-41.pu
; NAME/KEY: primer_bind
; LOCATION: 15460..15482
; OTHER INFORMATION: 17-41.rp complement
; NAME/KEY: primer_bind
; LOCATION: 42070..42090
; OTHER INFORMATION: 20-841.pu
; NAME/KEY: primer_bind
; LOCATION: 42572..42591
; OTHER INFORMATION: 20-841.rp complement
; NAME/KEY: primer_bind
; LOCATION: 45328..45347
; OTHER INFORMATION: 20-842.pu
; NAME/KEY: primer_bind
; LOCATION: 45863..45883
; OTHER INFORMATION: 20-842.rp complement
; NAME/KEY: primer_bind
; LOCATION: 76644..76664
; OTHER INFORMATION: 20-853.pu
; NAME/KEY: primer_bind
; LOCATION: 77166..77185
; OTHER INFORMATION: 20-853.rp complement
; NAME/KEY: primer_bind
; LOCATION: 1220..1238
; OTHER INFORMATION: 20-828-311.mis
; NAME/KEY: primer_bind
; LOCATION: 1240..1258
; OTHER INFORMATION: 20-828-311.mis complement
; NAME/KEY: primer_bind
; LOCATION: 12328..12346
; OTHER INFORMATION: 17-42-319.mis
; NAME/KEY: primer_bind
; LOCATION: 12348..12366
; OTHER INFORMATION: 17-42-319.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15222..15240
; OTHER INFORMATION: 17-41-250.mis
; NAME/KEY: primer_bind
; LOCATION: 15242..15260
; OTHER INFORMATION: 17-41-250.mis complement
; NAME/KEY: primer_bind
; LOCATION: 42199..42217
; OTHER INFORMATION: 20-841-149.mis
; NAME/KEY: primer_bind
; LOCATION: 42219..42237
; OTHER INFORMATION: 20-841-149.mis complement
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NAME/KEY: primer_bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match 1.5%; Score 43; DB 4; Length 8001;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1198 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCC 1240
|||||
DB 59318 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCC 59360

RESULT 48

US-09-791-211-10/C

Sequence 10, Application US/09791211

Patent No. 648080

GENERAL INFORMATION:

APPLICANT: Donna T. Ward

APPLICANT: Andrew T. Watt

TITLE OF INVENTION: ANTISENSE MODULATION OF WNK EXPRESSION

FILE REFERENCE: RTS-0205

CURRENT APPLICATION NUMBER: US/09/791,211

CURRENT FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 10

LENGTH: 98844

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure

LOCATION: 24962

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 64383

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 65468

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 65469

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 65470

OTHER INFORMATION: unknown

NAME/KEY: unsure
LOCATION: 65471
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 87130
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 89049
OTHER INFORMATION: unknown
US-09-791-211-10

Query Match 1.5%; Score 43; DB 4; Length 98844;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1189 GGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGC 1231
|||||
DB 55998 GGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGC 55956

RESULT 49

US-09-798-096-10/C

Sequence 10, Application US/09798096

Patent No. 639978

GENERAL INFORMATION:

APPLICANT: Donna T. Ward

APPLICANT: Andrew T. Watt

TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION

FILE REFERENCE: RTS-0207

CURRENT APPLICATION NUMBER: US/09/798,096

CURRENT FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 89

SEQ ID NO 10

LENGTH: 99500

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

US-09-798-096-10

Query Match 1.5%; Score 43; DB 4; Length 93500;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1198 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCC 1240
|||||
DB 79008 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCC 78966

RESULT 50

US-08-812-204-1

Sequence 1, Application US/08812204

Patent No. 5965790

GENERAL INFORMATION:

APPLICANT: Acton, Susan L.

TITLE OF INVENTION: SR-BI REGULATORY SEQUENCES AND

TITLE OF INVENTION: THERAPEUTIC METHODS OF USE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, ROAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/812,204

FILING DATE: 06-MAR-1997

```

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-014.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-812-204-1

Query Match      1.5%   Score 42;   DB 2;   Length 1613;
Best Local Similarity 100.0%;   Pred. No. 2.5e-09;
Matches 42;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  1040 GCCTCCCGGGTCAAGCGATTCTCCGCTCAGGCTCTGAG 1681
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Db   447  GCCTCCCGGGTCAAGCGATTCTCCGCTCAGGCTCTGAG 486

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Search completed: May 10, 2003, 04:39:45
Job time : 4287.72 secs

GenCore version 5.1.1.5
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DM nucleic - nucleic search, using sw model

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(without alignments)
2376.654 Million comp. updates/sec

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Title: US-09-846-456-5
perfect score: 159
Sequence: 1 ttaatgacacagccacagggc.....cttctcagagagagagagagag 159

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext. 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0
Total number of hits satisfying chosen parameters: 410000

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Minimum DH seq length: 0
Maximum DH seq length: 2000000000
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Post processing: Listing first 45 summaries

Labelbase :	GenEmbl :	*
	1:	gb_ba:*
	2:	qb_htg:*
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	34:	em_htg_pin:*
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	38:	em_sy:*
	39:	em_htgo_hum:*
	40:	em_htgo_mus:*
	41:	em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		ID	Description
		Match	Length		
1	159	100.0	159	6	AX351033 Sequence
2	159	100.0	457	6	AX351030 Sequence
3	77	48.4	10442	6	AX060713 Sequence
4	77	48.4	10442	6	AX060892 Sequence
5	77	48.4	10442	9	AF285167 Homo sapi
6	77	48.4	10474	6	AX060719 Sequence
7	77	48.4	10474	6	AX060721 Sequence
8	77	48.4	10474	6	AX060898 Sequence
9	77	48.4	10474	6	AX060900 Sequence
10	77	48.4	149034	9	AF275948 Homo sapi
11	60	37.7	200	9	AF258623S2
12	60	37.7	298	9	AH037924 Homo sapi
13	60	37.7	446	6	AX127764 Sequence
14	60	37.7	446	6	AX139751 Sequence
15	60	37.7	480	9	HS4252277 Homo sapi
16	60	37.7	597	9	AF258627 Homo sapi
17	60	37.7	5786	9	AB055982 Homo sapi
18	60	37.7	7260	6	AX253452 Sequence
19	60	37.7	7860	6	AX092594 Sequence
20	60	37.7	7862	6	AX135712 Sequence
21	60	37.7	9741	6	AX127830 Sequence
22	60	37.7	9741	6	AX139817 Sequence
23	60	37.7	9741	6	AX351038 Sequence
24	60	37.7	9854	6	AX127831 Sequence
25	60	37.7	9854	6	AX139818 Sequence
26	60	37.7	129606	9	AL353685 Human DNA
27	60	37.7	175064	2	AC012230 Homo sapi
28	60	37.7	183999	6	AX092589 Sequence
29	60	37.7	201144	9	AF287262 Homo sapi
30	51	32.1	1556	9	AC024328 Homo sapi
31	44	27.7	50598	2	AC021345 Homo sapi
32	35	23.0	37	6	AX092843 Sequence
33	21	14.2	21	6	AX092705 Sequence
34	21	14.2	21	6	AX092707 Sequence
35	21	14.2	144809	4	AC091506 Homo sapi
36	20	12.6	152155	9	AC007388 Homo sapi
37	19	11.9	470	6	AX1389585 Sequence
38	19	11.9	624	6	AX066487 Sequence
39	19	11.9	624	6	AR074300 Sequence
40	19	11.9	624	6	AR143622 Sequence
41	19	11.9	624	6	BD005548 Materials
42	19	11.9	684	6	AB074135 Sequence
43	19	11.9	684	6	BD005544 Materials
44	19	11.9	6542	9	AC14324 Homo sapi
45	19	11.9	6155	9	AY099459 Homo sapi

ALIGNMENTS

RESULT 1					
AX351034	AX351034	159 bp	DNA	linear	JAT 06 FEB-2002
LOCUS	Sequence 5				
DEFINITION	from Patent W0183746.				
ACCESSION	AX351034				
VERSION	AX351034.1	GI:18616389			
KEYWORDS	human.				
SOURCE	Homo Sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 Kosier, Marius, M.F., Prades, C., Lemoine, C., Naudin, L., Benetle, P., Brewer, B., Diverger, N., Komaley, A. and Santamarina-Fajó, S. Relative frequency and sequences of the abel gene				
AUTHORS					
TITLE					

KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Lawn, R.M., Wade, D. and Garvin, M.
TITLE Regulation with binding cassette transporter protein: abcl
JOURNAL Patent: WO 0078972-A 1 28-DEC-2000;
CV EMBL/GENB/CCDS, INC. (US)
FEATURES
Source 1..10442
/accession="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
ORIGIN

Query Match 48.4%; Score 77; DB 6; Length 10442;
Best local Similarity 99.2%; Pred. No. 4.3e-32;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 AGCTCTGGCTGCTTCCAGGGCTCCGAGGCCACACGCTGGGGTCTGGCTGAGGGA 91
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Db 229 AGCTCTGGCTGCTTCCAGGGCTCCGAGGCCACACGCTGGGGTCTGGCTGAGGGA 288
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 92 ACATGGCATGTGGCTTCAAGTGTGAGTGTGCTGTGGAGAACCTCACTTTCAGAGAA 151
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 289 ACATGGCATGTGGCTTCAAGTGTGAGTGTGCTGTGGAGAACCTCACTTTCAGAGAA 348
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 152 GACAAACA 159
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Db 349 GACAAACA 356
|||||

RESULT 4
AXC00892
LOCUS AXC00892 Sequence 1 from Patent WO0078971.
DEFINITION AXC00892
ACCESSION AXC00892
VERSION AXC00892.1 GI:12406270
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Lawn, R.M., Wade, D., Gram, J.F. and Garvin, M.
TITLE Abcl binding cassette transporter protein: abcl polypeptides
JOURNAL Patent: WO 0078972-A 1 28-DEC-2000;
CV EMBL/GENB/CCDS, INC. (US)
FEATURES
Source 1..10442
/accession="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
ORIGIN

Query Match 48.4%; Score 77; DB 6; Length 10442;
Best local Similarity 99.2%; Pred. No. 4.3e-32;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 AGCTCTGGCTGCTTCCAGGGCTCCGAGGCCACACGCTGGGGTCTGGCTGAGGGA 91
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 229 AGCTCTGGCTGCTTCCAGGGCTCCGAGGCCACACGCTGGGGTCTGGCTGAGGGA 288
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 92 ACATGGCATGTGGCTTCAAGTGTGAGTGTGCTGTGGAGAACCTCACTTTCAGAGAA 151
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 289 ACATGGCATGTGGCTTCAAGTGTGAGTGTGCTGTGGAGAACCTCACTTTCAGAGAA 348
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 152 GACAAACA 159
|||||
Db 349 GACAAACA 356
|||||

useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis.

Disclosure: Page 122-128; 215pp; English.

The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell membranes and utilizes ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilization of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterized by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for other disorders associated with hypercholesterolemia.

Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 48.4%; Score 77; DB 22; Length 10442;
Best Local Similarity 99.2%; Pred. No. 6.5e-29;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

32 AGCTGCGCGCTGGCTTCAGGGCTCCGAGCCACACGCTGGCGTGTGCTGAGGGA 91
|||||
229 AGCTGCGCGCTGGCTTCAGGGCTCCGAGCCACACGCTGGCGTGTGCTGAGGGA 288

92 ACATGGCAATGTTGGCTTCAGCTGAGGTGCTGCTGGAGAACCTCCTCTTCAAGAA 151
|||||
289 ACATGGCTTGTGGCTTCAGCTGAGGTGCTGCTGGAGAACCTCCTCTTCAAGAA 344

152 GACAAACA 159
|||||
349 GACAAACA 356

RESULT 4
AAF24702
ID AAF24702 standard; DNA: 10442 BP.

AC AAF24702;

UT 20 APR-2001 (first entry)

Nucleotide sequence of a human ABC1 polypeptide.

Human: adenosine triphosphate binding cassette protein 1; ABC1;
apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
chromosome 9q22-9q31; heart disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

Key Location/Qualifiers
CDS 291..7076

/tag- a

/product- "ABC1 polypeptide"

W:200078971 A2.

Z:8-DEC-2000.

16-JUN-2000; 2000W0-0516591.

18-JUN-1999; 99US-0140264.

14-SEP-1999; 99US-0153872.

19-NOV-1999; 99US-0166573.

PA (CVTH-) CV THERAPEUTICS INC.
PA (UNIW) UNIV WASHINGTON.

XX Lawn RM, Wade D, Oram JF, Garvin M;

XX WPI; 2001-137611/14.

XX P-PSDB; AAB3145.

XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
polynucleotides and polypeptides, useful for treatment of heart disease
and other disorders associated with hypercholesterolemia and
atherosclerosis.

XX Claim 3; Page 117-123; 211pp; English.

XX The present sequence encodes a human adenosine triphosphate (ATP)
binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
membranes and utilizes ATP hydrolysis to transport a wide variety of
substrates across the plasma membrane. ABC1 is a pivotal protein in
the apolipoprotein-mediated mobilisation of intracellular cholesterol
stores. ABC1 is defective in Tangier disease, a genetic disorder
characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
useful for developing pharmaceutical agents for the treatment of heart
disease and other disorders associated with hypercholesterolemia and
atherosclerosis. The genes are useful for developing screening assays to
screen for compounds that regulate the expression of genes associated
with cholesterol transport. The genes and proteins are also useful for
other disorders associated with hypercholesterolemia.

XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 48.4%; Score 77; DB 22; Length 10442;
Best Local Similarity 99.2%; Pred. No. 6.5e-29;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

32 AGCTGCGCGCTGGCTTCAGGGCTCCGAGCCACACGCTGGCGTGTGCTGAGGGA 91
|||||
229 AGCTGCGCGCTGGCTTCAGGGCTCCGAGCCACACGCTGGCGTGTGCTGAGGGA 288

92 ACATGGCAATGTTGGCTTCAGCTGAGGTGCTGCTGGAGAACCTCCTCTTCAAGAA 151
|||||
289 ACATGGCTTGTGGCTTCAGCTGAGGTGCTGCTGGAGAACCTCCTCTTCAAGAA 348

152 GACAAACA 159

|||||
349 GACAAACA 356

RESULT 5

AAF24685

ID AAF24685 standard; DNA: 10474 BP.

XX AAF24685;

UT 20-APR-2001 (first entry)

Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
Human: adenosine triphosphate binding cassette protein 1; ABC1;
apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
chromosome 9q22-9q31; heart disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

Key Location/Qualifiers
CDS 323..7108

/tag- a

/product- "defective ABC1 polypeptide"

W:200078972-A2.


```
PR 30-NOV-2000: 2060US-0728422.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX WPI: 2001-476283/51.
DR P-PSDB: AAM78550.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PI useful in diagnosis and gene therapy
XX
XX Claim 1: Page 1086-1096; 6221pp: English.
XX
XX The invention relates to polynucleotides (AAK5145, AAK5145) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation of which may induce
CC production of other cytokines in other cell populations, the
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC
CC Note: Records for SEQ ID NO.2110 (AAK52581), 2111 (AAK52582) and 1666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 7281 BP: 1831 A; 1773 C; 1915 G; 1762 T; 1 other;
XX
XX Query Match 37.7%; Score 60; DB 21; Length 7857;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-20;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 100 TGTGGGCTCAGCTGAGGTTCCTGCTGGAGAGAACCTTCTCAGAGAGAACAAACA 159
XX
XX 349 TGTGGGCTCAGCTGAGGTTCCTGCTGGAGAGAACCTTCTCAGAGAGAACAAACA 407
XX
XX RESULT 15
XX AAC69488
XX
XX AAC69488 standard; CUNA; 7857 BP.
XX
XX AAC69498:
XX
XX 29-JAN-2001 (first entry)
XX
XX Human ABC1 cholesterol transporter FHA-4 mutant cDNA (U014575.2)
XX
XX Human ABC1 cholesterol transporter; chromosome 9p31
XX ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
XX Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
XX cardiovascular disease; coronary artery disease; coronary restenosis;
XX cerebrovascular disease; peripheral vascular disease;
XX Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
XX X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
XX prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
XX
XX Homo sapiens.
XX
XX W0200055318-A2.
XX
XX 21 SEP-2000.
XX
XX 15-MAR-2000; 2000WO-1800532.
XX
XX 15-MAR-1999; 99US-0124702.
XX 08 JUN-1999; 99US-0138048.
XX 17-JUN-1999; 99US-0139600.
XX 01-SEP-1999; 99US-0151977.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (XENO-) XENON BIORESEARCH INC.
XX
XX Hayden MR, Wilson AK, Pimstone SN;
XX
XX WPI: 2000-587528/55.
XX P-PSDB: AAB38107.
XX
XX New ABC1 polypeptide is useful for treating diseases associated with
XX ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
XX disease and cancer
XX
XX Examples: Page 1: 229pp: English.
XX
XX The invention relates to the human ABC1 cholesterol transporter protein
XX (B36082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
XX a member of the ATP-binding cassette (ABC transporter) superfamily of
XX proteins, and plays a crucial role in cholesterol transport, particularly
XX intracellular cholesterol trafficking in monocytes and fibroblasts, being
XX involved in cholesterol efflux from the cell. The gene encoding ABC1 is
XX located on chromosome 9q31, and mutations in this gene are associated
XX with two genetic HDL (high density lipoprotein) deficiency disorders
XX Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
XX are distinguishable in that TD is an autosomal recessive disorder, while
XX FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
XX cholesterol") in the blood correlate with a high risk of cardiovascular
XX disease, particularly coronary artery disease, but also cerebrovascular
XX disease, coronary restenosis, and peripheral vascular disease.
XX Conversely, a high level of HDL has protective effects against
XX cardiovascular disease. The invention provides genetic constructs and
XX transgenic cells and non-human animals comprising human ABC1 nucleic
XX acids, and methods of gene therapy for the treatment or prevention of
XX cardiovascular disease comprising the administration of an expression
XX vector encoding ABC1 or an active fragment thereof. The invention also
XX encompasses compounds which mimic ABC1 activity, compounds which
XX stimulate ABC1 expression and methods of screening for such compounds.
XX It further relates to methods for determining whether a patient has an
XX increased risk for cardiovascular disease due to polymorphisms in the
XX ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
XX or prevent cardiovascular disease, especially coronary artery disease,
XX cerebrovascular disease, coronary restenosis or peripheral vascular
XX disease. They may also be used in the treatment of diseases associated
XX with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
XX disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
XX The invention specifically excludes proteins with the exact amino acid
XX sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic
XX acid with the exact sequence as Genbank Accession No: AJ012476.1. The
XX present sequence represents cDNA encoding a mutant human ABC1 cholesterol
XX transporter associated with an altered cholesterol level and therefore an
XX altered risk of cardiovascular disease.
XX Note: The present sequence is not shown in the specification, but is
XX derived from the native human ABC1 cDNA shown on pages 157-160.
XX
XX Sequence 7857 BP: 2011 A; 1860 C; 2008 G; 1977 T; 1 other;
XX
XX Query Match 37.7%; Score 60; DB 21; Length 7857;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-20;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 100 TGTGGGCTCAGCTGAGGTTCCTGCTGGAGAGAACCTTCTCAGAGAGAACAAACA 159
XX
XX 81 TGTGGGCTCAGCTGAGGTTCCTGCTGGAGAGAACCTTCTCAGAGAGAACAAACA 140
XX
XX Search completed: May 10, 2003, 02:15:55
XX Job time : 242 secs
```

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OH nucleic - nucleic search, using sw model

Run on: May 10, 2003, 02:16:03 : Search time 1580 seconds
(without alignments)
1623.794 Million cell updates/sec

Title: US-09-846-456-5

Perfect score: 159

Sequence: 1 ttaatgaccagccacggcg.....ctttacaaagaaacaaaca 159

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1213172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Listing first 45 summaries

Database :

- EST.*
1: em_estba.*
2: em_esthum.*
3: em_estim.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by program to have a score greater than or equal to the score of the results being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	48.4	547	9	AL698654
2	51	32.1	736	9	AU135588
3	39	24.5	535	12	BG384217
4	24	15.1	292	14	Z44377
5	20	12.6	661	13	BI391126
6	19	11.9	216	12	BF756949

19	11.9	454	17	AQ369174
19	11.9	470	9	AI351952
19	11.9	493	17	AQ709464
19	11.9	546	10	AV953274
19	11.9	568	14	BQ259614
19	11.9	618	9	AA495487
19	11.9	643	9	AI497295
19	11.9	694	10	AV997283
19	11.9	705	13	BI160520
19	11.9	730	10	AW116004
17	18	231	12	BF898523
17	18	275	17	BH402163
18	11.3	299	9	AA098714
18	11.3	303	12	BF903506
18	11.3	340	17	BH859759
18	11.3	346	17	BH859242
18	11.3	375	17	BH127062
18	11.3	397	12	BF911983
18	11.3	461	14	BQ751693
18	11.3	492	14	BQ752118
18	11.3	512	14	BQ751545
18	11.3	529	17	BH396354
18	11.3	532	17	AQ776697
18	11.3	532	17	AQ779444
18	11.3	544	10	AV974535
18	11.3	548	14	BQ752139
18	11.3	554	17	AZ236353
18	11.3	558	17	AZ510640
18	11.3	566	17	AZ510673
18	11.3	597	14	BP010466
18	11.3	599	9	AA720413
18	11.3	627	11	AY067297
18	11.3	631	9	AL652524
18	11.3	645	10	BB614720
18	11.3	645	13	BI996668
18	11.3	647	17	CNS03C31
18	11.3	652	14	BQ751274
18	11.3	654	12	BG308188
18	11.3	668	14	BQ751485

ALIGNMENTS

AL698654 547 bp mRNA linear EST 21-MAR-2002
DKFZp686N12109.t1:686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686N12109.5, mRNA sequence.

AL698654
EST:
AL698654.1 ct:19619194

human.

Homo Sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wicmann

EST (Duesterhoeft, et al.)

Unpublished (1999)

Contact: Duesterhoeft A

MIPS

Am Klopsterspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by Qiaugen (Hilden/Germany) within the cDNA sequencing

consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp686N12109) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers

1. 547
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKF2p686N12109"
 /clone_lib="686 (synonym: hicc3)"
 /tissue_type="human skeletal muscle"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pTR19pEx2; Site: 1; Strain: Site 2; Sfi18;
 cDNA-collection"

BASE COUNT 112 a 154 c 157 g 124 t

ORIGIN

Query Match 48.48; Score 77; DB 9; Length 547
 Best Local Similarity 99.28; Pred. No. 4.5e+28;
 Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 AGCTCTGGCGCTCCCTCCAGGCTCCGAGGCACAGCTGAGTGTGCTGAGTGAAGA 91

DB 253 AGCTCTGGCGCTCCCTCCAGGCTCCGAGGCACAGCTGAGTGTGCTGAGTGAAGA 312

QY 92 ACATGGCATGTGGCTTCAGCTCAGCTGAGTGTGCTGAGTGAAGAAGCTCACTTTCAGAGAA 151

DB 313 ACATGGCATGTGGCTTCAGCTCAGCTGAGTGTGCTGAGTGAAGAAGCTCACTTTCAGAGAA 372

QY 152 GACAAACA 159

DB 473 GACAAACA 380

RESULT 2

AU135588

LOCUS

DEFINITION AU135588 PLACE1 Homo sapiens cDNA clone PLACE100497 5' mRNA

SEQUENCE

VERSION AU135588.1 GI:10996127

KEYWORDS EST

SOURCE human

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 (bases 1 to 736)
 Authors: Ohta, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawata, Y.,
 Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nakamura, S., and
 Isojima, T.

TITLE

JOURNAL

COMMENT

hri human cDNA project
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5' and 3' end zone pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

Location/Qualifiers

1. 736
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="PLACE100247"
 /clone_lib="PLACE1"
 /tissue_type="placenta"
 /note="Vector: pME18SFL4"

BASE COUNT 163 a 199 c 199 g 170 t

ORIGIN

Query Match 32.18; Score 51; DB 9; Length 736

Best Local Similarity 100.0%; Pred. No. 5.1e+15;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 CAGCTGAGGTGCTGCTGCTGGAAGACCTCAGCTTTCAGAGAGACAAACA 159

DB 329 CAGCTGAGGTGCTGCTGCTGGAAGACCTCAGCTTTCAGAGAGACAAACA 375

RESULT 3

BG384217

LOCUS

DEFINITION BG384217 535 bp mRNA linear EST 12 MAR-2001

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;

REFERENCE

AUTHORS

1 (bases 1 to 535)
 Fabrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, I.P.L., Casas, E.,
 Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.,
 and Keeler, J.W.

TITLE

JOURNAL

COMMENT

Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine
 Contact: Smith, I.P.L.
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68913-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@meat.mars.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.c. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.

PCR PRIMERS

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCGAGTCACGAG

Plate: 90 row: 3 column: 13

Seq primer: ATTAGCTGACACTATAG.

FEATURES

source

1. 535
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC lp1c"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /vector="vector: pCMV SPOR6"
 Library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryos.

BASE COUNT 122 a 155 c 136 g 119 t

ORIGIN

Query Match 24.54; Score 39; DB 12; Length 535;

Best Local Similarity 100.0%; Pred. No. 4.9e+09;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 CTGCTGTGGAAGACCTCAGCTTTCAGAGAGACAAACA 159

DB 311 CTGCTGTGGAAGACCTCAGCTTTCAGAGAGACAAACA 349

RESULT 4

Z44377

LOCUS

DEFINITION HSC12B081 normalized infant brain cDNA Homo sapiens cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

244377
 HSC12B081 normalized infant brain cDNA Homo sapiens cDNA clone
 C-12B08, mRNA sequence.
 244377
 244377.1 GI:574506
 EST
 Human
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Small: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

BASE COUNT 48 a 39 c 49 g 80 t

ORIGIN

Query Match 11.9%; Score 19; DB 12; Length 454
Best Local Similarity 100.0%; Pred. No. 41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 TTTCAGAGAGACAAACA 159

DB 160 TTTCAGAGAGACAAACA 142

RESULT 7

AQ369174

LOCUS

DEFINITION HS_5032_A2_F04_SP6E RPC111 Human Male BAC Library Homo sapiens

ACCESSION AQ369174

VERSION AQ369174.1

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;

1 (bases 1 to 454)

MAHAIKAS,G.G., WALLACE,J.C., SMITH,K., SWARTZELL,S., HOLZMAN,T.,

KELLER,A., SHAKER,R., FURLONG,J., YOUNG,J., ZHAO,S., ADAMS,M.D., and

BLAD,L.

Sequence-tagged connectors: A sequence approach to mapping and

sequencing the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (12), 9709-9713 (1999)

99080-89

CONTACT: MahaiKas GG, Wallace JC, Broad L

High Throughput Sequencing Center

University of Washington

491 Queen Anne Avenue North, Seattle, WA 98199, USA

TEL: (206) 616-3618

FAX: (206) 616-3887

Email: jwallace@u.washington.edu

Clones may be purchased from Kestrel Genetics (Kestrel@KGC.com).

BAC end Web Server: http://www.hi-st.washington.edu

Plate: 608 row: K column: 9

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 454.

Location/Qualifiers

1..454

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Plate-608 Col-8 Row-K"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBAC3.6; Kestell Human Male BAC Library"

BASE COUNT 144 a 82 c 90 g 136 t

ORIGIN

Query Match 11.9%; Score 19; DB 17; Length 454

Best Local Similarity 100.0%; Pred. No. 51;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 CAGCTGCGGCTGCTGGCT 85

DB 286 CAGCTGCGGCTGCTGGCT 303

A1354952/c

LOCUS

DEFINITION zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio

ACCESSION A1353952

VERSION A1353952.1

KEYWORDS EST.

SOURCE zebrafish.

ORGANISM Danio rerio

Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

; Cyprinidae; Danio.

1 (bases 1 to 470)

Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and Liew

C.C.

Identification and Characterization of Expressed Sequence Tags from

an Embryonic Zebrafish Heart cDNA Library

Unpublished (1999)

Contact: Drew CC

Brigham and Women's Hospital

Harvard Medical School

75 Francis St. Boston, MA 02115, USA

Tel: 6177328915

Fax: 6179750945

Email: clemetrics.bwh.harvard.edu

PCR Primers

FORWARD: 5' GCGAAGTCGAAATTAACCTTCACATAAGGG 3'

BACKWARD: 5' GCACTGAAATGTAATACGACCTACCTATAGGCG 3'

Seq primer: 5' GAAATTAACCTTCATAAGGG 3'

Location/Qualifiers

1..470

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone_lib="Zebrafish Embryonic Heart cDNA library"

/clone_stage="embryonic day 3 post-fertilization"

/lab_host="E-coli XL1-blue mF"

/note="organ: heart; Vector: lambda ZAP Express; Site:1:

ECORI; Site:2: XhoI; mRNA was purified from embryonic

zebrafish hearts (3 day post-fertilization). cDNA was

synthesized using a XhoI-Oligo dT adaptor-primer. EORI

adaptors were ligated, followed by digestion with XhoI,

for directional cloning into pre-digested lambda ZAP

Express vector."

BASE COUNT 123 a 112 c 130 g 105 t

ORIGIN

Query Match 11.9%; Score 19; DB 9; Length 470;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 TGGCTCAGCTGAGGTTGG 121

DB 395 TGGCTCAGCTGAGGTTGG 377

RESULT 9

AQ709464/c

LOCUS

DEFINITION HS_5459_A2_F04_17A RPC1-11 Human Male BAC Library Homo sapiens

ACCESSION AQ709464

VERSION AQ709464.1

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 493)

MAHAIKAS,G.G., WALLACE,J.C., SMITH,K., SWARTZELL,S., HOLZMAN,T.,

KELLER,A., SHAKER,R., FURLONG,J., YOUNG,J., ZHAO,S., ADAMS,M.D. and

BLAD,L.

Sequence-tagged connectors: A sequence approach to mapping and

sequencing the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (12), 9709-9713 (1999)

99080-89

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

A1353952 470 bp mRNA linear EST 04-JAN-1999
zeh1204.seq.f Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5' mRNA sequence.

JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
79380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human HAC library (F01-11). For BAC
library availability, please contact Peter de Jong
(peter@redjond.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/bacpac.htm>)
or from Research Genetics (<http://www.resgen.com>) BAC and Web Server:
<http://www.htsc.washington.edu>
Plate: 1035 Row: K Column: B
Seq primer: T7
Class: HAC ends
High quality sequence stop: 493.
Location/Qualifiers
1..493
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/db_xref="taxon:9606"
/clone_lib="RPCT-11 Human Male HAC library"
/sex="male"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites."
171 a 94 c 69 g 152 t 7 others
BASE COUNT
ORIGIN

Query Match 11.9%; Score 19; Length 157
Best local Similarity 100.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AV954274
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AV954274 546 bp mRNA linear EST 14-MAR-2002
AV954274 Nori Satoh unpublished cDNA library; cleavage stage embryo
Clona intestinalis cDNA clone cl12109.57, mRNA sequence.
AV954274
EST
Clona intestinalis.
Eukaryota; Metazoa; Chordata; Branchiata; Ascidiacea; Enterogona;
Platybranchia; Clonidae; Clona.
1 (bases 1 to 546)
Satoh, N., Satou, Y., Kohara, Y. and Shimizu
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohe@scid.ian.zoo1.kyoto-u.ac.jp
Location/Qualifiers
1..546
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="cl102109"
/clone_lib="Nori Satoh unpublished cDNA library, cleavage
stage embryo"

AV954274
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AV954274 546 bp mRNA linear EST 06-MAY-2002
AV954274 zebrafish fin day1 regeneration Danio rerio cDNA clone
5908564 5' similar to SW-UCR2_BOVIN P23004 UB1QUINOL-CYCLOHOME C
REDUCTASE COMPLEX CORE PROTEIN 2 PRECURSOR ;, mRNA sequence.
B0259614
B0259614 1 GI:20460387
EST
zebrafish.
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 568)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, J., Underwood
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shan, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1870
Email: zbrfish@wustl.edu
cDNA Library Preparation: Raymond Lee, cDNA Library Arrayed by:
Matthew Clark, DNA Sequencing by: Washington University Genome
Sequencing Center clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
kessouren@zenitumprimatdatenbank.berlin.germany (web address:
www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to:
gil2224979|gb|AA45487|AA45487 fa09h12.r1 zebrafish ICRFzfls Danio
rerio cDNA
Seq primer: T3 Et from Amersham
High quality sequence stop: 411.
Location/Qualifiers
1..568
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/db_xref="taxon:7955"
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/sex="mixed male and female"
/tissue_type="1 day fin regenerates"
/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XbaI; 1st
strand cDNA primed with (CA)10ACTAGTCTCGAG(T)18, followed
by second strand synthesis, and ligated to 5' adapter (5'
) atttcgacacgaag 3', 3'-gccgctc-5'. cDNA was cloned
directionally (EcoRI/XbaI) into Stratagene Zap express
lambda phage arms. Mass in vivo excision done to obtain
inserts in pBK-CMV phagemid."

AV954274
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AV954274 546 bp mRNA linear EST 14-MAR-2002
AV954274 Nori Satoh unpublished cDNA library; cleavage stage embryo
Clona intestinalis cDNA clone cl12109.57, mRNA sequence.
AV954274
EST
Clona intestinalis.
Eukaryota; Metazoa; Chordata; Branchiata; Ascidiacea; Enterogona;
Platybranchia; Clonidae; Clona.
1 (bases 1 to 546)
Satoh, N., Satou, Y., Kohara, Y. and Shimizu
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohe@scid.ian.zoo1.kyoto-u.ac.jp
Location/Qualifiers
1..546
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="cl102109"
/clone_lib="Nori Satoh unpublished cDNA library, cleavage
stage embryo"

AV954274
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AV954274 546 bp mRNA linear EST 06-MAY-2002
AV954274 zebrafish fin day1 regeneration Danio rerio cDNA clone
5908564 5' similar to SW-UCR2_BOVIN P23004 UB1QUINOL-CYCLOHOME C
REDUCTASE COMPLEX CORE PROTEIN 2 PRECURSOR ;, mRNA sequence.
B0259614
B0259614 1 GI:20460387
EST
zebrafish.
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 568)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, J., Underwood
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shan, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1870
Email: zbrfish@wustl.edu
cDNA Library Preparation: Raymond Lee, cDNA Library Arrayed by:
Matthew Clark, DNA Sequencing by: Washington University Genome
Sequencing Center clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
kessouren@zenitumprimatdatenbank.berlin.germany (web address:
www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to:
gil2224979|gb|AA45487|AA45487 fa09h12.r1 zebrafish ICRFzfls Danio
rerio cDNA
Seq primer: T3 Et from Amersham
High quality sequence stop: 411.
Location/Qualifiers
1..568
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="5908564"
/clone_lib="zebrafish (fin day1) regeneration"
/sex="mixed male and female"
/tissue_type="1 day fin regenerates"
/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XbaI; 1st
strand cDNA primed with (CA)10ACTAGTCTCGAG(T)18, followed
by second strand synthesis, and ligated to 5' adapter (5'
) atttcgacacgaag 3', 3'-gccgctc-5'. cDNA was cloned
directionally (EcoRI/XbaI) into Stratagene Zap express
lambda phage arms. Mass in vivo excision done to obtain
inserts in pBK-CMV phagemid."

/tissue_type="whole animal"
/dev_stage="cleavage stage embryo"
/note="Vector: pBluescript SK"

BASE COUNT 160 a 117 c 86 g 183 t
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Query Match 11.9%; Score 19; Length 546;
Best local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 CCCTACTTTTGAAGAAGA 153
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DB 145 CCCTACTTTTGAAGAAGA 163

RESULT 11
B0259614/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

B0259614 568 bp mRNA linear EST 06-MAY-2002
B0259614 zebrafish fin day1 regeneration Danio rerio cDNA clone
5908564 5' similar to SW-UCR2_BOVIN P23004 UB1QUINOL-CYCLOHOME C
REDUCTASE COMPLEX CORE PROTEIN 2 PRECURSOR ;, mRNA sequence.
B0259614
B0259614 1 GI:20460387
EST
zebrafish.
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 568)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, J., Underwood
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shan, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1870
Email: zbrfish@wustl.edu
cDNA Library Preparation: Raymond Lee, cDNA Library Arrayed by:
Matthew Clark, DNA Sequencing by: Washington University Genome
Sequencing Center clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
kessouren@zenitumprimatdatenbank.berlin.germany (web address:
www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to:
gil2224979|gb|AA45487|AA45487 fa09h12.r1 zebrafish ICRFzfls Danio
rerio cDNA
Seq primer: T3 Et from Amersham
High quality sequence stop: 411.
Location/Qualifiers
1..568
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="5908564"
/clone_lib="zebrafish (fin day1) regeneration"
/sex="mixed male and female"
/tissue_type="1 day fin regenerates"
/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XbaI; 1st
strand cDNA primed with (CA)10ACTAGTCTCGAG(T)18, followed
by second strand synthesis, and ligated to 5' adapter (5'
) atttcgacacgaag 3', 3'-gccgctc-5'. cDNA was cloned
directionally (EcoRI/XbaI) into Stratagene Zap express
lambda phage arms. Mass in vivo excision done to obtain
inserts in pBK-CMV phagemid."

FEATURES
source

Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters of single clones were sequenced additional times to assess quality control."

BASE COUNT 164 a 158 c 170 g 159 t 1 others

Query Match 11.9% Score 19; DB 9; Length 644
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 TGGCTCAGCTGAGGTGC 121

DB 395 TGGCTCAGCTGAGGTGC 377

RESULT 14

AV997283/c

LOCUS

DEFINITION

AV997283

AV997283

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AV997283

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AV997283

STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,000
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US 08-713-050-9

Query Match 11.9% Score 19; DB 2; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 70 GCTGGGCTGCTGGCTGAG 88
|||||
DB 261 GCTGGGCTGCTGGCTGAG 279

RESULT 3
US-08-975-316-9
Sequence 9, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4125
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/100001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-9

Query Match 11.9% Score 19; DB 2; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 70 GCTGGGCTGCTGGCTGAG 88
|||||
DB 261 GCTGGGCTGCTGGCTGAG 279

RESULT 4
US-09-211-710-9
Sequence 9, Application US/09211710A
Patent No. 6204434
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N.
APPLICANT: HAVUKKALA, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.100003
CURRENT APPLICATION NUMBER: US/09/211,710A
CURRENT FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 624
TYPE: DNA
ORGANISM: Pinus radiata
US-09-211-710-9

Query Match 11.9% Score 19; DB 4; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 70 GCTGGGCTGCTGGCTGAG 88
|||||
DB 261 GCTGGGCTGCTGGCTGAG 279

RESULT 5
US-09-615-192A-9
Sequence 9, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N.
APPLICANT: HAVUKKALA, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1000040
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 624
TYPE: DNA
ORGANISM: Pinus radiata
US 09-615,192A-9

Query Match 11.9% Score 19; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGCGCTGCTGGCTGAG 88
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Db 261 GCTGGCGCTGCTGGCTGAG 279

RESULT 6
US-09 975 316-45
Sequence 45, Application US/08/975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT GROWTH IN NUTRIT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
FILING DATE:
CLASSIFICATION: 800
PARENT APPLICATION DATA:
APPLICATION NUMBER: 08/714,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 110067/100301
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09 975 316-45
Query Match 11.9% Score 19; DB 2; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGCGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGCGCTGCTGGCTGAG 279

RESULT 7
US-09 615 192A-45
Sequence 45, Application US/09/615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: BLOKBERG, Leonard N.
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
TITLE OF INVENTION: MATERIALS AND METHODS FOR PLANT GROWTH IN NUTRIT
FILE REFERENCE: 11000.1003040

Query Match 11.9% Score 19; DB 2; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGCGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGCGCTGCTGGCTGAG 279

RESULT 8
US-09 519-777-63/c
Sequence 63, Application US/08/519777
Patent No. 5739307
GENERAL INFORMATION:
APPLICANT: JOHNSON, JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: TAMPE, PATRICIA A.
TITLE OF INVENTION: NEUTROTIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
STREET: 7733 PARSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,777
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BELLAND, DONALD R.
REGISTRATION NUMBER: 65,197
REFERENCE/DOCKET NUMBER: 953095
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6392
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MEDIUM TYPE: floppy disk
US-09 519-777-63/c

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Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 11.9% Score 19; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGCGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGCGCTGCTGGCTGAG 279

RESULT 8
US-09 519-777-63/c
Sequence 63, Application US/08/519777
Patent No. 5739307
GENERAL INFORMATION:
APPLICANT: JOHNSON, JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: TAMPE, PATRICIA A.
TITLE OF INVENTION: NEUTROTIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
STREET: 7733 PARSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,777
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BELLAND, DONALD R.
REGISTRATION NUMBER: 65,197
REFERENCE/DOCKET NUMBER: 953095
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6392
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MEDIUM TYPE: floppy disk
US-09 519-777-63/c

Query Match 11.9% Score 19; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGCGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGCGCTGCTGGCTGAG 279

RESULT 7
US-09 615 192A-45
Sequence 45, Application US/09/615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: BLOKBERG, Leonard N.
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
TITLE OF INVENTION: MATERIALS AND METHODS FOR PLANT GROWTH IN NUTRIT
FILE REFERENCE: 11000.1003040

Query Match 11.9% Score 19; DB 2; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGCGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGCGCTGCTGGCTGAG 279

RESULT 8
US-09 519-777-63/c
Sequence 63, Application US/08/519777
Patent No. 5739307
GENERAL INFORMATION:
APPLICANT: JOHNSON, JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: TAMPE, PATRICIA A.
TITLE OF INVENTION: NEUTROTIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
STREET: 7733 PARSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,777
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BELLAND, DONALD R.
REGISTRATION NUMBER: 65,197
REFERENCE/DOCKET NUMBER: 953095
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6392
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MEDIUM TYPE: floppy disk
US-09 519-777-63/c

Query Match 11.9% Score 19; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 953095
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-775-414-63

Query Match 10.18; Score 16; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GCGCGCTGCTTCAG 53
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 DB 36 GCGCGCTGCTTCAG 21

RESULT 12
 US-08-775-414-63/c
 Sequence 63, Application US/08775414
 Patent No. 6090779
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 90
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/775,414
 FILING DATE: 31-DEC-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 955805
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-775-414-63

Query Match 10.18; Score 16; DB 3; Length 39;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GCGCGCTGCTTCAG 53
 ||||| ||||| ||||| |||||
 DB 36 GCGCGCTGCTTCAG 21

US-08-775-414-63
 Sequence 63, Application US/08775414
 Patent No. 6090779
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US

Query Match 10.18; Score 16; DB 3; Length 39;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GCGCGCTGCTTCAG 53
 ||||| ||||| ||||| |||||
 DB 36 GCGCGCTGCTTCAG 21

RESULT 13
 US-08-931-858E-63/c
 Sequence 63, Application US/08931858E
 Patent No. 6220222
 GENERAL INFORMATION:
 APPLICANT: JOHNSON, EUGENE M.
 APPLICANT: MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUVAGE, FRED
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-63

Query Match 10.18; Score 16; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GCGCGCTGCTTCAG 53
 ||||| ||||| ||||| |||||
 DB 36 GCGCGCTGCTTCAG 21

US-08-931-858E-63
 Sequence 63, Application US/08931858E
 Patent No. 6220222
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US

Query Match 10.18; Score 16; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GCGCGCTGCTTCAG 53
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 DB 36 GCGCGCTGCTTCAG 21

RESULT 14
 US-08-981-739-63/c
 Sequence 63, Application US/08981739
 Patent No. 6232449
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US

Query Match 10.18; Score 16; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GCGCGCTGCTTCAG 53
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 DB 36 GCGCGCTGCTTCAG 21

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1  ZIP: 63105-1817
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  SOFTWARE: Patent Release #1.0, Version #1.0
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/08/981,739
9  FILING DATE: 31-Aug-1998
10 CLASSIFICATION: <Unknown>
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: PCT/US97/03441
13 FILING DATE: <Unknown>
14 ATTORNEY/AGENT INFORMATION:
15 NAME: HOLLAND, DONALD R.
16 REGISTRATION NUMBER: 35,197
17 REFERENCE/DOCKET NUMBER: 976164
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (314) 727-5188
20 TELEFAX: (314) 727-6092
21
22 INFORMATION FOR SEQ ID NO: 63:
23     SEQUENCE CHARACTERISTICS:
24         LENGTH: 39 base pairs
25         TYPE: nucleic acid
26         STRANDEDNESS: single
27         TOPOLOGY: linear
28     MOLECULE TYPE: cDNA
29     SEQUENCE DESCRIPTION: SEQ ID NO: 63:
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Query Match      10.1%; Score 16; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy  36 GCGCCGTCAGTTCAG 53
Db  36 GCGCCGTCAGTTCAG 21

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Result 1:
US 09-128-026-64
Sequence 63, Application US/09128025
Patent No. 640335
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANT, JEFFREY D.
APPLICANT: KOCZKAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED DEWET ACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSER: HOWELL & HAFERKAMP, L.L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 64195-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,026
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976164
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092

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1  INFORMATION FOR SEQ ID NO: 63:
2  SEQUENCE CHARACTERISTICS:
3  LENGTH: 39 base pairs
4  TYPE: nucleic acid
5  STRANDEDNESS: single
6  TOPOLOGY: linear
7  MOLECULE TYPE: cDNA
8  US 09-128-026-64
9
10 Query Match      10.1%; Score 16; DB 4; Length 39;
11 Best Local Similarity 100.0%; Pred. No. 22;
12 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
13
14 Qy  36 GCGCCGTCAGTTCAG 53
15 Db  36 GCGCCGTCAGTTCAG 21
16
17 Search completed: May 10, 2003, 03:18:23
18 Job time : 48 secs

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Computer, Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 02:15:59 : Search time 124 Sec on
(without alignment)
1593485 Million cell updates/sec

Title: US-09-846-456-5

Perfect score: 159

Sequence: 1 ttaatgaccagcagcagggcgc.....ctttccagaaagagatata 159

Scoring table: G1G0_NUC

Gapop 60.0 , Gapext 60.0

Seatched: 783854 seqs, 521352466 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1593776

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA :
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB_SEQ :
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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB_SEQ :
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB_SEQ :
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB_SEQ :
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB_SEQ :

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	159	100.0	357	9	US-09-984-827-4
3	159	100.0	357	10	US-09-846-456-2
4	143	89.9	158	9	US-09-984-827-25
5	108	67.9	159	9	US-09-984-827-26
6	60	37.7	1062	9	US-09-924-340-101
7	60	37.7	1062	9	US-09-992-600A-101
8	60	37.7	9741	9	US-09-984-827-1
9	60	37.7	9741	10	US-09-846-456-10
10	60	37.7	9870	9	US-09-984-827-92
11	60	37.7	9870	9	US-09-984-827-93
12	60	37.7	9870	9	US-09-984-827-94
13	60	37.7	9870	9	US-09-984-827-95
14	60	37.7	9870	9	US-09-984-827-96
15	60	37.7	9870	9	US-09-984-827-97
16	60	37.7	9870	9	US-09-984-827-98
17	60	37.7	9870	9	US-09-984-827-99
18	60	37.7	9870	9	US-09-984-827-100
19	60	37.7	9870	9	US-09-984-827-101

20	60	37.7	9870	9	US-09-984-827-102
21	60	37.7	9870	9	US-09-984-827-103
22	60	37.7	9870	9	US-09-984-827-104
23	60	37.7	9870	9	US-09-984-827-105
24	60	37.7	9870	9	US-09-984-827-106
25	60	37.7	9870	9	US-09-984-827-107
26	60	37.7	9870	9	US-09-984-827-108
27	60	37.7	9870	9	US-09-984-827-109
28	60	37.7	9870	9	US-09-984-827-110
29	60	37.7	9870	9	US-09-984-827-111
30	60	37.7	9870	9	US-09-984-827-112
31	60	37.7	9870	9	US-09-984-827-113
32	60	37.7	9870	9	US-09-984-827-114
33	60	37.7	9870	9	US-09-984-827-115
34	60	37.7	9870	9	US-09-984-827-116
35	60	37.7	9870	9	US-09-984-827-117
36	60	37.7	9870	9	US-09-984-827-118
37	60	37.7	9870	9	US-09-984-827-119
38	60	37.7	9870	9	US-09-984-827-120
39	60	37.7	9870	9	US-09-984-827-121
40	60	37.7	9870	9	US-09-984-827-122
41	60	37.7	9870	9	US-09-984-827-123
42	60	37.7	9870	9	US-09-984-827-124
43	60	37.7	9870	9	US-09-984-827-125
44	60	37.7	9870	9	US-09-984-827-126
45	20	12.6	474	9	US-09-918-995-19151

ALIGNMENTS

RESULT 1
US-09-846-456-5
: Sequence 5, Application US/09846456
: Patent No. US20020146792A1
: GENERAL INFORMATION:
: APPLICANT: Rosier, Marie
: APPLICANT: Prades, Catherine
: APPLICANT: Lemoine, Cendrine
: APPLICANT: Naudin, Laurent
: APPLICANT: Deneffe, Patrice
: APPLICANT: Duverget, Nicolas
: APPLICANT: Brewer, Bryan
: APPLICANT: Remaley, Allan
: APPLICANT: Fojo, Silvia
: TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modif
: FILE OF INVENTION: Activity and Therapeutic Uses
: FILE REFERENCE: 3806.0505
: CURRENT FILING DATE: 2001-05-02
: PRIOR APPLICATION NUMBER: US/09/846.456
: PRIOR FILING DATE: 2000-05-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 5
: LENGTH: 159
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-846-456-5

Query Match	100.0%	Score 159;	DB 10;	Length 159;
Best Local Similarity	100.0%	Pred. No. 8.le-79;		
Matches 159;	Conservative	0;	Mismatches 0;	Indels 0;
0;	Gaps	0;		
QY	1	TTAATGACGAGCAGCGGGCGTCCCTGCTGTACAGTCTGTGCGCGCTGCTTCCAGGCGTCCC	60	
DB	1	TTAATGACGAGCAGCGGGCGTCCCTGCTGTACAGTCTGTGCGCGCTGCTTCCAGGCGTCCC	60	
QY	61	GAGCCACAGCTGGGGGTGTGGCTGAGGGAACATGGCATGTGGCGCTCAGCTGAGGTG	120	
DB	61	GAGCCACAGCTGGGGGTGTGGCTGAGGGAACATGGCATGTGGCGCTCAGCTGAGGTG	120	
QY	121	CTGCTGTGAGGAAGCTCAGCTTTCAGAGAGACAAACA	159	

Db 121 CTGCTGTGGAGAACCTCCTCTTCAGAGAGAACAAACA 159
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RESULT 2

US-09-984-827-4

: Sequence 4, Application US/09984827

: Publication No. US20030056234A1

: GENERAL INFORMATION:

: APPLICANT: DENEFFLE, PATRICE

: APPLICANT: ROSIER-MONTIUS, MARIE-FRANCOISE

: APPLICANT: ARNOULD-REGUIGNE, ISABELLE

: APPLICANT: DUVERGER, NICOLAS

: APPLICANT: CAMBIEN, FRANCOIS

: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ARAA1 GENE, THEIR USES, AND

: FILE REFERENCE: 03806.0522-00000

: CURRENT APPLICATION NUMBER: US/09/984,827

: PRIOR FILING DATE: 2002-04-01

: PRIOR APPLICATION NUMBER: 60/254,108

: PRIOR FILING DATE: 2000-12-11

: PRIOR APPLICATION NUMBER: FR 00/14037

: NUMBER OF SEQ ID NOS: 161

: SOFTWARE: Patent In Ver. 2.1

: SEQ ID NO 4

: LENGTH: 357

: TYPE: DNA

: ORGANISM: Homo sapiens

: US-09-984-827-4

Query Match 100.0% Score 159; DB 9; Length 357;

Best Local Similarity 100.0%; Pred. No. 7.9e-79;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 100 TTAATGACACAGCCAGCGGCTGCTGTCAGCTGCGCTGAGGAGATGTTTCAAGGCTGCTG 159

QY 61 GAGCCACACAGCTGGCGCTGCTGCTGAGGAGATGTTTCAAGGCTGCTG 120

DB 169 GAGCCACACAGCTGGCGCTGCTGCTGAGGAGATGTTTCAAGGCTGCTG 219

QY 121 TGTCTGTGGAAGAACCTCCTCTTCAGAGAGAACAAACA 159

DB 220 TGTCTGTGGAAGAACCTCCTCTTCAGAGAGAACAAACA 258

RESULT 3

US-09-846-456-2

: Sequence 4, Application US/09846456

: Patent No. US20020146792A1

: GENERAL INFORMATION:

: APPLICANT: Rosier, Marie

: APPLICANT: Prades, Catherine

: APPLICANT: Lemoine, Cendrine

: APPLICANT: Naudin, Laurent

: APPLICANT: Deneffle, Patrice

: APPLICANT: Duverger, Nicolas

: APPLICANT: Brewer, Bryan

: APPLICANT: Remaley, Alan

: APPLICANT: Foto, Silvia

: TITLE OF INVENTION: Regulatory Nucleic Acid for the ARA1 Gene, Molecules Modifying its

: FILE REFERENCE: 3806.0505

: CURRENT APPLICATION NUMBER: US/09/846,456

: CURRENT FILING DATE: 2001-05-02

: PRIOR APPLICATION NUMBER: US 60/261,289

: PRIOR FILING DATE: 2000-05-02

: NUMBER OF SEQ ID NOS: 20

: SOFTWARE: Patent In version 3.0

: SEQ ID NO 2

: LENGTH: 357

: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-846-456-2

Query Match

100.0% Score 159; DB 10; Length 357;

Best Local Similarity 100.0%; Pred. No. 7.9e-79;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAATGACACAGCCAGCGGCTGCTGTCAGCTGCGCTGAGGAGATGTTTCAAGGCTGCTG 60

DB 100 TTAATGACACAGCCAGCGGCTGCTGTCAGCTGCGCTGAGGAGATGTTTCAAGGCTGCTG 159

QY 61 GAGCCACACAGCTGGCGCTGCTGCTGAGGAGATGTTTCAAGGCTGCTG 120

DB 160 GAGCCACACAGCTGGCGCTGCTGCTGAGGAGATGTTTCAAGGCTGCTG 219

QY 121 CTGCTGTGGAAGAACCTCCTCTTCAGAGAGAACAAACA 159

DB 220 CTGCTGTGGAAGAACCTCCTCTTCAGAGAGAACAAACA 258

RESULT 4

US-09-984-827-25

: Sequence 25, Application US/09984827

: Publication No. US20030056234A1

: GENERAL INFORMATION:

: APPLICANT: DENEFFLE, PATRICE

: APPLICANT: ROSIER-MONTIUS, MARIE-FRANCOISE

: APPLICANT: ARNOULD-REGUIGNE, ISABELLE

: APPLICANT: DUVERGER, NICOLAS

: APPLICANT: CAMBIEN, FRANCOIS

: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ARAA1 GENE, THEIR USES,

: FILE REFERENCE: 03806.0522-00000

: CURRENT APPLICATION NUMBER: US/09/984,827

: PRIOR FILING DATE: 2002-04-01

: PRIOR APPLICATION NUMBER: 60/254,108

: PRIOR FILING DATE: 2000-12-11

: PRIOR APPLICATION NUMBER: FR 00/14037

: PRIOR FILING DATE: 2000-10-31

: NUMBER OF SEQ ID NOS: 161

: SOFTWARE: Patent In Ver. 2.1

: SEQ ID NO 25

: LENGTH: 158

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-984-827-25

Query Match

89.9% Score 143; DB 9; Length 158;

Best Local Similarity 100.0%; Pred. No. 6.5e-70;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GGCGTCCCTGCTGTCAGCTGTCAGGCTGCGCTGCTTCCAGGGCTCCCGAGCCACACGCTGGGC 76

DB 16 GGCGTCCCTGCTGTCAGCTGTCAGGCTGCGCTGCTTCCAGGGCTCCCGAGCCACACGCTGGGC 75

QY 77 GCTCTGCTGAGGAGACATGGATGTTGCGCTCAGCTGAGGTTGCTGTGGAGAGACC 136

DB 76 GCTCTGCTGAGGAGACATGGATGTTGCGCTCAGCTGAGGTTGCTGTGGAGAGACC 135

QY 137 TCACCTTCAGACAGACAAACA 159

DB 136 TCACCTTCAGACAGACAAACA 158

RESULT 5

US-09-984-827-26

: Sequence 26, Application US/09984827

: Publication No. US20030056234A1

: GENERAL INFORMATION:

: APPLICANT: DENEFFLE, PATRICE

: APPLICANT: ROSIER-MONTIUS, MARIE-FRANCOISE

: APPLICANT: ARNOULD-REGUIGNE, ISABELLE


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Matches 60: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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Db 320 TGTGGGCTCAGCTGAGTTGCTGCTGTGGAGAACCTCATTTCAGAAAGAAACAAACA 379

RESULT 12
US-09-984-827-94
? Sequence 94, Application US/09984827
? Publication No. US20030056234A1
? GENERAL INFORMATION:
? APPLICANT: DENEFELE, PATRICE
? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
? APPLICANT: ARNOULD-REGUIGNE, ISABELLE
? APPLICANT: DUVERGER, NICOLAS
? APPLICANT: CAMBIEN, FRANCOIS
? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
? FILE REFERENCE: 03806.0522-00000
? CURRENT APPLICATION NUMBER: US/09/984.827
? PRIOR FILING DATE: 2002-04-01
? PRIOR APPLICATION NUMBER: 60/254,108
? PRIOR FILING DATE: 2000-12-11
? PRIOR APPLICATION NUMBER: FR 00/14037
? NUMBER OF SEQ ID NOS: 161
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 94
? LENGTH: 9870
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: modified_base
? LOCATION: (7138)
? OTHER INFORMATION: a, t, c or g
US-09-984-827-94

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Best Local Similarity 100.0% Pred. No. 9e-24:
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Db 320 TGTGGGCTCAGCTGAGTTGCTGCTGTGGAGAACCTCATTTCAGAAAGAAACAAACA 379

RESULT 13
US-09-984-827-95
? Sequence 95, Application US/09984827
? Publication No. US20030056234A1
? GENERAL INFORMATION:
? APPLICANT: DENEFELE, PATRICE
? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
? APPLICANT: ARNOULD-REGUIGNE, ISABELLE
? APPLICANT: DUVERGER, NICOLAS
? APPLICANT: CAMBIEN, FRANCOIS
? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
? FILE REFERENCE: 03806.0522-00000
? CURRENT APPLICATION NUMBER: US/09/984.827
? PRIOR FILING DATE: 2002-04-01
? PRIOR APPLICATION NUMBER: 60/254,108
? PRIOR FILING DATE: 2000-12-11
? PRIOR APPLICATION NUMBER: FR 00/14037
? NUMBER OF SEQ ID NOS: 161
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 95
? LENGTH: 9870
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
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? NAME/KEY: modified_base
? LOCATION: (7138)
? OTHER INFORMATION: a, t, c or g
US-09-984-827-95

Query Match 37.7% Score 60: DB 9: Length 9870:
Best Local Similarity 100.0% Pred. No. 9e-24:
Matches 60: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 100 TGTGGGCTCAGCTGAGTTGCTGCTGTGGAGAACCTCATTTCAGAAAGAAACAAACA 159
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RESULT 14
US-09-984-827-96
? Sequence 96, Application US/09984827
? Publication No. US20030056234A1
? GENERAL INFORMATION:
? APPLICANT: DENEFELE, PATRICE
? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
? APPLICANT: ARNOULD-REGUIGNE, ISABELLE
? APPLICANT: DUVERGER, NICOLAS
? APPLICANT: CAMBIEN, FRANCOIS
? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
? FILE REFERENCE: 03806.0522-00000
? CURRENT APPLICATION NUMBER: US/09/984.827
? PRIOR FILING DATE: 2002-04-01
? PRIOR APPLICATION NUMBER: 60/254,108
? PRIOR FILING DATE: 2000-12-11
? PRIOR APPLICATION NUMBER: FR 00/14037
? NUMBER OF SEQ ID NOS: 161
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 96
? LENGTH: 9870
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: modified_base
? LOCATION: (7138)
? OTHER INFORMATION: a, t, c or g
US-09-984-827-96

Query Match 37.7% Score 60: DB 9: Length 9870:
Best Local Similarity 100.0% Pred. No. 9e-24:
Matches 60: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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Db 320 TGTGGGCTCAGCTGAGTTGCTGCTGTGGAGAACCTCATTTCAGAAAGAAACAAACA 379

RESULT 15
US-09-984-827-97
? Sequence 97, Application US/09984827
? Publication No. US20030056234A1
? GENERAL INFORMATION:
? APPLICANT: DENEFELE, PATRICE
? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
? APPLICANT: ARNOULD-REGUIGNE, ISABELLE
? APPLICANT: DUVERGER, NICOLAS
? APPLICANT: CAMBIEN, FRANCOIS
? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
? FILE REFERENCE: 03806.0522-00000
? CURRENT APPLICATION NUMBER: US/09/984.827
? PRIOR FILING DATE: 2002-04-01
? PRIOR APPLICATION NUMBER: 60/254,108
? PRIOR FILING DATE: 2000-12-11
? PRIOR APPLICATION NUMBER: FR 00/14037
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 97
? LENGTH: 9870
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
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1 NUMBER OF SEQ IDS: 161
2 SOFTWARE: PatentIn Ver. 2.1
3 SEQ ID NO: 97
4 LENGTH: 9870
5 TYPE: DNA
6 ORGANISM: Homo sapiens
7 FEATURE:
8 NAME/KEY: modified_base
9 LOCATION: (7148)
10 OTHER INFORMATION: a, t, c or g
US-09-846-456-5

Query Match 37.7% Score 60 DB 97 Length 9870
Best Local Similarity 100.0% Pred. No. 98 24
Matches 60 Conservative 0 Mismatches 0 Indels 0 Gaps 0

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DB 100 GTTGGCTCAGCTGAGGTTGCTGCTGGAGAGACCTTCAGTTCAGTAAAGAGTAAACA 159

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Job time: 140 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 16:36:12 ; Search time 470.364 seconds
(without alignments)
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Title: US-09-846-456-3

Perfect score: 2893

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Scoring table: OLIGO_NUC

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Word size : 30

Total number of hits satisfying chosen parameters: 10484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 49	49	1.7	448	9	US-09-918-995-2616
c 50	49	1.7	866	10	US-09-729-835-11
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c 52	49	1.7	4140	10	US-09-764-877-3620
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c 81	48	1.7	311	10	US-09-764-847-211
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c 92	48	1.7	9566	9	US-10-091-572-834

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c 249	1.6	1395	9	US-09-997-166-35	Sequence 45, Appl	322	45	1.6	10093	10	US-09-764-869-1390	Sequence 1390, Ap
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c 258	1.6	1395	9	US-10-063-518-9	Sequence 45, Appl	331	45	1.6	17397	9	US-10-091-504-1945	Sequence 1945, Ap
c 259	1.6	1395	9	US-10-063-598-9	Sequence 45, Appl	332	45	1.6	17397	10	US-09-764-869-1945	Sequence 1945, Ap
c 260	1.6	1395	9	US-10-227-693-9	Sequence 45, Appl	333	45	1.6	18692	9	US-10-092-154-1682	Sequence 1682, Ap
c 261	1.6	1395	9	US-09-990-443-35	Sequence 45, Appl	334	45	1.6	18692	10	US-09-764-847-1682	Sequence 1682, Ap
c 262	1.6	1395	9	US-09-990-726-35	Sequence 45, Appl	335	45	1.6	19334	9	US-10-091-504-1943	Sequence 1943, Ap
c 263	1.6	1395	9	US-09-997-559-35	Sequence 45, Appl	336	45	1.6	19334	10	US-09-764-869-1943	Sequence 1943, Ap
c 264	1.6	1395	9	US-09-997-601-35	Sequence 45, Appl	337	45	1.6	19345	9	US-10-091-504-1944	Sequence 1944, Ap
c 265	1.6	1395	9	US-09-989-7294-35	Sequence 45, Appl	338	45	1.6	19345	10	US-09-764-869-1944	Sequence 1944, Ap
c 266	1.6	1395	9	US-09-990-440-35	Sequence 45, Appl	339	45	1.6	21727	9	US-09-764-864-1603	Sequence 1603, Ap
c 267	1.6	1395	9	US-09-991-853-35	Sequence 45, Appl	340	45	1.6	21727	10	US-09-764-864-1604	Sequence 1604, Ap
c 268	1.6	1395	9	US-09-997-449-35	Sequence 45, Appl	341	45	1.6	22161	9	US-10-092-154-1020	Sequence 1020, Ap
c 269	1.6	1395	9	US-09-997-449-35	Sequence 45, Appl	342	45	1.6	22161	10	US-09-764-847-1020	Sequence 1020, Ap
c 270	1.6	1395	9	US-09-997-628-35	Sequence 45, Appl	343	45	1.6	22484	9	US-09-875-114-2	Sequence 2, Appl
c 271	1.6	1395	9	US-09-997-683-35	Sequence 45, Appl	344	45	1.6	22484	10	US-09-880-107-3341	Sequence 3341, Ap
c 272	1.6	1395	9	US-09-997-469-35	Sequence 45, Appl	345	45	1.6	24983	9	US-09-863-0494-1	Sequence 1, Appl
c 273	1.6	1395	9	US-09-997-448-35	Sequence 45, Appl	346	45	1.6	24983	10	US-09-764-891-5950	Sequence 5950, Ap
c 274	1.6	1395	9	US-09-997-442-35	Sequence 45, Appl	347	45	1.6	26995	9	US-09-764-891-8475	Sequence 8475, Ap
c 275	1.6	1395	9	US-10-063-562-9	Sequence 45, Appl	348	45	1.6	26995	10	US-10-079-854-227	Sequence 227, App
c 276	1.6	1395	9	US-09-990-427-35	Sequence 45, Appl	349	45	1.6	26995	10	US-09-764-878-227	Sequence 227, App
c 277	1.6	1395	9	US-09-990-439-35	Sequence 45, Appl	350	45	1.6	40175	10	US-09-738-878-3	Sequence 3, Appl
c 278	1.6	1395	9	US-09-989-428-35	Sequence 45, Appl	351	45	1.6	40175	10	US-10-163-381-3	Sequence 3, Appl
c 279	1.6	1395	9	US-09-993-683-35	Sequence 45, Appl	352	45	1.6	40515	9	US-10-092-154-1208	Sequence 1208, Ap
c 280	1.6	1395	9	US-10-063-573-9	Sequence 45, Appl	353	45	1.6	40515	10	US-09-764-847-1208	Sequence 1208, Ap
c 281	1.6	1395	9	US-09-993-992-35	Sequence 45, Appl	354	45	1.6	42176	9	US-10-091-504-1953	Sequence 1953, Ap
c 282	1.6	1395	9	US-09-992-421-35	Sequence 45, Appl	355	45	1.6	42176	10	US-09-764-869-1953	Sequence 1953, Ap
c 283	1.6	1395	9	US-10-063-573-9	Sequence 45, Appl	356	45	1.6	42176	9	US-10-091-504-1954	Sequence 1954, Ap
c 284	1.6	1395	10	US-09-989-428-35	Sequence 45, Appl	357	45	1.6	42178	10	US-09-764-869-1954	Sequence 1954, Ap
c 285	1.6	1395	10	US-09-989-428-35	Sequence 45, Appl	358	45	1.6	42185	10	US-09-764-877-3171	Sequence 3171, Ap
c 286	1.6	1395	10	US-09-989-428-35	Sequence 45, Appl	359	45	1.6	42189	9	US-10-079-854-379	Sequence 379, App
c 287	1.6	1395	10	US-09-989-428-35	Sequence 45, Appl	360	45	1.6	42189	10	US-09-764-878-379	Sequence 379, App
c 288	1.6	1395	10	US-09-989-428-35	Sequence 45, Appl	361	45	1.6	42216	9	US-09-764-891-9613	Sequence 9613, Ap
c 289	1.6	1395	10	US-09-989-428-35	Sequence 45, Appl	362	45	1.6	42221	10	US-10-079-854-377	Sequence 377, App
c 290	1.6	1395	10	US-09-993-074-35	Sequence 45, Appl	363	45	1.6	42221	10	US-09-880-107-3327	Sequence 3327, Ap
c 291	1.6	1395	10	US-09-990-424-35	Sequence 45, Appl	364	45	1.6	43433	10	US-10-282-048-3	Sequence 3, Appl
c 292	1.6	1395	10	US-09-993-114-35	Sequence 45, Appl	365	45	1.6	43763	9	US-10-844-053-32	Sequence 32, Appl
c 293	1.6	1395	10	US-09-993-604-35	Sequence 45, Appl	366	45	1.6	48841	10	US-09-835-081-3	Sequence 3, Appl
c 294	1.6	1395	10	US-09-993-456-35	Sequence 45, Appl	367	45	1.6	57130	10	US-10-237-859-3	Sequence 3, Appl
c 295	1.6	1395	10	US-09-994-727-35	Sequence 45, Appl	368	45	1.6	74677	9	US-10-274-974-3	Sequence 3, Appl
c 296	1.6	1395	12	US-10-095-862-9	Sequence 45, Appl	369	45	1.6	74962	9	US-09-654-883-243	Sequence 243, App
c 297	1.6	1424	9	US-09-729-673-71	Sequence 45, Appl	370	45	1.6	75899	10	US-09-962-436-36	Sequence 36, Appl
c 298	1.6	1539	9	US-10-043-487-144	Sequence 45, Appl	371	45	1.6	84539	10	US-09-880-107-3428	Sequence 428, Ap
c 299	1.6	2648	10	US-09-822-674-243	Sequence 45, Appl	372	45	1.6	99914	10	US-09-563-728A-36	Sequence 36, Appl
c 300	1.6	3011	9	US-10-163-114-630	Sequence 45, Appl	373	45	1.6	122186	9	US-09-910-185-11	Sequence 11, Appl
c 301	1.6	3091	9	US-10-074-095-1001	Sequence 1001, Ap	374	45	1.6	124526	9	US-09-920-671-11	Sequence 11, Appl
c 302	1.6	3091	9	US-10-074-095-1002	Sequence 1002, Ap	375	45	1.6	149257	10	US-09-962-436-281	Sequence 281, App
c 303	1.6	3091	10	US-09-764-860-1001	Sequence 1001, Ap	376	45	1.6	167343	10	US-09-964-824A-213	Sequence 213, App
c 304	1.6	3844	9	US-10-127-124-1	Sequence 1001, Ap	377	45	1.6	167343	10	US-09-835-232-7	Sequence 7, Appl
c 305	1.6	5834	9	US-10-091-572-299	Sequence 45, Appl	378	45	1.6	170034	9	US-10-238-709-3	Sequence 3, Appl
c 306	1.6	5834	9	US-09-764-891-9793	Sequence 9793, Ap	379	45	1.6	224493	10	US-09-804-471A-3	Sequence 3, Appl
c 307	1.6	5834	9	US-10-074-095-1001	Sequence 1001, Ap	380	45	1.6	224493	10	US-09-764-877-2836	Sequence 2836, Ap
c 308	1.6	5834	10	US-09-764-869-1945	Sequence 1945, Ap	381	45	1.6	224493	10	US-09-764-891-9888	Sequence 9888, Ap
c 309	1.6	6191	9	US-10-092-154-1020	Sequence 1020, Ap	382	45	1.6	224493	10	US-09-764-891-9889	Sequence 9889, Ap
c 310	1.6	6191	10	US-09-764-847-1020	Sequence 1020, Ap	383	45	1.6	224493	10	US-09-818-995-28293	Sequence 28293, A
c 311	1.6	6191	10	US-09-764-847-1020	Sequence 1020, Ap	384	45	1.6	224493	10	US-09-818-995-28293	Sequence 28293, A

c 185	44	1.5	487	9	US-09-916-995-21275	Sequence 23275, A	c 458	43	1.5	2650	9	US-09-954-556-28	Sequence 28, Appl
c 186	44	1.5	558	9	US-09-736-457-554	Sequence 554, App	c 459	43	1.5	3613	9	US-10-079-854-416	Sequence 416, App
c 187	44	1.5	558	9	US-09-902-94-554	Sequence 554, App	c 460	43	1.5	3613	9	US-09-764-878-416	Sequence 416, App
c 188	44	1.5	558	9	US-09-849-626-554	Sequence 554, App	c 461	43	1.5	4854	10	US-09-764-877-3882	Sequence 3882, App
c 189	44	1.5	558	9	US-10-017-754-554	Sequence 554, App	c 462	43	1.5	4854	10	US-09-764-891-7901	Sequence 7901, App
c 190	44	1.5	1066	10	US-09-822-816A-314	Sequence 314, App	c 463	43	1.5	4854	10	US-09-764-891-7901	Sequence 7901, App
c 191	44	1.5	2510	10	US-09-822-849A-465	Sequence 465, App	c 464	43	1.5	4854	10	US-09-764-891-7901	Sequence 7901, App
c 192	44	1.5	3471	9	US-10-092-154-1893	Sequence 1893, App	c 465	43	1.5	4854	10	US-09-764-891-7901	Sequence 7901, App
c 193	44	1.5	3471	9	US-09-764-847-1893	Sequence 1893, App	c 466	43	1.5	4854	10	US-09-764-891-7901	Sequence 7901, App
c 194	44	1.5	4900	9	US-09-977-221-1	Sequence 1, Appl	c 467	43	1.5	5430	9	US-10-091-438-279	Sequence 279, App
c 195	44	1.5	5239	10	US-09-909-147-22	Sequence 22, Appl	c 468	43	1.5	5430	9	US-10-091-438-279	Sequence 279, App
c 196	44	1.5	6107	9	US-09-764-891-8370	Sequence 8370, App	c 469	43	1.5	5768	10	US-09-764-846-328	Sequence 328, App
c 197	44	1.5	6286	9	US-09-764-868-1463	Sequence 1463, App	c 470	43	1.5	5893	10	US-09-764-846-328	Sequence 328, App
c 198	44	1.5	6792	9	US-10-121-235-20	Sequence 20, Appl	c 471	43	1.5	5893	10	US-09-764-846-328	Sequence 328, App
c 199	44	1.5	7588	9	US-09-764-891-9724	Sequence 9724, App	c 472	43	1.5	8957	9	US-10-091-572-815	Sequence 815, App
c 200	44	1.5	7703	9	US-10-073-961-415	Sequence 415, App	c 473	43	1.5	8957	9	US-09-764-891-9239	Sequence 9239, App
c 201	44	1.5	7703	9	US-10-073-961-415	Sequence 415, App	c 474	43	1.5	11221	10	US-09-764-864-1773	Sequence 1773, App
c 202	44	1.5	7703	9	US-09-764-887-415	Sequence 415, App	c 475	43	1.5	11221	10	US-09-764-864-1773	Sequence 1773, App
c 203	44	1.5	7703	9	US-09-764-887-415	Sequence 415, App	c 476	43	1.5	11557	9	US-10-102-627-103	Sequence 103, App
c 204	44	1.5	10634	9	US-09-764-887-456	Sequence 456, App	c 477	43	1.5	11557	9	US-10-102-627-104	Sequence 104, App
c 205	44	1.5	15266	10	US-09-764-877-3797	Sequence 3797, App	c 478	43	1.5	11557	9	US-09-764-891-9063	Sequence 9063, App
c 206	44	1.5	15271	10	US-09-764-877-3798	Sequence 3798, App	c 479	43	1.5	11557	9	US-09-764-891-9064	Sequence 9064, App
c 207	44	1.5	17216	10	US-09-764-877-3565	Sequence 3565, App	c 480	43	1.5	12045	9	US-09-984-827-5	Sequence 5, Appl
c 208	44	1.5	17217	10	US-09-764-877-3566	Sequence 3566, App	c 481	43	1.5	12045	9	US-09-764-891-9754	Sequence 1579, App
c 209	44	1.5	17450	9	US-09-764-891-8641	Sequence 8641, App	c 482	43	1.5	12822	10	US-09-764-847-1579	Sequence 1579, App
c 210	44	1.5	20869	10	US-10-091-504-2427	Sequence 2427, App	c 483	43	1.5	14176	10	US-09-764-864-1644	Sequence 1644, App
c 211	44	1.5	20869	10	US-09-764-869-2427	Sequence 2427, App	c 484	43	1.5	14176	10	US-09-764-864-1644	Sequence 1644, App
c 212	44	1.5	20966	10	US-09-776-976-7	Sequence 7, Appl	c 485	43	1.5	14796	10	US-09-954-456-1636	Sequence 1636, App
c 213	44	1.5	20966	10	US-09-758-055-7	Sequence 7, Appl	c 486	43	1.5	14796	10	US-09-918-186A-3	Sequence 3, Appl
c 214	44	1.5	20966	10	US-09-909-547-7	Sequence 7, Appl	c 487	43	1.5	14796	10	US-09-880-107-3421	Sequence 1421, App
c 215	44	1.5	21423	10	US-09-764-877-2845	Sequence 2845, App	c 488	43	1.5	15275	9	US-10-091-504-1475	Sequence 1475, App
c 216	44	1.5	24132	9	US-10-074-095-661	Sequence 661, App	c 489	43	1.5	15275	9	US-09-764-869-1475	Sequence 1475, App
c 217	44	1.5	24132	9	US-09-764-860-561	Sequence 661, App	c 490	43	1.5	20966	10	US-09-776-976-7	Sequence 7, Appl
c 218	44	1.5	31168	9	US-09-764-868-1464	Sequence 1464, App	c 491	43	1.5	20966	10	US-09-758-055-7	Sequence 7, Appl
c 219	44	1.5	31168	9	US-09-764-891-9556	Sequence 9556, App	c 492	43	1.5	20966	10	US-09-909-547-7	Sequence 7, Appl
c 220	44	1.5	32134	9	US-09-764-891-6763	Sequence 6763, App	c 493	43	1.5	32082	9	US-09-764-877-3297	Sequence 3297, App
c 221	44	1.5	32188	9	US-09-764-891-7300	Sequence 7300, App	c 494	43	1.5	32134	9	US-09-764-891-9679	Sequence 9679, App
c 222	44	1.5	32188	9	US-10-074-095-799	Sequence 799, App	c 495	43	1.5	32134	9	US-10-092-154-1057	Sequence 1057, App
c 223	44	1.5	32188	9	US-09-764-860-799	Sequence 799, App	c 496	43	1.5	32134	9	US-09-764-891-6357	Sequence 6357, App
c 224	44	1.5	46218	9	US-10-274-873-3	Sequence 3, Appl	c 497	43	1.5	32134	10	US-09-764-847-1057	Sequence 1057, App
c 225	44	1.5	46218	10	US-09-616-093-3	Sequence 3, Appl	c 498	43	1.5	32134	10	US-09-764-877-3535	Sequence 1057, App
c 226	44	1.5	68804	10	US-09-740-041-3	Sequence 3, Appl	c 499	43	1.5	32190	9	US-10-079-854-201	Sequence 201, App
c 227	44	1.5	84539	10	US-09-962-436-46	Sequence 3, Appl	c 500	43	1.5	32190	9	US-09-764-878-201	Sequence 201, App
c 228	44	1.5	176373	9	US-10-095-407-17	Sequence 17, Appl	c 501	43	1.5	32190	9	US-10-079-854-200	Sequence 200, App
c 229	43	1.5	105	9	US-10-125-547-608	Sequence 598, App	c 502	43	1.5	32193	10	US-09-764-878-200	Sequence 200, App
c 230	43	1.5	105	9	US-10-074-095-696	Sequence 696, App	c 503	43	1.5	32207	10	US-09-764-891-6966	Sequence 6966, App
c 231	43	1.5	105	10	US-09-764-870-604	Sequence 608, App	c 504	43	1.5	32207	10	US-09-764-877-3250	Sequence 3250, App
c 232	43	1.5	105	10	US-09-764-860-595	Sequence 696, App	c 505	43	1.5	32249	9	US-10-079-854-202	Sequence 202, App
c 233	43	1.5	304	10	US-09-867-701-949	Sequence 969, App	c 506	43	1.5	32249	9	US-09-764-891-8024	Sequence 8024, App
c 234	43	1.5	309	9	US-10-092-154-1476	Sequence 1476, App	c 507	43	1.5	32249	10	US-09-764-878-202	Sequence 202, App
c 235	43	1.5	309	9	US-10-092-154-1476	Sequence 1476, App	c 508	43	1.5	38374	10	US-09-880-107-3463	Sequence 3463, App
c 236	43	1.5	309	10	US-09-764-847-1476	Sequence 1476, App	c 509	43	1.5	49744	10	US-09-927-091-4	Sequence 4, Appl
c 237	43	1.5	309	10	US-09-764-847-1476	Sequence 1476, App	c 510	43	1.5	60153	9	US-10-222-334-7	Sequence 7, Appl
c 238	43	1.5	324	9	US-09-764-891-691	Sequence 691, App	c 511	43	1.5	81001	9	US-09-842-364-1	Sequence 1, Appl
c 239	43	1.5	324	9	US-09-764-891-691	Sequence 691, App	c 512	43	1.5	81001	10	US-09-751-877-1	Sequence 1, Appl
c 240	43	1.5	324	9	US-09-764-891-691	Sequence 691, App	c 513	43	1.5	12762	9	US-09-954-556-17	Sequence 17, Appl
c 241	43	1.5	361	10	US-09-867-701-6452	Sequence 6452, App	c 514	43	1.5	133893	9	US-10-161-510-1	Sequence 1, Appl
c 242	43	1.5	391	10	US-09-867-701-7901	Sequence 7901, App	c 515	43	1.5	174493	9	US-10-238-709-3	Sequence 3, Appl
c 243	43	1.5	412	9	US-09-918-995-7919	Sequence 7919, App	c 516	43	1.5	174493	10	US-09-804-471A-3	Sequence 3, Appl
c 244	43	1.5	418	9	US-09-918-995-3499	Sequence 3499, App	c 517	42	1.5	174493	9	US-09-844-653-5	Sequence 5, Appl
c 245	43	1.5	443	9	US-09-918-995-12842	Sequence 12842, App	c 518	42	1.5	174493	9	US-09-844-653-5	Sequence 5, Appl
c 246	43	1.5	462	9	US-09-918-995-5458	Sequence 5458, App	c 519	42	1.5	174493	9	US-09-764-891-10229	Sequence 10229, App
c 247	43	1.5	462	9	US-09-918-995-6488	Sequence 6488, App	c 520	42	1.5	174493	10	US-09-764-860-660	Sequence 660, App
c 248	43	1.5	474	9	US-09-918-995-6607	Sequence 6607, App	c 521	42	1.5	253	10	US-09-867-701-5005	Sequence 5005, App
c 249	43	1.5	487	10	US-09-867-701-6728	Sequence 6728, App	c 522	42	1.5	253	9	US-09-764-891-6009	Sequence 6009, App
c 250	43	1.5	504	9	US-09-918-995-11203	Sequence 11203, App	c 523	42	1.5	310	9	US-09-796-692-5928	Sequence 5928, App
c 251	43	1.5	506	9	US-09-918-995-2444H	Sequence 2444H, App	c 524	42	1.5	310	9	US-10-040-862-5928	Sequence 5928, App
c 252	43	1.5	646	9	US-10-091-504-1882	Sequence 1882, App	c 525	42	1.5	360	10	US-09-867-701-6979	Sequence 6979, App
c 253	43	1.5	670	9	US-09-764-869-1882	Sequence 1882, App	c 526	42	1.5	396	9	US-09-918-995-5901	Sequence 5901, App
c 254	43	1.5	1100	9	US-09-764-891-9054	Sequence 9054, App	c 527	42	1.5	425	10	US-09-764-877-2736	Sequence 2736, App
c 255	43	1.5	1635	10	US-10-108-677-2	Sequence 2, Appl	c 528	42	1.5	468	9	US-09-918-995-14394	Sequence 14394, App
c 256	43	1.5	2104	9	US-09-954-1311-1	Sequence 1, Appl	c 529	42	1.5	468	9	US-09-918-995-3151	Sequence 3151, App
c 257	43	1.5					c 530	42	1.5	503	10	US-09-764-877-3646	Sequence 3646, App

541	42	1.5	554	10	US-09-764-877-3776	Sequence 3776, App	604	42	1.5	32192	9	US-09-764-891-8319	Sequence 8319, App
542	42	1.5	747	10	US-09-828-641-51	Sequence 51, Appl	605	42	1.5	32192	10	US-09-764-847-1416	Sequence 1416, App
543	42	1.5	1101	10	US-09-711-872-54	Sequence 54, Appl	606	42	1.5	32193	10	US-09-764-877-2623	Sequence 2623, App
544	42	1.5	1450	10	US-09-822-830A-251	Sequence 251, Appl	607	42	1.5	41907	10	US-09-967-013-5	Sequence 5, Appl
545	42	1.5	3064	9	US-10-042-154-1289	Sequence 1289, App	608	42	1.5	58817	10	US-09-982-091A-5	Sequence 3, Appl
546	42	1.5	3064	9	US-10-042-154-1290	Sequence 1290, App	609	42	1.5	62804	12	US-10-096-960-3	Sequence 3, Appl
547	42	1.5	3064	10	US-09-764-847-1289	Sequence 1289, App	610	42	1.5	92139	10	US-09-918-686-1	Sequence 1, Appl
548	42	1.5	3138	10	US-09-764-847-1290	Sequence 1290, App	611	42	1.5	113604	9	US-10-227-195A-1	Sequence 1, Appl
549	42	1.5	3305	9	US-09-764-891-7823	Sequence 7823, App	612	42	1.5	113604	9	US-10-227-195A-2	Sequence 2, Appl
550	42	1.5	3828	9	US-09-764-891-7518	Sequence 7518, App	613	42	1.5	132762	9	US-09-954-556-17	Sequence 17, Appl
551	42	1.5	3961	9	US-09-764-891-6205	Sequence 6205, App	614	42	1.5	378351	9	US-09-901-136-3	Sequence 3, Appl
552	42	1.5	3961	9	US-09-764-891-6206	Sequence 6206, App	615	41	1.4	114	9	US-10-092-154-1868	Sequence 1868, App
553	42	1.5	4431	9	US-10-091-572-665	Sequence 665, App	616	41	1.4	114	10	US-09-764-847-1868	Sequence 1868, App
554	42	1.5	4431	9	US-09-764-891-6867	Sequence 6867, App	617	41	1.4	254	10	US-09-867-701-1718	Sequence 1718, App
555	42	1.5	4433	9	US-10-091-572-668	Sequence 668, App	618	41	1.4	280	10	US-09-867-701-7613	Sequence 7613, App
556	42	1.5	4433	9	US-09-764-891-6836	Sequence 6836, App	619	41	1.4	299	10	US-09-867-701-7087	Sequence 7087, App
557	42	1.5	4857	9	US-10-092-154-1329	Sequence 1329, App	620	41	1.4	329	9	US-10-073-961-53	Sequence 53, Appl
558	42	1.5	4857	10	US-09-764-847-1329	Sequence 1329, App	621	41	1.4	332	10	US-09-764-887-53	Sequence 53, Appl
559	42	1.5	5559	10	US-09-959-347-1799	Sequence 1799, App	622	41	1.4	332	10	US-09-920-300A-1154	Sequence 1154, App
560	42	1.5	5559	9	US-09-764-891-7252	Sequence 7252, App	623	41	1.4	332	12	US-10-033-528-1154	Sequence 1154, App
561	42	1.5	6053	9	US-09-764-891-7252	Sequence 7252, App	624	41	1.4	356	9	US-09-803-719-48	Sequence 48, Appl
562	42	1.5	6422	9	US-09-764-891-5414	Sequence 5414, App	625	41	1.4	356	10	US-09-925-300-361	Sequence 361, App
563	42	1.5	7470	9	US-10-073-961-397	Sequence 397, App	626	41	1.4	363	12	US-10-033-528-1863	Sequence 1863, App
564	42	1.5	7470	10	US-09-764-887-397	Sequence 397, App	627	41	1.4	394	9	US-09-803-719-2310	Sequence 2310, App
565	42	1.5	7470	10	US-09-764-887-398	Sequence 398, App	628	41	1.4	394	10	US-09-867-701-543	Sequence 543, App
566	42	1.5	8253	9	US-09-764-891-6722	Sequence 6722, App	629	41	1.4	405	10	US-09-867-701-9817	Sequence 9817, App
567	42	1.5	8253	9	US-10-074-095-468	Sequence 468, App	630	41	1.4	412	9	US-09-918-995-2846	Sequence 2846, App
568	42	1.5	8268	10	US-09-764-863-868	Sequence 868, App	631	41	1.4	412	9	US-09-918-995-23846	Sequence 23846, App
569	42	1.5	8268	9	US-09-764-863-868	Sequence 868, App	632	41	1.4	412	9	US-09-918-995-12121	Sequence 12121, App
570	42	1.5	8272	9	US-10-074-095-867	Sequence 867, App	633	41	1.4	415	9	US-09-764-891-233	Sequence 233, App
571	42	1.5	8272	10	US-09-764-891-5554	Sequence 5554, App	634	41	1.4	415	9	US-09-764-891-8739	Sequence 8739, App
572	42	1.5	8167	9	US-09-764-891-5554	Sequence 5554, App	635	41	1.4	416	9	US-09-803-719-59	Sequence 59, Appl
573	42	1.5	8253	9	US-09-764-891-6722	Sequence 6722, App	636	41	1.4	431	10	US-09-867-701-6659	Sequence 6659, App
574	42	1.5	8253	9	US-10-091-572-622	Sequence 622, App	637	41	1.4	444	9	US-09-918-995-14690	Sequence 14690, App
575	42	1.5	10378	10	US-09-764-847-1348	Sequence 1348, App	638	41	1.4	444	9	US-09-918-995-2725	Sequence 2725, App
576	42	1.5	10378	10	US-09-764-847-1348	Sequence 1348, App	639	41	1.4	445	9	US-09-918-995-23846	Sequence 23846, App
577	42	1.5	12118	10	US-09-764-891-6721	Sequence 6721, App	640	41	1.4	463	9	US-09-918-995-23846	Sequence 23846, App
578	42	1.5	12118	10	US-09-764-891-6721	Sequence 6721, App	641	41	1.4	472	9	US-09-918-995-12121	Sequence 12121, App
579	42	1.5	12503	9	US-10-125-540-549	Sequence 549, App	642	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
580	42	1.5	12503	9	US-10-125-540-549	Sequence 549, App	643	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
581	42	1.5	12503	10	US-09-764-870-549	Sequence 549, App	644	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
582	42	1.5	12503	10	US-09-764-870-549	Sequence 549, App	645	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
583	42	1.5	13392	9	US-10-091-572-621	Sequence 621, App	646	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
584	42	1.5	13392	9	US-09-764-891-6721	Sequence 6721, App	647	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
585	42	1.5	13392	9	US-09-764-891-6721	Sequence 6721, App	648	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
586	42	1.5	15054	9	US-10-091-572-577	Sequence 577, App	649	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
587	42	1.5	15054	9	US-09-764-891-6721	Sequence 6721, App	650	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
588	42	1.5	15843	9	US-10-091-504-2396	Sequence 2396, App	651	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
589	42	1.5	15843	9	US-09-764-891-6721	Sequence 6721, App	652	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
590	42	1.5	16423	9	US-09-989-442-165	Sequence 165, App	653	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
591	42	1.5	16423	9	US-09-989-442-165	Sequence 165, App	654	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
592	42	1.5	16774	9	US-10-091-504-2395	Sequence 2395, App	655	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
593	42	1.5	16774	9	US-10-091-504-2395	Sequence 2395, App	656	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
594	42	1.5	16774	10	US-09-764-891-6721	Sequence 6721, App	657	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
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596	42	1.5	17965	9	US-09-764-891-8198	Sequence 8198, App	659	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
597	42	1.5	19969	9	US-10-190-593-3	Sequence 3, Appl	660	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
598	42	1.5	20522	10	US-09-764-877-3774	Sequence 3774, App	661	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
599	42	1.5	21535	9	US-10-103-313-609	Sequence 609, App	662	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
600	42	1.5	21535	9	US-10-103-313-609	Sequence 609, App	663	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
601	42	1.5	21784	10	US-09-820-002-3	Sequence 3, Appl	664	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
602	42	1.5	23668	9	US-10-254-577-3	Sequence 3, Appl	665	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
603	42	1.5	23668	10	US-09-741-148A-3	Sequence 3, Appl	666	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
604	42	1.5	28588	9	US-10-073-961-399	Sequence 399, App	667	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
605	42	1.5	28588	10	US-09-764-887-399	Sequence 399, App	668	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
606	42	1.5	31766	9	US-10-288-478-5	Sequence 5, Appl	669	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
607	42	1.5	31766	10	US-09-765-348-5	Sequence 5, Appl	670	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
608	42	1.5	32134	9	US-09-764-891-6903	Sequence 6903, App	671	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
609	42	1.5	32187	9	US-10-102-627-109	Sequence 109, App	672	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
610	42	1.5	32191	9	US-09-764-891-6304	Sequence 6304, App	673	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
611	42	1.5	32192	9	US-10-092-154-1476	Sequence 1476, App	674	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
612	42	1.5	32192	9	US-09-764-891-7995	Sequence 7995, App	675	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App
613	42	1.5	32192	9	US-09-764-891-8225	Sequence 8225, App	676	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, App

c 677	41	1.4	2893	9	US-09-984-827-141	Sequence 141, App
c 678	41	1.4	2893	9	US-09-984-827-142	Sequence 142, App
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c 680	41	1.4	2893	9	US-09-984-827-144	Sequence 144, App
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c 686	41	1.4	2893	9	US-09-984-827-150	Sequence 150, App
c 687	41	1.4	2893	9	US-09-984-827-151	Sequence 151, App
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c 689	41	1.4	2893	9	US-09-984-827-153	Sequence 153, App
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c 691	41	1.4	2893	9	US-09-984-827-155	Sequence 155, App
c 692	41	1.4	2893	9	US-09-984-827-156	Sequence 156, App
c 693	41	1.4	2893	9	US-09-984-827-157	Sequence 157, App
c 694	41	1.4	2893	9	US-09-984-827-158	Sequence 158, App
c 695	41	1.4	2893	9	US-09-984-827-159	Sequence 159, App
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c 697	41	1.4	2893	9	US-09-984-827-161	Sequence 161, App
c 698	41	1.4	2893	9	US-09-984-827-162	Sequence 162, App
c 699	41	1.4	2893	9	US-09-984-827-163	Sequence 163, App
c 700	41	1.4	2893	9	US-09-984-827-164	Sequence 164, App
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c 705	41	1.4	2893	9	US-09-984-827-169	Sequence 169, App
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c 708	41	1.4	2893	9	US-09-984-827-172	Sequence 172, App
c 709	41	1.4	2893	9	US-09-984-827-173	Sequence 173, App
c 710	41	1.4	2893	9	US-09-984-827-174	Sequence 174, App
c 711	41	1.4	2893	9	US-09-984-827-175	Sequence 175, App
c 712	41	1.4	2893	9	US-09-984-827-176	Sequence 176, App
c 713	41	1.4	2893	9	US-09-984-827-177	Sequence 177, App
c 714	41	1.4	2893	9	US-09-984-827-178	Sequence 178, App
c 715	41	1.4	2893	9	US-09-984-827-179	Sequence 179, App
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C 825	41	1.4	1503841	10	US-09-795-688-1	Sequence 1, Appli	C 898	40	1.4	26995	9	US-10-079-854-227	Sequence 227, App
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C 827	40	1.4	345	9	US-09-831-719-1571	Sequence 1571, Ap	C 900	40	1.4	31718	9	US-09-764-872-812	Sequence 812, App
C 828	40	1.4	358	9	US-09-918-995-29818	Sequence 29818, A	C 901	40	1.4	31718	9	US-09-764-872-812	Sequence 812, App
C 829	40	1.4	394	9	US-09-918-995-29818	Sequence 29818, A	C 902	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 830	40	1.4	401	9	US-09-946-807-729	Sequence 729, App	C 903	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 831	40	1.4	401	10	US-09-795-668-729	Sequence 729, App	C 904	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
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C 834	40	1.4	402	10	US-09-867-701-6517	Sequence 6517, Ap	C 907	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 835	40	1.4	402	10	US-09-867-701-6517	Sequence 6517, Ap	C 908	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 836	40	1.4	461	9	US-09-918-995-29818	Sequence 29818, A	C 909	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 837	40	1.4	463	9	US-09-918-995-29818	Sequence 29818, A	C 910	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
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C 839	40	1.4	497	9	US-09-918-995-29818	Sequence 29818, A	C 912	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 840	40	1.4	521	9	US-09-796-692-8285	Sequence 8285, Ap	C 913	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 841	40	1.4	521	9	US-09-796-692-8285	Sequence 8285, Ap	C 914	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 842	40	1.4	542	9	US-09-918-995-29818	Sequence 29818, A	C 915	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 843	40	1.4	577	9	US-09-918-995-29818	Sequence 29818, A	C 916	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 844	40	1.4	666	10	US-09-822-830A-547	Sequence 547, App	C 917	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
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C 852	40	1.4	1671	9	US-10-073-961-513	Sequence 513, App	C 925	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 853	40	1.4	1671	9	US-10-073-961-513	Sequence 513, App	C 926	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 854	40	1.4	1671	9	US-10-073-961-513	Sequence 513, App	C 927	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 855	40	1.4	1671	10	US-09-764-891-9103	Sequence 9103, Ap	C 928	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
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C 857	40	1.4	1671	10	US-09-764-891-9103	Sequence 9103, Ap	C 930	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 858	40	1.4	2241	10	US-09-764-891-9103	Sequence 9103, Ap	C 931	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 859	40	1.4	2364	9	US-10-073-961-513	Sequence 513, App	C 932	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 860	40	1.4	2364	10	US-09-764-891-9103	Sequence 9103, Ap	C 933	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 861	40	1.4	2418	10	US-09-771-161A-10	Sequence 10, App	C 934	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 862	40	1.4	2482	9	US-09-822-846-599	Sequence 599, App	C 935	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 863	40	1.4	3196	9	US-09-764-891-9103	Sequence 9103, Ap	C 936	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 864	40	1.4	3243	9	US-10-092-154-1176	Sequence 1176, Ap	C 937	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 865	40	1.4	3243	10	US-09-764-891-9103	Sequence 9103, Ap	C 938	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 866	40	1.4	3898	9	US-09-764-891-9103	Sequence 9103, Ap	C 939	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 867	40	1.4	3899	9	US-09-764-891-9103	Sequence 9103, Ap	C 940	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 868	40	1.4	3899	9	US-09-764-891-9103	Sequence 9103, Ap	C 941	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 869	40	1.4	4747	9	US-09-764-891-9103	Sequence 9103, Ap	C 942	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 870	40	1.4	4747	9	US-09-764-891-9103	Sequence 9103, Ap	C 943	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 871	40	1.4	4747	9	US-09-764-891-9103	Sequence 9103, Ap	C 944	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
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C 874	40	1.4	7072	9	US-09-764-891-9103	Sequence 9103, Ap	C 947	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
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C 876	40	1.4	9691	9	US-10-073-961-513	Sequence 513, App	C 949	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 877	40	1.4	10503	9	US-10-125-540-134	Sequence 134, App	C 950	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 878	40	1.4	10503	9	US-10-074-095-1042	Sequence 1042, Ap	C 951	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 879	40	1.4	10503	9	US-10-103-413-582	Sequence 582, App	C 952	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
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C 882	40	1.4	11221	10	US-09-778-963A-3	Sequence 3, App	C 955	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 883	40	1.4	11839	9	US-09-764-891-9103	Sequence 9103, Ap	C 956	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 884	40	1.4	13021	9	US-10-103-413-612	Sequence 612, App	C 957	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 885	40	1.4	13021	9	US-10-224-494-29	Sequence 29, App	C 958	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 886	40	1.4	15071	9	US-10-225-013-29	Sequence 29, App	C 959	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 887	40	1.4	15071	9	US-10-225-013-29	Sequence 29, App	C 960	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 888	40	1.4	15071	10	US-09-358-082A-29	Sequence 29, App	C 961	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 889	40	1.4	16163	9	US-09-764-891-9103	Sequence 9103, Ap	C 962	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 890	40	1.4	16607	9	US-09-764-891-9103	Sequence 9103, Ap	C 963	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 891	40	1.4	18877	10	US-09-764-891-9103	Sequence 9103, Ap	C 964	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 892	40	1.4	17431	9	US-10-072-149-247	Sequence 247, App	C 965	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 893	40	1.4	17431	9	US-09-764-891-9103	Sequence 9103, Ap	C 966	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 894	40	1.4	18866	10	US-09-764-891-9103	Sequence 9103, Ap	C 967	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap
C 895	40	1.4	22494	10	US-09-768-439-5	Sequence 5, Appli	C 968	40	1.4	31718	9	US-09-764-891-9103	Sequence 9103, Ap

114: TCATCATGTTGGCCAGGTTGGTTTCGAACCTCTGACCTGAGGTGAGTCTACCTTGGC 1206
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DB 1202 CTCCTCAAGTCTGGGATTACAGCATGAGCCACTGCGCCAGCTCAGATCCTATCCTTT 1260
QY 1261 CTAAAGGCAAAAGTCCATGGTCAAAAGGGCCATGCAACCCAGCTTATGAGTACTG 1320
DB 1262 CTAAAGGCAAAAGTCCATGGTCAAAAGGGCCATGCAACCCAGCTTATGAGTACTG 1320
QY 1321 GACTCCAGAAATTCCTTCGCTGGTGGCTCCACATGCACTTCCAGGCTGCTTGGGCTTC 1380
DB 1322 GACTCCAGAAATTCCTTCGCTGGTGGCTCCACATGCACTTCCAGGCTGCTTGGGCTTC 1380
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DB 1382 TCTATGCTGCTGCTGAGTGTGATAGAACCACTGATGAGTACCTGAGCTTGGAGC 1440
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DB 1442 GTGGCTGGAGATCTGTTGACTGTAGCATGGAGGGGCTTGTGAGCTGAAATGCTGCA 1500
QY 1501 TGCAGGTGGTGGGAGTCTGGAATATGATGAGCTGAGGTGGGAGGAGAGTGGCTTG 1560
DB 1502 TGCAGGTGGTGGGAGTCTGGAATATGATGAGCTGAGGTGGGAGGAGAGTGGCTTG 1560
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DB 1802 TGGCAGATTAAGTGGATTTAGTTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1860
QY 1861 TGGTGTGAGGCTGGATTCCTAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1920
DB 1862 TGGTGTGAGGCTGGATTCCTAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1920
QY 1921 AGTTTGTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1980
DB 1922 AGTTTGTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1980
QY 1981 AATTTACAGCTGCAATCTCTGGCTGCACTTCAAAATGATACAAATGATACAAATGATAC 2040
DB 1982 AATTTACAGCTGCAATCTCTGGCTGCACTTCAAAATGATACAAATGATACAAATGATAC 2040
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DB 2042 GTCTGTGCTTTTATCAGGAGGCTGATCAATATATCAATATCAATATCAATATCAATATCA 2100
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DB 2102 CATATGCTGCTTTTGTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCT 2160
QY 2161 TCTTCTCTCAATTTATGAG 2220
DB 2162 TCTTCTCTCAATTTATGAG 2220
QY 2221 CCTGGGAGCTCAGGCTGGGAATCTCCAAGCAGTGGCTGGCTGGCTGGCTGGCTGGCTGG 2280
DB 2222 CCTGGGAGCTCAGGCTGGGAATCTCCAAGCAGTGGCTGGCTGGCTGGCTGGCTGGCTGG 2280

QY 2281 CAGGTTTGTGGGGGAAACAAAGAGAGCCATTTACCCAGAGACTGTCCGGCTTCCCT 2340
DB 2282 CAGGTTTGTGGGGGAAACAAAGAGAGCCATTTACCCAGAGACTGTCCGGCTTCCCT 2340
QY 2341 CACCCAGCTTAGGCTTTTGAAGGAAACAAAGAGAGAAATGATTGGCTTCCCTGA 2400
DB 2342 CACCCAGCTTAGGCTTTTGAAGGAAACAAAGAGAGAAATGATTGGCTTCCCTGA 2400
QY 2401 GGGAGATTGAGCTTAGGCTTCTCTCCCAATTCCTTCCCTCCGCTGAGGAACTAAC 2460
DB 2402 GGGAGATTGAGCTTAGGCTTCTCTCCCAATTCCTTCCCTCCGCTGAGGAACTAAC 2460
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DB 2462 AAAGGAAACAAATTCGCGGAGAGAGATTTAGAGAGAGAAATTCCTTCCCTT 2520
QY 2521 GGCTGGCGGAGAGCTGAGCTTAGAGCTTCTCGGCGAGCCCGAGCCAGCTTCCCT 2580
DB 2522 GGCTGGCGGAGAGCTGAGCTTAGAGCTTCTCGGCGAGCCCGAGCCAGCTTCCCT 2580
QY 2581 GCGTCTTAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2640
DB 2582 GCGTCTTAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2640
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DB 2642 CCTCTGTAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 2700
QY 2701 TCGTGGCGGCTGAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 2760
DB 2702 TCGTGGCGGCTGAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 2760
QY 2761 TCACTGAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 2820
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RESULT 2

US-09-846-456-3
: Sequence 3, Application US/09846456
: Patent No. US20020146792A1
: GENERAL INFORMATION:
: APPLICANT: Rosier, Marie
: APPLICANT: Prades, Catherine
: APPLICANT: Lemoine, Cendrino
: APPLICANT: Naudin, Laurence
: APPLICANT: Benfle, Patrice
: APPLICANT: Duverger, Nicolas
: APPLICANT: Brewer, Bryan
: APPLICANT: Remaley, Alan
: APPLICANT: Folio, Silvia
: TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
: FILE REFERENCE: 3806.0505
: CURRENT APPLICATION NUMBER: US/09/846,456
: PRIOR FILING DATE: 2001-05-02
: PRIOR APPLICATION NUMBER: US 60/201,280
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens

US-09-846-456-3

Query Match		100.0%	Score 2893	Db 10	Length 2893
Best Local Similarity		100.0%	Pred. No. 0		
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			0	Indels	0
			0	Gaps	0
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Qy	361	AAGTTCAGCTTTTCAAGAAACCCCTTTGAGGAGACAGCAATATACATTTCTCTCAAT	420		
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Qy	421	CTGAGGCGAGAGGATCGCTTCAAGCTCCAGAGCTTCAAGGAGCTTCAAGGAGCT	480		
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Qy	901	GCTGGGCTTGGGCTTTAGAAAGCTCATCTGAGGAGGAGGAGGAGGAGGAGGAG	960		
Db	901	GCTGGGCTTGGGCTTTAGAAAGCTCATCTGAGGAGGAGGAGGAGGAGGAGGAG	960		
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Qy	1261	CTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1320		
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Qy	1681	GTGGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1740		
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Qy	1801	TGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1860		
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Qy	1981	AAATTTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2040		
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Qy	2041	GTGGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2100		
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QY 901 CTTGGGCTTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTTCAGATGCAATCTTTCTTT 960
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Db 1021 TCGACTCACTGTAAGCTCTGCTCCGCGCTTCAAGGATCTCTCTCACTGAGGCTGAGGCTGAGG 1080
QY 1081 GATAACAGGCGCGCGCCACACATCTGGCTAATTTTATTTTATTAAGAACTGGGTT 1140
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QY 1201 CTTCCAAAGTCTGGGATTAAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGG 1260
Db 1201 CTTCCAAAGTCTGGGATTAAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGG 1260
QY 1261 CTAGGCAAAACAGTCCATGGTGCAGAGGCGGATGAGGCTATGAGGCTATGAGGCTATGAGG 1320
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QY 1321 GATTCAGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 1321 GATTCAGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
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Db 1441 GTGCTGAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
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Db 1501 TCGAGTGGTGGGAGTCTGGAATATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1560
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QY 1801 TGGCAGAAATAGGTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
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QY 1861 TGGTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
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QY 1921 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Db 1921 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980

QY 1981 AATTTTACAGGCTGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Db 1981 AATTTTACAGGCTGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
QY 2041 GCTCTGCTGCTTATACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Db 2041 GCTCTGCTGCTTATACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
QY 2101 CATATGCTGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2101 CATATGCTGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
QY 2161 TCTTCTCTCTCAATTTATCAAGAGCAATTAAGATGCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 2220
Db 2161 TCTTCTCTCTCAATTTATCAAGAGCAATTAAGATGCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 2220
QY 2221 CTTGGGAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Db 2221 CTTGGGAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
QY 2281 CAGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Db 2281 CAGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
QY 2341 CACCCAGCTGAGGCTTGTGAAGAGCAAAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCA 2400
Db 2341 CACCCAGCTGAGGCTTGTGAAGAGCAAAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCA 2400
QY 2401 GGGAGATTCAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Db 2401 GGGAGATTCAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
QY 2461 AAGGAG 2520
Db 2461 AAGGAG 2520
QY 2521 GCTG 2580
Db 2521 GCTG 2580
QY 2581 GCTG 2640
Db 2581 GCTG 2640
QY 2641 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
Db 2641 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
QY 2701 TCTG 2760
Db 2701 TCTG 2760
QY 2761 TGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
Db 2761 TGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
QY 2821 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
Db 2821 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
QY 2881 CGGCAAAAGAGGCT 2893
Db 2881 CGGCAAAAGAGGCT 2893

RESULT 4

US-09-846-456-1
; Sequence 1, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine

1561 GGGGAGCTCTCTCATGCGCCTCATCTGCGCAAAACTCAGGTCAAACTGGAAGAGTCT 1620
QY 1621 AAATCTGATCTGCGCTTCAAGGTGGCTACAAAGGTATCTTTCGCAAGGTAGAGACCTT 1680
DB 1621 AAATGTAATCTGCGCTTCAAGGTGGCTACAAAGGTATCTTTCGCAAGGTAGAGACCTT 1680
QY 1681 GTGGCTCCAGCTGCACTTCCAGGGCTGCTTGGGGCTCTTTCAGGGCTCTTTCAGGT 1740
DB 1681 GTGGCTCCAGCTGCACTTCCAGGGCTGCTTGGGGCTCTTTCAGGGCTCTTTCAGGT 1740
QY 1741 CTTCTATGATCTTCAAGGAGATTCATATTTAGACTCTTTCAGGTCTTTCAGGT 1800
DB 1741 CTTCTATGATCTTCAAGGAGATTCATATTTAGACTCTTTCAGGTCTTTCAGGT 1800
QY 1801 TGGCCAGAAATAGGTGACATTTAGTTTGGCTTCATGATGACATTAATAA:ITAGACA 1860
DB 1801 TGGCCAGAAATAGGTGACATTTAGTTTGGCTTCATGATGACATTAATAA:ITAGACA 1860
QY 1861 TGGTGTAGGCTGCAATCTCTACTCTTGGCTTTTTCGCGCTGCAAG:TTTTGGGT 1920
DB 1861 TGGTGTAGGCTGCAATCTCTACTCTTGGCTTTTTCGCGCTGCAAG:TTTTGGGT 1920
QY 1921 AGTTTCTCTCCCTACAGCCAAAGGCAAGAGAGAGAGTGGAGTCTGGAGTCTGATCA 1980
DB 1921 AGTTTCTCTCCCTACAGCCAAAGGCAAGAGAGAGAGTGGAGTCTGGAGTCTGATCA 1980
QY 1981 AATTTACAGCACTGCAATCTCTGCTGCACTTCAAAATGTAACAA:AAATACAA 2040
DB 1981 AATTTACAGCACTGCAATCTCTGCTGCACTTCAAAATGTAACAA:AAATACAA 2040
QY 2041 GTGCTGTGTTTATCAGGAGGCTGATCATATATATATATATATATATATATATATAT 2100
DB 2041 GTGCTGTGTTTATCAGGAGGCTGATCATATATATATATATATATATATATATATAT 2100
QY 2101 CATATGCTGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2160
DB 2101 CATATGCTGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2160
QY 2161 TCTTCTCTCTAAATTTAG 2220
DB 2161 TCTTCTCTCTAAATTTAG 2220
QY 2221 GTTGGGAGCTCAGCTGGGATCTCCAAAGTCTAGTCTGCTTATCAAAATCAAGTC 2280
DB 2221 GTTGGGAGCTCAGCTGGGATCTCCAAAGTCTAGTCTGCTTATCAAAATCAAGTC 2280
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DB 2281 CAGGTTTGTGGGGGAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
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DB 2341 CAGCCAGCTAGGCTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
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DB 2401 GGGAGATTCAGCTTAGAGCTCTCTCTCCCAATCTCTCTCTCTCTCTCTCTCTCTCT 2460
QY 2461 AAAGGAAAAAATTTGGGAAAGAGAGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
DB 2461 AAAGGAAAAAATTTGGGAAAGAGAGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
QY 2521 GCTCTCGGAGAGCTGAGAGTCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
DB 2521 GCTCTCGGAGAGCTGAGAGTCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
QY 2581 GCGTCTTAGGCG 2640
DB 2581 GCGTCTTAGGCG 2640
QY 2641 CTGCTGTACCTTCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2700
DB 2641 CTGCTGTACCTTCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2700

QY 2701 TCGTGGCGGTGAACGTGCGCCGTTTAAAGGGCGGCCCGGCTCCACGTCTTCTTCG 2760
DB 2701 TCGTGGCGGTGAACGTGCGCCGTTTAAAGGGCGGCCCGGCTCCACGTCTTCTTCG 2760
QY 2761 TGAGTGACTGAATACATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
DB 2761 TGAGTGACTGAATACATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
QY 2821 GCTTTGACCGAATAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
DB 2821 GCTTTGACCGAATAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
QY 2881 CGGCAAAACCC 2893
DB 2881 CGGCAAAACCC 2893

RESULT 7
US-09-984-827-139
; Sequence 139, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION
; APPLICANT: DENEPE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-139

Query Match 98.2%, Score 2842, DB 9, Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAGGGCATGCTGGCAGCTGCTGTAACTCTCAGTTACTCTGGGAGGTGGAGGTGCAATGA 60
DB 1 ACAGGGCATGCTGGCAGCTGCTGTAACTCTCAGTTACTCTGGGAGGTGGAGGTGCAATGA 60
QY 61 GCCAGATCGCCACCAATTCAGCTCCAGCTGGGCAACAAAGGTGAACTCCATCTCAAT 120
DB 61 GCCAGATCGCCACCAATTCAGCTCCAGCTGGGCAACAAAGGTGAACTCCATCTCAAT 120
QY 121 AAAAAAANCAATGATTTGGTGGCTGCTCAATAGTAGTAGGAGAGAGAGAGAGAGG 180
DB 121 AAAAAAANCAATGATTTGGTGGCTGCTCAATAGTAGTAGGAGAGAGAGAGAGAGG 180
QY 181 AGATGGAGGTTCAGGAGATCTAATTACTCTCTAAATCATGCTAGGAAAGATACACCT 240
DB 181 AGATGGAGGTTCAGGAGATCTAATTACTCTCTAAATCATGCTAGGAAAGATACACCT 240
QY 241 TTTAATAACACTCTCTGCTTTTAAACATCATCTGCCAGGAGCTCAAGAGTTCAACA 300
DB 241 TTTAATAACACTCTCTGCTTTTAAACATCATCTGCCAGGAGCTCAAGAGTTCAACA 300
QY 301 AGATTCACTTTCAGAAAAACCTTTTGAGGAAGACAGATATACATCTTCTCTCCATT 360
DB 301 AGATTCACTTTCAGAAAAACCTTTTGAGGAAGACAGATATACATCTTCTCTCCATT 360

QY 361 AAGATGAGAAACAGCGCGGACAAATGGCTAATGCCCTGTAAATCCAGCAATTTGGGAGG 420
DB 361 AAGATGAGAAACAGCGCGGACAAATGGCTAATGCCCTGTAAATCCAGCAATTTGGGAGG 420
QY 421 CTGAGGCCAGAGATCGCTTGGCTCCAGAGTTTCAGACAGCCCTGGATAAATGAGCAAA 480
DB 421 CTGAGGCCAGAGATCGCTTGGCTCCAGAGTTTCAGACAGCCCTGGATAAATGAGCAAA 480
QY 481 ACCCTGTCTCTACAAAAAATACAAAAATACAAAAATAGATGGGCTGTGGCTGGCTGGCTGG 540
DB 481 ACCCTGTCTCTACAAAAAATACAAAAATACAAAAATAGATGGGCTGTGGCTGGCTGGCTGG 540
QY 541 CCGAGCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTGGAGCCAGGAGCTAACTCTACA 500
DB 541 CCGAGCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTGGAGCCAGGAGCTAACTCTACA 500
QY 601 CTGAGCCATGATTGGATCACTGCACCTCCAGCTGGGTAGACAGCAAGATCTGCTCA 560
DB 601 CTGAGCCATGATTGGATCACTGCACCTCCAGCTGGGTAGACAGCAAGATCTGCTCA 560
QY 661 AAAAAAGAAATGAAAGAGAAAGAAAGAGAGAGAGAGAGAGATGAGGAGAGG 720
DB 661 AAAAAAGAAATGAAAGAGAAAGAAAGAGAGAGAGAGAGATGAGGAGAGG 720
QY 721 GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 721 GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 781 GATGAACAGAGCGGAGAGAGACATTTACGTAATATGCTATGATGATGATGATGATGATG 840
DB 781 GATGAACAGAGCGGAGAGAGACATTTACGTAATATGCTATGATGATGATGATGATGATG 840
QY 841 CTTCAAAACCAATTTATGACCAAGTTATCTTTCATGAGGAGGAGGAGGAGGAGGAGG 900
DB 841 CTTCAAAACCAATTTATGACCAAGTTATCTTTCATGAGGAGGAGGAGGAGGAGGAGG 900
QY 901 CTGAGGCTTGGGCTTTAGAAAGCTCATCTGCTGGCTTTCTGAGATGCAATGATGCTTT 960
DB 901 CTGAGGCTTGGGCTTTAGAAAGCTCATCTGCTGGCTTTCTGAGATGCAATGATGCTTT 960
QY 961 TTAATTTCTGACAGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 961 TTAATTTCTGACAGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1021 TGAATCACTGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 TGAATCACTGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 GATAAAGGCGCGGCGGACACATCTGGCTAATTTCTGATCTTTCTGATCTTTCTGATCTTT 1140
DB 1081 GATAAAGGCGCGGCGGACACATCTGGCTAATTTCTGATCTTTCTGATCTTTCTGATCTTT 1140
QY 1141 TCAATCACTGTTGGCAGCTTGGTTTGGAACTGCTGAGCTTGAATGAGCTGAGCTGAGCT 1200
DB 1141 TCAATCACTGTTGGCAGCTTGGTTTGGAACTGCTGAGCTTGAATGAGCTGAGCTGAGCT 1200
QY 1201 CTCCCAAGTCTGGGATTAACGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
DB 1201 CTCCCAAGTCTGGGATTAACGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
QY 1261 CTANGGCAACAGCTCCATGGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
DB 1261 CTANGGCAACAGCTCCATGGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
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DB 1321 GACTCCAGAAATTCCTTGGCTGGGCTCCACATGCAATTCAGGAGGAGGAGGAGGAGGAGG 1380
QY 1381 TTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1381 TTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 CTGAGCTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500

DB 1441 GTGGCTTGGAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 TGCAGGTGGTGGAGTTCTGGAAATATGATCGAGCTGGAGGTGGGAGAGAGAGTGGCTTG 1560
DB 1501 TGCAGGTGGTGGAGTTCTGGAAATATGATCGAGCTGGAGGTGGGAGAGAGTGGCTTG 1560
QY 1561 GGGCAGCTCTCTCATGCCACCTCATCTTCTGGCCAAAACCTCAGGTCAAACTGTCAGAGTCT 1620
DB 1561 GGGCAGCTCTCTCATGCCACCTCATCTTCTGGCCAAAACCTCAGGTCAAACTGTCAGAGTCT 1620
QY 1621 AAATGTGAATCTGCTCTTCAAGGTGCTTCAAGAGTATCTTGTCAAGGTAGGAGCTT 1680
DB 1621 AAATGTGAATCTGCTCTTCAAGGTGCTTCAAGAGTATCTTGTCAAGGTAGGAGCTT 1680
QY 1681 GTGGCTTCCAGGTGCTGCTTCCAGGGCTGCTTGGGGCTCTTCTACGGGTCTGCTGCTGAGT 1740
DB 1681 GTGGCTTCCAGGTGCTGCTTCCAGGGCTGCTTGGGGCTCTTCTACGGGTCTGCTGCTGAGT 1740
QY 1741 CTTCTATGAATCTTCCAGGCGAGATTCATATTTAGACTCTTCCAGGTGCTGCTGCTGAGT 1800
DB 1741 CTTCTATGAATCTTCCAGGCGAGATTCATATTTAGACTCTTCCAGGTGCTGCTGCTGAGT 1800
QY 1801 TGGCCAGAAATAAGGTGACATTTAGTTTGTGGCTTGGATGAGTAAATATTTAGACA 1860
DB 1801 TGGCCAGAAATAAGGTGACATTTAGTTTGTGGCTTGGATGAGTAAATATTTAGACA 1860
QY 1861 TGGTGTGAGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
DB 1861 TGGTGTGAGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
QY 1921 AGTTTGTCTGCTTACAGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
DB 1921 AGTTTGTCTGCTTACAGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
QY 1981 AATTTACAGCTGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
DB 1981 AATTTACAGCTGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
QY 2041 GTCTGTGTTTATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100
DB 2041 GTCTGTGTTTATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
QY 2101 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
DB 2101 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
QY 2161 TCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
DB 2161 TCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
QY 2221 CTTGGGAGCTGAGGCTGGGAAATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280
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QY 2281 CAGTTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
DB 2281 CAGTTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
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DB 2341 CAGCCGAGCTGAGGCTGGGAAATCTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400
QY 2401 GGGAGATGAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
DB 2401 GGGAGATGAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
QY 2461 AAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
DB 2461 AAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
QY 2521 GGGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580

2521 GGTTCGGGGAAGCTGTAAGAGAGTGTGATGGGCAAGGCGGAGGCGCAATGTTGCGCG 2550
2581 GATCTTAGCG 2640
2581 GGTCTTAGCG 2640
2641 GCTGCTGACCTCCACCCCG 2700
2701 TGTGGGCG 2760
2701 TGTGGGCG 2760
2761 TGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2820
2761 TGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2820
2821 GCTTTGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880
2821 GCTTTGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880
2881 GCGCAAAACCC 2893
2881 GCGCAAAACCC 2893

RESULTS

US-09-846-827-140

Sequence 140, Application US/09984827

Publication No. US20030056234A

GENERAL INFORMATION:

APPLICANT: DENEPIE, PATRICE

APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

APPLICANT: ARNOULD-REGUIGNE, ISABELLE

APPLICANT: DUVERGER, NICOLAS

APPLICANT: CAMBIEN, FRANCOIS

TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN APO A1 GENE, THEIR USES, AND

METHODS OF INVENTION: DETECTION METHODS AND KITS THEREFOR

FILE REFERENCE: 03806, 0522-00000

CURRENT APPLICATION NUMBER: US/09/984,827

PRIOR FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 60/254,108

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: FR 00/24037

PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 161

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 140

LENGTH: 2893

TYPE: DNA

ORGANISM: Homo sapiens

US-09-846-827-140

Query Match 98.2% Score 2842, DB 9, Expect 2e-63

Best Local Similarity 100.0% Prod No 32

Matches 2892, Conservative 0, Mismatches 1, Indels 6, Gaps 1

1 ACAGGCAATGCTGCGAGTGCCTGTAATCTGATTAATCTGCGGATGATGATGATGATGATG 50

1 ACAGGCAATGCTGCGAGTGCCTGTAATCTGATTAATCTGCGGATGATGATGATGATGATG 60

61 GCGGCAATGCGACCATTCGATCTGCGGATGATGATGATGATGATGATGATGATGATGATG 120

61 GCGGCAATGCGACCATTCGATCTGCGGATGATGATGATGATGATGATGATGATGATGATG 120

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

121 AAAAAAAGCAATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 180

QY 1321 GACTCCAGAAATTCCTTGCTGGTGGCCCTCCACATCCAGCCTCCAGGCGCTGTTGGGGCTC 1380
DB 1321 GACTCCAGAAATTCCTTGCTGGTGGCCCTCCACATCCAGCCTCCAGGCGCTGTTGGGGCTC 1380
QY 1381 TTTATGCTGTCTGCTGAGTCTTGATAGAACCACTGATGAGTACGCTGAGCTTACAGT 1440
DB 1381 TTTATGCTGTCTGCTGAGTCTTGATAGAACCACTGATGAGTACGCTGAGCTTACAGT 1440
QY 1441 TTGGCTGGAGATCCTGTTTACCTGACCTGAGGAGGCTGAGTACGCTGAGGCTGAGT 1500
DB 1441 TTGGCTGGAGATCCTGTTTACCTGACCTGAGGAGGCTGAGTACGCTGAGGCTGAGT 1500
QY 1501 TCCAGTGTGGGAGTCTGGAATATGATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1560
DB 1501 TCCAGTGTGGGAGTCTGGAATATGATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1560
QY 1561 GGGCAGCTCTCTCATGCCACCTCAATCTGGCCAAACTCAGTCAAACTCAGAGAGTCT 1620
DB 1561 GGGCAGCTCTCTCATGCCACCTCAATCTGGCCAAACTCAGTCAAACTCAGAGAGTCT 1620
QY 1621 AATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTGTCAAGGTAGAGAGCTT 1680
DB 1621 AATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTGTCAAGGTAGAGAGCTT 1680
QY 1681 GTGGCTCCACCTGCTCAGGCGCTGCTGGCGCTCTTCTACAGCTCTTCTCTGAGT 1740
DB 1681 GTGGCTCCACCTGCTCAGGCGCTGCTGGCGCTCTTCTACAGCTCTTCTCTGAGT 1740
QY 1741 TTCTATGAATCTTCAGGGGAGATTCATATACAGCTCTTCTACAGCTCTTCTCTGAGT 1800
DB 1741 TTCTATGAATCTTCAGGGGAGATTCATATACAGCTCTTCTACAGCTCTTCTCTGAGT 1800
QY 1801 TGGCAGAAATAGGTGACATATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
DB 1801 TGGCAGAAATAGGTGACATATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
QY 1861 TGGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
DB 1861 TGGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
QY 1921 AATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
DB 1921 AATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
QY 1981 AATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
DB 1981 AATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
QY 2041 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
DB 2041 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
QY 2101 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
DB 2101 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
QY 2161 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
DB 2161 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
QY 2221 TTTGGGAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
DB 2221 TTTGGGAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
QY 2281 CAGGTTTGTGGGGGAAACAAAGCAGCCTATAGTACAGGAGCTGCTGCTGCTGCTGCTG 2340
DB 2281 CAGGTTTGTGGGGGAAACAAAGCAGCCTATAGTACAGGAGCTGCTGCTGCTGCTGCTG 2340
QY 2341 CACCCAGCCTAGGCTTTGAAGAGCAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2400
DB 2341 CACCCAGCCTAGGCTTTGAAGAGCAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2400
QY 2401 GAGAGATTCAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460

DB 2401 GGGAGATTGAGCTAGAGTCTCTCTCCCAATCCCTCCCTCCCTGAGGAACTAAC 2460
QY 2461 AAGAGAAAAAAATTCGGAAGCAGGATTTAGAGGAAGCAAAATTCACCTGGTGGCTT 2520
DB 2461 AAGAGAAAAAAATTCGGAAGCAGGATTTAGAGGAAGCAAAATTCACCTGGTGGCTT 2520
QY 2521 GGC1GCCGGGAAGTGGATAGAGAGTCTGGGGCAGCAGCCCGAGCCGAGCGCTTCGCG 2580
DB 2521 GGC1GCCGGGAAGTGGATAGAGAGTCTGGGGCAGCAGCCCGAGCCGAGCGCTTCGCG 2580
QY 2581 GGCCTTAGGCTGGGGGCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
DB 2581 GGCCTTAGGCTGGGGGCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
QY 2641 CCGTGTGACCTTCCAGCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCT 2700
DB 2641 CCGTGTGACCTTCCAGCCACCCACCCACCCACCCACCCACCCACCCACCCACCT 2700
QY 2701 TCGTGGGCGGCTGAACGCTGGCGGCTTTAAGGGGGGGGGGGGGGGGGGGGGGGGGGG 2760
DB 2701 TCGTGGGCGGCTGAACGCTGGCGGCTTTAAGGGGGGGGGGGGGGGGGGGGGGGGGGG 2760
QY 2761 TGAGTGACTGAACACTACATAAAGCAGGCGGGAAGGGGGGGGGGGGGGGGGGGGGGG 2820
DB 2761 TGAGTGACTGAACACTACATAAAGCAGGCGGGAAGGGGGGGGGGGGGGGGGGGGGGG 2820
QY 2821 GCTTACCGGATAGTAATCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
DB 2821 GCTTACCGGATAGTAATCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
QY 2881 CGGCAAAAGCC 2893
DB 2881 CGGCAAAAGCC 2893
RESULT 9
US-09-984-827-141
Sequence 141: Application US/09984827
Publication No. US2003056234A1
GENERAL INFORMATION:
APPLICANT: DENEFE, PATRICE
APPLICANT: KOSTER-MONTUS, MARIE FRANCOISE
APPLICANT: ARNOUD-RECUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBLEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
FILE REFERENCE: 03805-0522-00000
CURRENT APPLICATION NUMBER: US/09/984-827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 141
LENGTH: 2893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-827-141
Query Match 98.2% Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pctd. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAGGGCAGTGTGGAGTGGCTGTGTAATCTCAGTTACTCGGAGGTGAGGTTGCAATGA 60
DB 1 ACAGGGCAGTGTGGAGTGGCTGTGTAATCTCAGTTACTCGGAGGTGAGGTTGCAATGA 60
QY 61 GGGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 143
LENGTH: 2893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-846-456-3.oli30.rnpb

Query Match 98.2%; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred No 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAGGGAGTGGGAGGTGCTGTAAATCTCAGTACTCGGGAGGTGGAGTGCAGATGA 60
|||||
DB 1 ACAGGGAGTGGGAGGTGCTGTAAATCTCAGTACTCGGGAGGTGGAGTGCAGATGA 60
|||||

QY 61 GCCAGATCGGACCAATTCAGCTCCAGCTGGGCAACAAAGGTGCAACTCATCTCAAT 120
|||||
DB 61 GCCAGATCGGACCAATTCAGCTCCAGCTGGGCAACAAAGGTGCAACTCATCTCAAT 120
|||||

QY 121 AAAAAAAGAAATGATTTGGTGGTGCACCTTCAATAGGTAGGAGAGAGAGAGAGG 180
|||||
DB 121 AAAAAAAGAAATGATTTGGTGGTGCACCTTCAATAGGTAGGAGAGAGAGAGAGG 180
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QY 181 AGATGGAGGTGAGGAGATCTAATTAATCTCTAATATGCTAGGAAAGATAACTCT 240
|||||
DB 181 AGATGGAGGTGAGGAGATCTAATTAATCTCTAATATGCTAGGAAAGATAACTCT 240
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QY 241 TTTAATACACTCTCTGCTTTTATAACATCATCTGCCAGAGAGTCAAAATTTCAACA 300
|||||
DB 241 TTTAATACACTCTCTGCTTTTATAACATCATCTGCCAGAGAGTCAAAATTTCAACA 300
|||||

QY 301 AAGTTCACTTTTCAGAAAACCCCTTTGAGGAAGACAGAAATATATATTTTTCATTTA 360
|||||
DB 301 AAGTTCACTTTTCAGAAAACCCCTTTGAGGAAGACAGAAATATATATTTTTCATTTA 360
|||||

QY 361 AAGATGAAGAAACAGCCGGGCGGACAAATGGCTAATGCTGTAAATCCAGAGTATTCGGAGG 420
|||||
DB 361 AAGATGAAGAAACAGCCGGGCGGACAAATGGCTAATGCTGTAAATCCAGAGTATTCGGAGG 420
|||||

QY 421 CTGAGGCGAGAGATCGGTTGAGCTCCAGAGTTTCAGAGCTGAGCTGATATATATATAT 480
|||||
DB 421 CTGAGGCGAGAGATCGGTTGAGCTCCAGAGTTTCAGAGCTGAGCTGATATATATATAT 480
|||||

QY 481 ACCCTGTCTACAAAAAATAACAAAAATAGATGAGTGTGGTGGCAATATATATATATAT 540
|||||
DB 481 ACCCTGTCTACAAAAAATAACAAAAATAGATGAGTGTGGTGGCAATATATATATATAT 540
|||||

QY 541 CCCAGCTACTTTGGGAGGCTAAGGTGGAGATGCTTCAGAGCTGAGCTGATATATATAT 600
|||||
DB 541 CCCAGCTACTTTGGGAGGCTAAGGTGGAGATGCTTCAGAGCTGAGCTGATATATATAT 600
|||||

QY 601 CTGAGCCATGATTTGATCAGTCTGACCTCCAGCTGGTATAGACAGAGTGAAGAATTTGTCTCA 660
|||||
DB 601 CTGAGCCATGATTTGATCAGTCTGACCTCCAGCTGGTATAGACAGAGTGAAGAATTTGTCTCA 660
|||||

QY 661 AAAAAAAGAAATGAAG 720
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DB 661 AAAAAAAGAAATGAAG 720
|||||

QY 721 GAGGGGGAGGAG 780
|||||
DB 721 GAGGGGGAGGAG 780
|||||

QY 781 GATGAACAGAGGCGAGAGAGCTTTACGTAATTTGCTATCACTGCTGTGTAAATTTGA 840
|||||
DB 781 GATGAACAGAGGCGAGAGAGCTTTACGTAATTTGCTATCACTGCTGTGTAAATTTGA 840
|||||

QY 841 CCCCCAACCCCAATTTATTGACCAAGGTTATCTTTTACCTGAGGAGAGAGAGAGAGAG 900
|||||
DB 841 CCCCCAACCCCAATTTATTGACCAAGGTTATCTTTTACCTGAGGAGAGAGAGAGAGAG 900
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QY 901 CTGGGCGCTGGGCTTTAGAAAGCTCATCTCTGAGCTTTCTGAGATCACTCCCTTTCT 960
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DB 901 CTGGGCGCTTTAGAAAGCTCATCTCTGGCCTTTCTGAGATCACTCCCTTTCTTT 960
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QY 961 TTAATTTCTTGACAGGAGTCTTCTCTCTGCTCACTCAGGCTGGAGTGCAGTGGCATATC 1020
|||||

DB 961 TTAATTTCTTGACAGGAGTCTTCTCTCTGCTCACTCAGGCTGGAGTGCAGTGGCATATC 1020
|||||

QY 1021 TCGACTCACTGTAATCTCTGCTCCGGGTTCAAGCCATTCTCTGCTCAGCTCCCTGA 1080
|||||

DB 1021 TCGACTCACTGTAATCTCTGCTCCGGGTTCAAGCCATTCTCTGCTCAGCTCCCTGA 1080
|||||

QY 1081 GATACAGGCGGCGCCACACATCTGCTAATTTTGTATTTTGTAGTAAAGATGGGTT 1140
|||||

DB 1081 GATACAGGCGGCGCCACACATCTGCTAATTTTGTATTTTGTAGTAAAGATGGGTT 1140
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QY 1141 TCATCATGTTGTCAGTGTGTTTCGAACCTCTGACCTGAGTGCAGCTGCACCTTGGC 1200
|||||

DB 1141 TCATCATGTTGTCAGTGTGTTTCGAACCTCTGACCTGAGTGCAGCTGCACCTTGGC 1200
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QY 1201 CTCCAAAGTCTGGGATTTACAGGATGAGCCACTGCGCCAGCTCAGATCCATCCCTTT 1260
|||||

DB 1201 CTCCAAAGTCTGGGATTTACAGGATGAGCCACTGCGCCAGCTCAGATCCATCCCTTT 1260
|||||

QY 1261 CTAAAGGCAACAGTCCATGTTGCAAGGGGCCATGCCACCCAGAGTTATGATACCTGG 1320
|||||

DB 1261 CTAAAGGCAACAGTCCATGTTGCAAGGGGCCATGCCACCCAGAGTTATGATACCTGG 1320
|||||

QY 1321 GACTCCAGAAATTCCTTGGCTGCTGCCATCCACATGCTCCAGGGCTGCTTGGGCTC 1380
|||||

DB 1321 GACTCCAGAAATTCCTTGGCTGCTGCCATCCACATGCTCCAGGGCTGCTTGGGCTC 1380
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QY 1381 TTCTATGCTCTGCTCAGTGTGATAGAACCTGATGATGATGATGATGATGATGATGATG 1440
|||||

DB 1381 TTCTATGCTCTGCTCAGTGTGATAGAACCTGATGATGATGATGATGATGATGATGATG 1440
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QY 1441 GTGGCTCGAGATCTGTTGCTGAGTGTAGCTGAGGAGGCTGTCAGCTGATGATGATG 1500
|||||

DB 1441 GTGGCTCGAGATCTGTTGCTGAGTGTAGCTGAGGAGGCTGTCAGCTGATGATGATG 1500
|||||

QY 1501 TCCAGTGTGCTGAGTCTTGGAAATATGATGAGGCTGGAGGTGGGAAGAGAGTGGCTTG 1560
|||||

DB 1501 TCCAGTGTGCTGAGTCTTGGAAATATGATGAGGCTGGAGGTGGGAAGAGAGTGGCTTG 1560
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QY 1561 GGGAGCTCTCTCATGCGACCTTCTTGGCCAAACTCAGTCCAACTGATGATGATGATGAT 1620
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DB 1561 GGGAGCTCTCTCATGCGACCTTCTTGGCCAAACTCAGTCCAACTGATGATGATGATGAT 1620
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QY 1621 AAATGTGAATCTGCGCTTCAAGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGACTT 1680
|||||

DB 1621 AAATGTGAATCTGCGCTTCAAGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGACTT 1680
|||||

QY 1681 GTGGCTTCCAGCTGACTTCCAGGGCTGCTTGGGCTCTTCTAGGGTCTGCTCTGAGT 1740
|||||

DB 1681 GTGGCTTCCAGCTGACTTCCAGGGCTGCTTGGGCTCTTCTAGGGTCTGCTCTGAGT 1740
|||||

QY 1741 CTCTATGAATCTTTCAGGCGAGATTCATATTTAGACTCTTTCAGCTTTGACCTGAGTTT 1800
|||||

DB 1741 CTCTATGAATCTTTCAGGCGAGATTCATATTTAGACTCTTTCAGCTTTGACCTGAGTTT 1800
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QY 1801 TGCCAGAAATAGGTGACATTTAGTTTGTGCTTGTAGTGGATGACTTAAATATTAGACA 1860
|||||

DB 1801 TGCCAGAAATAGGTGACATTTAGTTTGTGCTTGTAGTGGATGACTTAAATATTAGACA 1860
|||||

QY 1861 TGGTGTGAGGCTGCATCT 1920
|||||

DB 1861 TGGTGTGAGGCTGCATCT 1920
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QY 1921 AGTTTGTCTCCCTTACGCCAAGCAACAGAGAGTGTGGAGTCTGGAGTGGCTACAT 1980
|||||

DB 1921 AGTTTGTCTCCCTTACGCCAAGCAACAGAGAGTGTGGAGTGGCTGGAGTGGCTACAT 1980
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QY 1981 AATTTTACAGGCTGCAATCTCTGGCTGCACTTCAAAATGTATACAAACTAAATAACA 2040
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1981 AATTTTACAGACTGCAATCTCTGGCTGCACCTTACAAAATGATACAAAATAATACAA 2040
QY 2041 GTCTCTGTTTATACAGAGGAGCTGATCAATATAATGAATATAAAGAGAGCTGCTG 2100
DB 2041 GTCTCTGTTTATACAGAGGAGCTGATCAATATAATGAATATAAAGAGAGCTGCTG 2100
QY 2101 CATATGTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 2160
DB 2101 CATATGTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 2160
QY 2161 TCTTCTCTCAATATATCAAGAGAGAGCTGATGATGATGATGATGATGATGATGATG 2220
DB 2161 TCTTCTCTCAATATATCAAGAGAGAGCTGATGATGATGATGATGATGATGATGATG 2220
QY 2221 CTGGGAGCTCAGGCTGGAATCTCAAGGAGAGCTGATGATGATGATGATGATGATG 2280
DB 2221 CTGGGAGCTCAGGCTGGAATCTCAAGGAGAGCTGATGATGATGATGATGATGATG 2280
QY 2281 CAGGTTTGGGGGAAAACAAAGAGAGAGCTGATGATGATGATGATGATGATGATGAT 2340
DB 2281 CAGGTTTGGGGGAAAACAAAGAGAGAGCTGATGATGATGATGATGATGATGATGAT 2340
QY 2341 CACCCAGCTAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
DB 2341 CACCCAGCTAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
QY 2401 GAGAGATCAGGCTAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
DB 2401 GAGAGATCAGGCTAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
QY 2461 AAGGAG 2520
DB 2461 AAGGAG 2520
QY 2521 GAGTGGGAG 2580
DB 2521 GAGTGGGAG 2580
QY 2581 GAGTGGGAG 2640
DB 2581 GAGTGGGAG 2640
QY 2641 GCTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 2700
DB 2641 GCTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 2700
QY 2701 TGTGAGGAG 2760
DB 2701 TGTGAGGAG 2760
QY 2761 TGTGAGGAG 2820
DB 2761 TGTGAGGAG 2820
QY 2821 GCTTGGAGGAG 2880
DB 2821 GCTTGGAGGAG 2880
QY 2881 CGGCAAAAGCCCC 2893
DB 2881 CGGCAAAAGCCCC 2893

RESULT 12
US-09-984-827-144
; Sequence 144, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES
; FILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ. ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO: 144
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-144

Query Match 98.2%; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAGGGCATGTCGACGTCCTGTAATCTCAGTTACTCGGAGGTGGAGGTTGCAATCA 60
DB 1 ACAGGGCATGTCGACGTCCTGTAATCTCAGTTACTCGGAGGTGGAGGTTGCAATCA 60
QY 61 GCCCAGATCCACGATTCGACTCCAGCTGGGCAACAAAGGTGAAACTCCATCTCAATT 120
DB 61 GCCCAGATCCACGATTCGACTCCAGCTGGGCAACAAAGGTGAAACTCCATCTCAATT 120
QY 121 AAAAAAAGAAATGATTTTGGTGGCTTCAATAGTAGGAGAGAGAGAGAGAGAGAG 180
DB 121 AAAAAAAGAAATGATTTTGGTGGCTTCAATAGTAGGAGAGAGAGAGAGAGAGAG 180
QY 181 AGATGGAGGTCAGGAGATCTAATTACTCTCTAAATCATGCTAGGAGAGATACACCT 240
DB 181 AGATGGAGGTCAGGAGATCTAATTACTCTCTAAATCATGCTAGGAGAGATACACCT 240
QY 241 TTTAATAACACTCTCTCTCTTTAATACATCAATCTGCCAGGAGCTCAAGGTTTCAACA 300
DB 241 TTTAATAACACTCTCTCTCTTTAATACATCAATCTGCCAGGAGCTCAAGGTTTCAACA 300
QY 301 AAGTTCACTTTCAGAAAACCCCTTTGAGGAGAGACAGATATACATCTCTCTCCATTTA 360
DB 301 AAGTTCACTTTCAGAAAACCCCTTTGAGGAGAGACAGATATACATCTCTCTCCATTTA 360
QY 361 AAGATGAAGAAACAGCCCGGAGCAATGGTAAATGCTGTATATCCAGCACTTGGAGAG 420
DB 361 AAGATGAAGAAACAGCCCGGAGCAATGGTAAATGCTGTATATCCAGCACTTGGAGAG 420
QY 421 CTGAGGCAAGAGATCGCTTGAGCTCCAGAGTTTGAGACCAGCTCGATATAACATGCAAA 480
DB 421 CTGAGGCAAGAGATCGCTTGAGCTCCAGAGTTTGAGACCAGCTCGATATAACATGCAAA 480
QY 481 ACCCTGTCTTACAAAAAATACAAAAATAGATGGGTGTGGCATGCACCTGTGCT 540
DB 481 ACCCTGTCTTACAAAAAATACAAAAATAGATGGGTGTGGCATGCACCTGTGCT 540
QY 541 CCCAGCTACTTGGAGGCTAAGGTGGGAGGATCGCTTGAGCCAGGAGTCAAGCTACAC 600
DB 541 CCCAGCTACTTGGAGGCTAAGGTGGGAGGATCGCTTGAGCCAGGAGTCAAGCTACAC 600
QY 601 CTGAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 CTGAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 AAAAAAGAAATGAAG 720
DB 661 AAAAAAGAAATGAAG 720
QY 721 GAGGGGGAG 780
DB 721 GAGGGGGAG 780

781 GATGAACAGAGGAGAGAGACTTTAGCTAAATTCCTCATCATGTGGTGTGAAGTTGA 840
781 CATGAACAGAGGAGAGAGACTTTAGCTAAATTCCTCATCATGTGGTGTGAAGTTGA 840
841 CCCCCAACCCAAATTTATTGACCAAGGTATATCTTCTGACTGAGGCAAGGCTTCCGCTCT 900
841 CCCCCAACCCAAATTTATTGACCAAGGTATATCTTCTGACTGAGGCAAGGCTTCCGCTCT 900
901 CCTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATCCATPCTTTTCTTT 960
901 CCTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATCCATPCTTTTCTTT 960
961 TTATTTTCTTGACACGAGTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
961 TTATTTTCTTGACACGAGTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
1021 TCGACTCAGCTTAACCTCTGCTCCGGGTTCAAGGCAATCTCTGCTGCTGCTGCTGCTGCTG 1080
1021 TCGACTCAGCTTAACCTCTGCTCCGGGTTCAAGGCAATCTCTGCTGCTGCTGCTGCTGCTG 1080
1081 GATAACAGGCGGCGCCACCACATCTGGCTAAATTTTCTATTTTAGTAAAGCTTGGTT 1140
1081 GATAACAGGCGGCGCCACCACATCTGGCTAAATTTTCTATTTTAGTAAAGCTTGGTT 1140
1141 TCATCATCTTGGCCAGGTTGGTTTCCGACCTCTGACCTGACCTGACCTGACCTGACCTG 1200
1141 TCATCATCTTGGCCAGGTTGGTTTCCGACCTCTGACCTGACCTGACCTGACCTGACCTG 1200
1201 CTCGCAAGGCTGGGATTACAGGATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAG 1260
1201 CTCGCAAGGCTGGGATTACAGGATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAG 1260
1261 CTAAAGGCTAAAGCTTCCATGGTGCAGAGGCGGCTATGACCTGACCTGACCTGACCTG 1320
1261 CTAAAGGCTAAAGCTTCCATGGTGCAGAGGCGGCTATGACCTGACCTGACCTGACCTG 1320
1321 GACTCCAGAAATTCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1321 GACTCCAGAAATTCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1321 GACTCCAGAAATTCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1321 GACTCCAGAAATTCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
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1381 TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1441 GTGCTGCTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
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1501 TGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1501 TGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1561 GAGCAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
1561 GAGCAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
1621 AAATGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
1621 AAATGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
1681 GTGGCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
1681 GTGGCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
1741 CTCTATGAACTCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
1741 CTCTATGAACTCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
1801 TGGCAGAAATAGGCTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
1801 TGGCAGAAATAGGCTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
1861 TGGCAGAAATAGGCTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
1861 TGGCAGAAATAGGCTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920

RESULT 13

1861 TGGTGTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
1921 AGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
1921 AGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
1981 AATTTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
1981 AATTTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
2041 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
2041 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
2101 CATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
2101 CATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
2161 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
2161 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
2221 CTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
2221 CTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
2281 CAGGTTTGTGGGGGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2340
2281 CAGGTTTGTGGGGGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2340
2341 CACCCAGCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
2341 CACCCAGCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
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2461 AAGGAAAAAAATTCGGGAAAGGAGGATTTAGAGGAGGAGGATTTAGAGGAGGAGGATTTAG 2520
2461 AAGGAAAAAAATTCGGGAAAGGAGGATTTAGAGGAGGAGGATTTAGAGGAGGAGGATTTAG 2520
2521 GGTGCT 2580
2521 GGTGCT 2580
2581 GGTGCT 2640
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2641 GGTGCT 2700
2641 GGTGCT 2700
2701 TGTGCT 2760
2701 TGTGCT 2760
2761 TGTGCT 2820
2761 TGTGCT 2820
2821 GCTTTGCT 2880
2821 GCTTTGCT 2880
2881 GGTGCT 2940
2881 GGTGCT 2940

481 ACCTGTCTCTACAAAAAATACAAAAATTAGATGGGTGGTGGCATGTAATCTGGT 546
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541 CCCAGCTACTTGGGAGCTAAGGTGGGAGGATCGCTTGACCTCAGGAGCTAAGCTTACA 500
Qy
541 CCCAGCTACTTGGGAGCTAAGGTGGGAGGATCGCTTGACCTCAGGAGCTAAGCTTACA 500
Db
541 CCCAGCTACTTGGGAGCTAAGGTGGGAGGATCGCTTGACCTCAGGAGCTAAGCTTACA 500
Qy
601 CTGAGGCTATGATGGATCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 960
Db
601 CTGAGGCTATGATGGATCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 960
Qy
661 AAAAAAGAAATGAAG 720
Db
661 AAAAAAGAAATGAAG 720
Qy
721 CAGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db
721 CAGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Qy
781 GATGAAACAGAGGAG 840
Db
781 GATGAAACAGAGGAG 840
Qy
841 GCTGAAACAG 900
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841 GCTGAAACAG 900
Qy
901 GCTGAAACAG 960
Db
901 GCTGAAACAG 960
Qy
961 TATTTTCTGACAGGAGGCTTGGTCTGACAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db
961 TATTTTCTGACAGGAGGCTTGGTCTGACAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Qy
1021 TCGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG 1080
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1021 TCGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG 1080
Qy
1081 GATGAAACAG 1140
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1081 GATGAAACAG 1140
Qy
1141 TCATCATGTTGGGAGGCTTGGTCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
Db
1141 TCATCATGTTGGGAGGCTTGGTCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
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1201 CTGCAAGAGTCTGGGATACAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1260
Db
1201 CTGCAAGAGTCTGGGATACAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1260
Qy
1261 CTAGGAGTAAACAGTCCATGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
Db
1261 CTAGGAGTAAACAGTCCATGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
Qy
1321 GACTCCAGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db
1321 GACTCCAGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Qy
1381 TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Db
1381 TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Qy
1441 GGGGCTGGAGATCTGTTGACTGTTGACTGTTGACTGTTGACTGTTGACTGTTGACT 1500
Db
1441 GGGGCTGGAGATCTGTTGACTGTTGACTGTTGACTGTTGACTGTTGACTGTTGACT 1500
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1501 TCGAGTGGTGGGAGTCTGCAATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
Db
1501 TCGAGTGGTGGGAGTCTGCAATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
Qy
1561 GGGAGGCTCTCATGCGACCTCATCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620
Db
1561 GGGAGGCTCTCATGCGACCTCATCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620

1621 AAATGTGAATCTGGCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGCTT 1680
Qy
1621 AAATGTGAATCTGGCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGCTT 1680
Db
1681 GTGGCTCCAGTGGACCTTCAGGAGGCTTCAGGAGGCTTCCTTACGGGCTGCTGCTGAGT 1740
Qy
1681 GTGGCTCCAGTGGACCTTCAGGAGGCTTCAGGAGGCTTCCTTACGGGCTGCTGCTGAGT 1740
Db
1741 CTCTATCAATCTTCAGGAGGCTTCAGGAGGCTTCAGGAGGCTTCCTTACGGGCTGCTGCTGAGT 1800
Qy
1741 CTCTATCAATCTTCAGGAGGCTTCAGGAGGCTTCAGGAGGCTTCCTTACGGGCTGCTGCTGAGT 1800
Db
1801 TGGCAGAGTAAGGTGACATTTAGTTCCTTGGCTTGGATGATGACTTAAATATTTAGACA 1860
Qy
1801 TGGCAGAGTAAGGTGACATTTAGTTCCTTGGCTTGGATGATGACTTAAATATTTAGACA 1860
Db
1861 TGGTGTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Qy
1861 TGGTGTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Db
1921 AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Qy
1921 AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db
1921 AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Qy
1981 AATTTACAGGAGTGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Db
1981 AATTTACAGGAGTGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Qy
2041 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Db
2041 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
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2101 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
Db
2101 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
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2161 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Db
2161 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Qy
2221 CTTGGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 2280
Db
2221 CTTGGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 2280
Qy
2281 CAGGTTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
Db
2281 CAGGTTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
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2341 CACCCAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCT 2400
Db
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Db
2401 GGGAGATTCAGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCT 2460
Qy
2461 AAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
Db
2461 AAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
Qy
2521 GCT 2580
Db
2521 GCT 2580
Qy
2581 GCT 2640
Db
2581 GCT 2640
Qy
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Db
2641 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700

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QY 301 AAGTTCACCTTCAGAAACCCCTTTCAGGAAGACAGATATACACTTTCCTCCATTTCA 360
DB 301 AAGTTCACCTTCAGAAACCCCTTTCAGGAAGACAGATATACACTTTCCTCCATTTCA 360
QY 361 AAGTGAAGAAACAGGCGGGGCACAAATGGCTAATAGCTTATATCTCAAGACCTTTGGAGG 420
DB 361 AAGTGAAGAAACAGGCGGGGCACAAATGGCTAATAGCTTATATCTCAAGACCTTTGGAGG 420
QY 421 CTGAGGCCACAGGATCGCTTACGCTCCAGAGTTTGAACACAGCTGGAATAAATGGAATAA 480
DB 421 CTGAGGCCACAGGATCGCTTACGCTCCAGAGTTTGAACACAGCTTGAATAAATGGAATAA 480
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DB 481 ACCCTGTCTCTACAAAAAATACAAAAATTAGATGGGTGGTGGCATGTAATGTGGT 540
QY 541 CCCAGCTACTTGGGAGGCTAAGTGGGAGGATCGCTTGAAGGAGGAGGAGTCAAGTCTACA 600
DB 541 CCCAGCTACTTGGGAGGCTAAGTGGGAGGATCGCTTGAAGGAGGAGGAGTCAAGTCTACA 600
QY 601 CTGAGCCATGATTGGATCACTGCCTCCAGCTGGGTAGACAGCAAGACCTGTGTCTCA 660
DB 601 CTGAGCCATGATTGGATCACTGCCTCCAGCTGGGTAGACAGCAAGACCTGTGTCTCA 660
QY 661 AAAAAAGAAATGAAGAGAAAGAAAGAAAGAGAGAGAGAGATGAGGGGAGGAG 720
DB 661 AAAAAAGAAATGAAGAGAAAGAAAGAAAGAGAGAGAGAGATGAGGGGAGGAG 720
QY 721 GAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 721 GAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 GATGAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 GATGAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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DB 841 CCCAAACCCCAATTTATGACCAAGCTTATCTGATGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 CTGAGGCTTGGGCTTTAGAAAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CTGAGGCTTGGGCTTTAGAAAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TTATTTTCTGTACACGGAGTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 961 TTATTTTCTGTACACGGAGTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1021 TCGACTCACTGTAACCTTGCCTCCGGGTTCAAGGAGATCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 TCGACTCACTGTAACCTTGCCTCCGGGTTCAAGGAGATCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 GATAACAGGCGCGCCGACACATCTGGCTAAATTTTGTATTTTGTATTTTGTATTTTGT 1140
DB 1081 GATAACAGGCGCGCCGACACATCTGGCTAAATTTTGTATTTTGTATTTTGTATTTTGT 1140
QY 1141 TCATCATGTTGGCCAGGTTGGTTTCGAACTCTGCACTGAGCTGAGCTGAGCTGAGCTGAG 1200
DB 1141 TCATCATGTTGGCCAGGTTGGTTTCGAACTCTGCACTGAGCTGAGCTGAGCTGAGCTGAG 1200
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DB 1201 CTCCTCAAGTCTGGGATTACAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
QY 1261 CTAAGGGCAACAGCTCCATGGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
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DB 1321 GACTCCAGAAATCTCTGCTGGTGGCTCCACATGCACTTCCAGGCGCTCTTGGCGCTC 1380
QY 1381 TTTATGCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1381 TTTATGCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
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DB 1621 AAATGTGAATCTGCGCTTCAAGGTGGCTACAAAGGTATCTTGTCAAGGTAGAGAGCTT 1680
QY 1681 GTGGCTCCAGCTGCTTCCAGGGCTGCTTGGGCTCTTCTACGGCTCTGCTGCTGCTGCTGCT 1740
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DB 1801 TGGCAGAAATGAAGTGAATTTAGTCTTGGCTTGGATGATGATGATGATGATGATGATGATGATG 1860
QY 1861 TGGTGTGAGGCTGCTTCTGCTGCTTCTTCTGCTGCTTCTTCTGCTGCTTCTTCTGCTGCT 1920
DB 1861 TGGTGTGAGGCTGCTTCTGCTGCTTCTTCTGCTGCTTCTTCTGCTGCTTCTTCTGCTGCT 1920
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DB 1921 AGTTTGTCTGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
QY 1981 AATTTACACAGCTGCAATCTGCTGCTGCTTCAAAATGATACAAATGATACAAATGATACAA 2040
DB 1981 AATTTACACAGCTGCAATCTGCTGCTGCTTCAAAATGATACAAATGATACAAATGATACAA 2040
QY 2041 GTCTGCTGCTTCTTATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
DB 2041 GTCTGCTGCTTCTTATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
QY 2101 CATATTGCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 2160
DB 2101 CATATTGCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 2160
QY 2161 TCTTCTCTCTCAATTTATGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
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QY 2221 CCTGGGAGCTCAGGCTGGGAATCTCCAAGGAGTCTGCTGCTGCTTCTGCTGCTTCTGCTGCT 2280
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QY 2341 CAGGCTGCTGCTGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400
DB 2341 CAGGCTGCTGCTGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400
QY 2401 GGGAGATCTCAGGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460


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2401 GGGAGATTACGCTAGAGCTCTCTCTCCGCCAATCCCTCCCTCGGCTGA GAACATAAC 2450
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2461 AAGGAAAAAAATTCGGAAACAGGATTTAGACGAACCAATTCGATGATGACCTT 2520
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DB
2531 GCGTGGGGGAGCTGGACTAGAGATCTCGCGGCGAGCGCGAGCGCGAGCGCGAG 2580
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2581 GCGTCTTAGCGCGCGCGCGCGCGGGAAGGAGGAGAGAGAGAGAGAGAGAGAGAG 2640
DB
2591 GCGTCTTAGCGCGCGCGCGCGGGAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 2640
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DB
2651 GCTGCTGAGCTTACCTCCACCCACCCACCCACCCACCCACCCACCCACCCACCC 2700
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DB
2711 TCGTGGCGGCTGAACTGGCGCGCTTTAAGGGGGGGGAGGAGGAGGAGGAGGAGG 2760
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DB
2771 TCACTGAGCTGAACTACATAACAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820
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2821 GCTTTGACCGATGAACTGCGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2880
DB
2831 GCTTTGACCGATGAACTGCGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2880
QY
2881 GCGCAAAACCCC 2893
DB
2891 GCGCAAAACCCC 2893
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RESULT 17

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US-09-984-827-152
: Sequence 152, Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFLE, PATRICE
: APPLICANT: KOSIER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN APOA1 GENE, THEIR USES, AND
: FILE REFERENCE: DETECTION METHODS AND KITS THEREFOR
: CURRENT APPLICATION NUMBER: US/09/984,827
: PRIOR FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 152
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-984-827-152
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Query Match      98.2%; Score 2842; DB 9; Length 2893;
Best local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Caps 0;
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QY 1 ACAGGCGATGGTGGCAGGTGGCTGTAATCTCAGTTACTCGGAGAGTGCAGCTTCGAATGA 60
DB 1 ACAGGCGATGGTGGCAGGTGGCTGTAATCTCAGTTACTCGGAGAGTGCAGCTTCGAATGA 60
QY 61 GCGCAGATCGGACCAATTCAGCTCCAGCCTGGCGAACAAGAGTCAAACTCAATTAAT 120
DB 61 GCGCAGATCGGACCAATTCAGCTCCAGCCTGGCGAACAAGAGTCAAACTCAATTAAT 120
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QY 121 AAAAAAAGAAATGATTTGGTGGTGGCTCAATAGCTAGGAGAGAGAGAGAGAGG 180
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DB 181 AGATGGAGGGTTCAGGAGATCTAATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 TTTAATAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 241 TTTAATAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 AAGTTTCATCTTCAGAAACCCCTTTGAGGAAGACAGAAATATACATCTCTCTCTCTCT 360
DB 301 AAGTTTCATCTTCAGAAACCCCTTTGAGGAAGACAGAAATATACATCTCTCTCTCTCT 360
QY 361 AAGTGAAGAAGAACAGGCGGGGACAAATGGCTTAATGCCAGTGTGATCCAGACATCTGG 420
DB 361 AAGTGAAGAAGAACAGGCGGGGACAAATGGCTTAATGCCAGTGTGATCCAGACATCTGG 420
QY 421 CTGAGGCGAGAGGATCGCTTGAGCTCCAGAGCTTTGAGCAGCAGCTTGATAAATGCAAA 480
DB 421 CTGAGGCGAGAGGATCGCTTGAGCTCCAGAGCTTTGAGCAGCAGCTTGATAAATGCAAA 480
QY 481 ACCCTGTCTCTACAAAAAATACAAAAATAGATGGTGTGGTGGTGGTGGTGGTGGTGG 540
DB 481 ACCCTGTCTCTACAAAAAATACAAAAATAGATGGTGTGGTGGTGGTGGTGGTGGTGG 540
QY 541 CCCAGCTACTTGGAGGCTAAGGTGGGAGGATCGCTTGAGCCAGGAGTCAAGTGTCTACA 600
DB 541 CCCAGCTACTTGGAGGCTAAGGTGGGAGGATCGCTTGAGCCAGGAGTCAAGTGTCTACA 600
QY 601 CTGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 CTGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
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DB 661 AAAAAAAGAAATGAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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DB 721 GAGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 GATGAACAGAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 GATGAACAGAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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DB 841 CCCCCAACCCCAATTTATTTGACCAAGGTTATTTTCTTCTGAGCAGAGAGAGAGAG 900
QY 901 CCGTGGCCTTGGGCTTTAGAAAGCTCATCTCGGCCCTTTCTGAGATCCATCCCTTTCT 960
DB 901 CCGTGGCCTTGGGCTTTAGAAAGCTCATCTCGGCCCTTTCTGAGATCCATCCCTTTCT 960
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DB 961 TTTATTTTCTTGACAGGAGTCTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 TCGACTCACTGTAACCTCTCGCCCTCCGGGTTCAAGCGATTTCTCTGCTCAGCGCTCTGA 1080
DB 1021 TCGACTCACTGTAACCTCTCGCCCTCCGGGTTCAAGCGATTTCTCTGCTCAGCGCTCTGA 1080
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DB 1081 GATAACAGCGCCGCCACCACATCTGGCTAAATTTTGTATTTTGTATTTTGTATTAAGACT 1140
QY 1141 TCATCATGTGTGACAGGTGGTGTTCGAACCTCTGACCTGAGGTGAGGTGCGCCACTTGGC 1200
DB 1141 TCATCATGTGTGACAGGTGGTGTTCGAACCTCTGACCTGAGGTGAGGTGCGCCACTTGGC 1200
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QY 1201 CTCCAAAGTGTGGGATTACAGCATGACCCACTGCGCCAGCTCAGATCATCCCTTT 1260
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QY 1261 CTAAGGCAACAGTTCATGTCGAAGGGCCATGCCACCCAGAGTTATATATCTCTGG 1320
DB 1261 CTAAGGCAACAGTTCATGTCGAAGGGCCATGCCACCCAGAGTTATATATCTCTGG 1320
QY 1421 GACTCCAGAATTCCTTCCCTGGTGGCTGCACATGCACTCTGAGGAGCTGCTGAGGCTG 1480
DB 1421 GACTCCAGAATTCCTTCCCTGGTGGCTGCACATGCACTCTGAGGAGCTGCTGAGGCTG 1480
QY 1481 TTTCTATGCGTCTGCTCAGTGTGTATAGAACACATGATGTAGTACCTGATTTAGGCT 1440
DB 1481 TTTCTATGCGTCTGCTCAGTGTGTATAGAACACATGATGTAGTACCTGATTTAGGCT 1440
QY 1441 GTGCCCTGGAGATCCTGTTCACTGTAGCATGGAGGGGCTGTGACGCTGAATGCTGCA 1500
DB 1441 GTGCCCTGGAGATCCTGTTCACTGTAGCATGGAGGGGCTGTGACGCTGAATGCTGCA 1500
QY 1501 GCGAGTGTGGGAGTTCTGGAATATGATGGAGCTGGAGTGGGAAGAGAAATAGGCTTG 1560
DB 1501 GCGAGTGTGGGAGTTCTGGAATATGATGGAGCTGGAGTGGGAAGAGAAATAGGCTTG 1560
QY 1561 GCGAGTGTGGGAGTTCTGGAATATGATGGAGCTGGAGTGGGAAGAGAAATAGGCTTG 1620
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DB 1681 GTGATGTAGGCTGCAATCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1741 GTGATGTAGGCTGCAATCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
DB 1741 GTGATGTAGGCTGCAATCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 TGGGCAATTAAGTGTGACATTTAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1860
DB 1801 TGGGCAATTAAGTGTGACATTTAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1860
QY 1861 TGGGCAATTAAGTGTGACATTTAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1920
DB 1861 TGGGCAATTAAGTGTGACATTTAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1920
QY 1921 AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
DB 1921 AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
QY 1981 AATTTACAGACTGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
DB 1981 AATTTACAGACTGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
QY 2041 GTCTGTGTTTTTATCAGAGGGGCTGATCAATATATGAAATATGAAATATGAAATATGAAAT 2100
DB 2041 GTCTGTGTTTTTATCAGAGGGGCTGATCAATATATGAAATATGAAATATGAAATATGAAAT 2100
QY 2101 CATATTGTTCTGCTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG 2160
DB 2101 CATATTGTTCTGCTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG 2160
QY 2161 TCTCTGCTCTCAATTTATGAAGAAGCAGTACATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
DB 2161 TCTCTGCTCTCAATTTATGAAGAAGCAGTACATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
QY 2221 CTTGGGAGCTCAGGCTGGGAACTCTCAAGGAGTACGCTATCAAAAACAAAGTCT 2280
DB 2221 CTTGGGAGCTCAGGCTGGGAACTCTCAAGGAGTACGCTATCAAAAACAAAGTCT 2280
QY 2281 CAGGTTGTGGGGGAAACAAACAGCAGGCTGATTAAGCAGAGAGTGTGTTGTTGTTGTT 2340

DB 2281 CAGGTTGTGGGGGAAACAAACAGCAGGCTGATTAAGCAGAGTGTGTTGCTTCCCTT 2340
QY 2341 CACCCAGCTTGGGCTTTTGAAGGAAACAAACAGCAGGCTGATTAAGCAGAGTGTGTTGCTT 2400
DB 2341 CACCCAGCTTGGGCTTTTGAAGGAAACAAACAGCAGGCTGATTAAGCAGAGTGTGTTGCTT 2400
QY 2401 GGGAGTTACAGCTTAGAGCTCTCTCTCCCTCAATCCCTCCCTCCCTCCCTCCCTCCCTCCCT 2460
DB 2401 GGGAGTTACAGCTTAGAGCTCTCTCTCCCTCAATCCCTCCCTCCCTCCCTCCCTCCCTCCCT 2460
QY 2461 AAGGAAACAAACAAACAGCAGGCTTGAAGGAAACAAACAGCAGGCTTGAAGGAAACAAAC 2520
DB 2461 AAGGAAACAAACAAACAGCAGGCTTGAAGGAAACAAACAGCAGGCTTGAAGGAAACAAAC 2520
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DB 2521 GGCTGCCGGGAACTGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
QY 2581 GCGTCTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
DB 2581 GCGTCTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
QY 2641 CCGTCTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
DB 2641 CCGTCTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
QY 2701 TCGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
DB 2701 TCGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
QY 2761 TGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
DB 2761 TGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
QY 2821 GCTTTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
DB 2821 GCTTTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
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DB 2881 CGGCAAAACCTCC 2893

RESULT 18

US-09-984-827-153
; Sequence 153, Application US/09984827
; Publication No. US200300563441
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMELEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
; FILE REFERENCE: 03806.0522-00000
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-153

Query Match 94.2%; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;

Matches	2892:	Conservative	0:	Mismatches	1:	Indels	0:	Gaps
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DB	1	ACAGGCGATGGCGGAGTGGCTGTAAATCTCACTTACTCGGAGGTTGGAAATGA	60					
QY	61	GCCAGATGCGCAGTTCAGCTCCAGCTGCGGCGCAACAAAGGTGAACTCTATCTTAAT	120					
DB	61	GCCAGATGCGCAGTTCAGCTCCAGCTGCGGCGCAACAAAGGTGAACTCTATCTTAAT	120					
QY	121	AAAAAAAAGAATGATTTTGGTGGTGGAGCTTCAATATAGTATAGCAAGAAATA	180					
DB	121	AAAAAAAAGAATGATTTTGGTGGTGGAGCTTCAATATAGTATAGCAAGAAATA	180					
QY	181	AGATGGAGGTCAGGAGATCTAATTTACTCTTTAAATTAAGTATAGTATAGTAT	240					
DB	181	AGATGGAGGTCAGGAGATCTAATTTACTCTTTAAATTAAGTATAGTATAGTAT	240					
QY	241	TTAATAACACTCTCTGCTTTTATAACATCAITCTGCGAGGAGGTCAAATCTTCAACA	300					
DB	241	TTAATAACACTCTCTGCTTTTATAACATCAITCTGCGAGGAGGTCAAATCTTCAACA	300					
QY	301	AAATTCATTTTCAGAAACCCCTTTGAGGAGAGAGAGATATATATCTTCTTCCATTTTA	360					
DB	301	AAATTCATTTTCAGAAACCCCTTTGAGGAGAGAGAGATATATATCTTCTTCCATTTTA	360					
QY	361	AAATTCATTTTCAGAAACCCCTTTGAGGAGAGAGAGATATATATCTTCTTCCATTTTA	420					
DB	361	AAATTCATTTTCAGAAACCCCTTTGAGGAGAGAGAGATATATATCTTCTTCCATTTTA	420					
QY	421	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	480					
DB	421	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	480					
QY	481	ACATTCATTTTCAGAAACCCCTTTGAGGAGAGAGAGATATATATCTTCTTCCATTTTA	540					
DB	481	ACATTCATTTTCAGAAACCCCTTTGAGGAGAGAGAGATATATATCTTCTTCCATTTTA	540					
QY	541	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	600					
DB	541	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	600					
QY	601	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	660					
DB	601	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	660					
QY	661	AAAAAAGAAATGAAG	720					
DB	661	AAAAAAGAAATGAAG	720					
QY	721	GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780					
DB	721	GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780					
QY	781	GATGAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840					
DB	781	GATGAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840					
QY	841	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	900					
DB	841	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	900					
QY	901	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	960					
DB	901	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	960					
QY	961	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	1020					
DB	961	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	1020					
QY	1021	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	1080					
DB	1021	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	1080					
QY	1081	GATAACAGGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1140					
DB	1081	GATAACAGGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1140					
QY	1141	TCATCATGTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1200					
DB	1141	TCATCATGTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1200					
QY	1201	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	1260					
DB	1201	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	1260					
QY	1261	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	1320					
DB	1261	CTGAGGCGATGAGGATGCTTGAAGTTCAGAGTCTGAGTTCAGAGTTCAGAGTTCAGAGT	1320					
QY	1321	GATCCAGAAATGCTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT	1380					
DB	1321	GATCCAGAAATGCTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT	1380					
QY	1381	TTCTAAGGCTCTGTCTCTGAGTGTCTGATAGAACCACTGATGTGAGTACCTGGGCTTGA	1440					
DB	1381	TTCTAAGGCTCTGTCTCTGAGTGTCTGATAGAACCACTGATGTGAGTACCTGGGCTTGA	1440					
QY	1441	GTGGCTGAGATCTCTGTTGACCTGAGTATGGAGGGGGCTGTGACACTCAATCTGTGCA	1500					
DB	1441	GTGGCTGAGATCTCTGTTGACCTGAGTATGGAGGGGGCTGTGACACTCAATCTGTGCA	1500					
QY	1501	TGCAGTGGCTGAGTCTGTGGAATATGATGGAGTGGAGGTGGGAGAGAACTAGAGCTTG	1560					
DB	1501	TGCAGTGGCTGAGGATCTGTGGAATATGATGGAGTGGAGGTGGGAGAGAACTAGAGCTTG	1560					
QY	1561	GCGAGGCTCTCTATGGCACTCTCATCTGGCCCAAACTCAGGTCAGAACTGCGAGAGCTCT	1620					
DB	1561	GCGAGGCTCTCTATGGCACTCTCATCTGGCCCAAACTCAGGTCAGAACTGCGAGAGCTCT	1620					
QY	1621	AAATGTGAATCTGAGCTCTCAAGTGGCTGACAAAGGTATCTTTGTCAAGGTAGGAGACTT	1680					
DB	1621	AAATGTGAATCTGAGCTCTCAAGTGGCTGACAAAGGTATCTTTGTCAAGGTAGGAGACTT	1680					
QY	1681	GTGGCTGAGATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	1740					
DB	1681	GTGGCTGAGATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	1740					
QY	1741	CTCTCTGAATCTCTGAGGAGAGATTCATATTTAGACTCTTTCACAGTTTTCAGCTGAGT	1800					
DB	1741	CTCTCTGAATCTCTGAGGAGAGATTCATATTTAGACTCTTTCACAGTTTTCAGCTGAGT	1800					
QY	1801	TGGGCAAGATTAAGGTGAGATTTAGTTTGTGGCTTGAATGGATGACTTAAATATTTAGACA	1860					
DB	1801	TGGGCAAGATTAAGGTGAGATTTAGTTTGTGGCTTGAATGGATGACTTAAATATTTAGACA	1860					
QY	1861	TGGGCTGAGATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	1920					
DB	1861	TGGGCTGAGATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	1920					
QY	1921	AGTTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	1980					
DB	1921	AGTTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	1980					
QY	1981	AATTTTACAGATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	2040					
DB	1981	AATTTTACAGATCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	2040					
QY	2041	GAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	2100					
DB	2041	GAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	2100					
QY	2101	GAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	2160					
DB	2101	GAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	2160					

QY 2161 TCCTTCCTCAATTTATGAAGAGAGCAGTAGAAGTTCCTCTCTGGGTCCTCTGAGGGA 2220
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DB 2221 CTTGGGAGCTCAGGCTGGCAATCTCCAAAGGAGTAGGTCCTCTCAAAAGAGTGAAGT 2280
QY 2281 CAGGTTTGTGGGGGAAAGCAAAAGCAGGCTATTACAGAGAGAGTGTCTCTCTCTCT 2340
DB 2281 CAGGTTTGTGGGGGAAAGCAAAAGCAGGCTATTACAGAGAGAGTGTCTCTCTCTCT 2340
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DB 2341 CAGCCAGCTAGGCTTTTAAAGAGAAACAAAGCAAGCAACAAATGATCTCTCTCTCT 2400
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DB 2521 GGTTCGGGGAACCTGGACTAGAGAGTCTGCGGCGAGGCGCCAGGCGGCTCTCTCT 2580
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DB 2581 GGTTCGTTAGGCGGGGCGGGCGGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
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DB 2821 GCTTTCAGGATAGTAACTCTCGCTCGCTGAGGCGGAATCTATAAAGAGTAACT 2880
QY 2881 GGGCAAAACCCC 2893
DB 2881 GGGCAAAACCCC 2893

RESULT 19
US-09-846-827-154
Sequence 154, Application US/09984827
Publication No. US20030056234A1
GENERAL INFORMATION:
APPLICANT: DENEUF, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN APO(A) GENE, THEIR USES, AND
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0322-00000
CURRENT APPLICATION NUMBER: US/09/984.827
PRIOR FILING DATE: 2002-04-01
PRIOR FILING DATE: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 154
LENGTH: 2893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-827-154
Query Match 98.2%, Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 ACAGGGCATGCTGCTAGCTGCTCTAATCTCAGTTATCTGGGAGGTCGAGGTTGCAATGA 60
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DB 61 GCGCAGATCGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
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DB 121 AAAAAAAGCAATGATTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
QY 181 AGATGGAGGTCAGGAGATCTAATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 AGATGGAGGTCAGGAGATCTAATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 TTTAATAACACT 300
DB 241 TTTAATAACACT 300
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DB 301 AAGTTTACCTTTTCAAAACCCCTTTGAGGAGAGCAGATATACATCTCTCTCTCTCT 360
QY 361 AAGTGAAGAAACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
DB 361 AAGTGAAGAAACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 421 CTGAGGCGCAGAGATCGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 480
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DB 661 AAAAAAAGCAATGAAAG 720
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DB 1921 AGTTTCTCTCCCTACAGCCAAAGCCAAACAGACAGAGTTGGAGCTCTGACTGCTACAT 1980
QY 1981 AATTTTACAGGACTGCAATTTCTCTGGCTGACATTCACAAATGATATAAAATAAATACAA 2040
DB 1981 AATTTTACAGGACTGCAATTTCTCTGGCTGACATTCACAAATGATATAAAATAAATACAA 2040
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DB 2041 GTCTGTGTGTTTATACAGAGGAGGCTGATCAATAATGAATTAATAAAGTTCCTGCTG 2100
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QY 2161 TCTTCTCTCAATTTATGAAGAGAGCAGTAAGATTTCTCTGCTGCTGCTGCTGCTGCTG 2220
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DB 2581 GCGTCTTAGCGCGGGGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
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DB 2821 GCTTTGAGGAGTACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2880
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RESULT 2:

105-09-984-827-157

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; Sequence 157, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEPIE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806-0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-157
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Query Match 98.2%; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 121 AAAAAAAGAGATGATTTGGTGGTGGTCTCAATAGTGTAGAGAGAGAGAGAGAGAG 180
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DB 361 AAGATCAAGAAACAGCGCGGCGCAATGGCTAATGCCCTGTAAATCCAGCAGCTTTGGAGG 420
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DB 541 CCCAGCTACTTGGAGGCTAAGGTGGGAGGATCGCTTTCAGGCCAGGAGTCAAGTCTACA 600
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DB 601 CTGAGCCATGATTTGATCAGTCCAGCTCCAGCTGGGTAGACAGAGAGAGAGAGAGAG 660
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QY 1621 AAATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTCTCAAGTATGAGACCTT 1680
Db 1621 AAATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTCTCAAGTATGAGACCTT 1680
QY 1681 GTGGCTCCACGTCACTTCAGGGCCIGCTTGGGCTCTCTTACGGGTCTGTCCTCAGT 1740
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QY 1741 GTTCTATGAATCCCTTCAGGCGAGATTCATATTAGACTCTTCAGTITTCATGTAGTIT 1800
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Db 1801 TGCCAGAAATAGGTGACATTTAGTTTGGCTTTTATGATGATGATGATGATGATGATG 1859
QY 1860 -ATGCTGTAGGCTGCATCTCTACTCTTGCCTTTTCTTGGCTGCTGCTGCTGCTGCTGCTG 1918
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QY 1919 GTAGTTTGTCTCCCTTACAGCAAGGCAACAGAGAGAGTGGAGGTCTGAGTGGCTAC 1978
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Db 2761 GCTGAGTGAATCACTACATAAAGAGAGCGCGGAGGAGGCGGCGGAGGAGGAGGAGGAG 2820
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Db 2821 AGGCTTTGACCATATAGTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
QY 2879 CCGGCAAAAAAGCC 2893
Db 2881 CCGGCAAAAAAGCC 2895
RESULT 23
US-09-846-827-156
; Sequence 156, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PAIRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 2888
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-156
Query Match 92.3%, Score 2670, DB 9, Length 2888;
Best Local Similarity 100.0%, Pred. No. 0;
Matches 2670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGGCGATGTCGTCAGGTGGCTGTAATCTCAGTTACTCGGAGGTGGAGGTTCGAATGA 60
Db 1 ACAGGCGATGTCGTCAGGTGGCTGTAATCTCAGTTACTCGGAGGTGGAGGTTCGAATGA 60
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Db 61 GCCAGATCGGCACCATTTTGGTGGTGCATTCCTCCAGCTGGGCAACAAAGGTGAACTCCTCAAT 120
QY 121 AAAAAAAGAAATGATTTTGGTGGTGCATTCCTCAATAGGTAGGAGAGAGAGGAGG 180
Db 121 AAAAAAAGAAATGATTTTGGTGGTGCATTCCTCAATAGGTAGGAGAGAGAGGAGG 180
QY 181 AGATGAGGTCGAGGAGATCTAATTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
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QY 241 TTTAATAACACATCA 300
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QY 301 AAGTTTCACTTTTCAAGAAACCCCTTTGAGGAGAGAGAGATATACATCTCTCTCTCTCTCT 360
Db 301 AAGTTTCACTTTTCAAGAAACCCCTTTGAGGAGAGAGAGATATACATCTCTCTCTCTCTCT 360
QY 361 AAGATGAAGAAACAAACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420

361 AAGATGAAGAAACAGCGCGGCACAAATGGCTAATGGCTGTATATCCAGCA-ATTGGGAGG 420
421 CTGAGGCCAGAGATCGCTTGAGCTCCAGAGTTTGACACGAGCTGGATAAATGCGCAAA 480
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781 GATGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
781 GATGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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841 CCCCAAAACCCAAATTTATTGACCAAGGTTATCTCTGACGAGGAGGAGGAGGAGGAG 900
901 CTTGGGCTTGGGCTTTAGAAGGCTCATCTCTGAGGCTTTGAGAGTCAATCTTTTCTT 960
901 CTTGGGCTTGGGCTTTAGAAGGCTCATCTCTGAGGCTTTGAGAGTCAATCTTTTCTT 960
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1021 TCGACTCATCTGTAACCTCTGCCICCGGGTTCAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
1081 GATACAGGCGCGCCGACCATCTGGCTAAATTTTGCTGATCTGATCTGATCTGATCTG 1140
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1261 CTAAAGGCAACAGTCCATGCTGCAAGGCGGCAATCTGATCTGATCTGATCTGATCTGAT 1320
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1321 CACTCCAAATTCCTTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
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1621 AAATGTGAATCTGGCCTTCAAGTGGCTACAAAGGATATCTTTGTCAAGGTAGGAGACCT 1680
1681 GTGGCTCCAGCTGTACATCTCCAGGCGCTGCTTGGGCGCTCTTCTACAGGCTGTGCTGAGT 1740
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1741 CTCTATGAAATCTCTCAGGCGAGATTCATATTTAGACTCTTCACAGTTTGGACTCAGTTT 1800
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1861 TGGTGTAGGTCTGATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920
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1981 AATTTTACAGGAGTCAATTTCTTGGCTGACCTTCAAAATGATATACAACTTAAATACAA 2040
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2041 GTCCCTGTGTTTATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
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2161 TCTTCTCTCTCAATTTATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
2161 TCTTCTCTCTCAATTTATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
2221 CTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
2221 CTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
2281 CAGGTTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2340
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2461 AAAGTAAAAAATAAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
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2521 GAG 2580
2521 GAG 2580


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DB 1561 GGGAGGCTCTCTCATGCGACCTCATTTCTGGCCAAACACTCAGGTCAAACTGTAAGAGCTCT 1620
QY 1621 AAATGTGAATCGCCCTTCAAGGTGCTACAAAGGTATCTTTCTCAAGGTAAGAGCTCT 1680
DB 1621 AAATGTGAATCGCCCTTCAAGGTGCTACAAAGGTATCTTTCTCAAGGTAAGAGCTCT 1680
QY 1681 GTGGCTCGACGCTGCACTTCCAGGCGCTGCTTGGGCTGCTTCTAGGCTGCTTCTAGGCT 1740
DB 1681 GTGGCTCGACGCTGCACTTCCAGGCGCTGCTTGGGCTGCTTCTAGGCTGCTTCTAGGCT 1740
QY 1741 GTTCTATGAATCGCTTCAAGGCGAGATTCATATTTAGACCTCTTCAAGCTTTTCAAGCTTT 1800
DB 1741 GTTCTATGAATCGCTTCAAGGCGAGATTCATATTTAGACCTCTTCAAGCTTTTCAAGCTTT 1800
QY 1801 TGGGAGAAATAGGTGACATTTAGTCTTGGCTGTAGGATGATTTAAATATTAAGACA 1860
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QY 1921 AGTTTGTGCTGCTTACAGGCGAAAGCAAGAGAGAGTGGAGGCTGGAAGGCTGGAAGT 1980
DB 1921 AGTTTGTGCTGCTTACAGGCGAAAGCAAGAGAGAGTGGAGGCTGGAAGGCTGGAAGT 1980
QY 1981 AATTTACAGGCTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
DB 1981 AATTTACAGGCTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
QY 2041 GTCCTGTGTTTATCAGGCGAGGCTGATCAATATAATAGAAATTAAGAAATGCTGCTGCT 2100
DB 2041 GTCCTGTGTTTATCAGGCGAGGCTGATCAATATAATAGAAATTAAGAAATGCTGCTGCT 2100
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DB 2101 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
QY 2161 TCTGCTGCTCAATTTATGAAGAGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
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QY 2221 GCTGGGAGCTCAGGCTGGAATCTCGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
DB 2221 GCTGGGAGCTCAGGCTGGAATCTCGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
QY 2281 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
DB 2281 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
QY 2341 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
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QY 2401 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
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DB 2521 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
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DB 2757 TGAGTCACTGAACATACATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2816
QY 2821 GCTTTGACGATAGTAGTAACCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 2880
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US-09-984-827-151
; Sequence 151, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: KOSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOLD-REGUIGNIE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBLEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABC1 GENE, THEIR USES,
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.9522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254.108
; PRIOR FILING DATE: 2000-12-11
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 151
; LENGTH: 2884
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-151
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Query Match 78.9%; Score 2284; DB 9; Length 2884;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2884; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

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QY 181 AGATGGAGGCTCAGGAGATCTAATTACTCTCTAAATCATGCTAGGAAGATAACACCT 240
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QY 241 TTTAATAACACTCTCTGCTTTTAAACATCATTTCTCCAGGAGGTCAAAGGTTCACACA 300
DB 241 TTTAATAACACTCTCTGCTTTTAAACATCATTTCTCCAGGAGGTCAAAGGTTCACACA 300
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QY	421	CTGAGCCACAGGATCGCTTGAGCTCCAGAGTTTCAGACACAGCCCTGGATAACATGCGTAAA	480
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QY	481	ACCTGTCTCTACAAAAAAATACAAAAATTAGATGGGTGTGCTGGCATGTACTGTGGT	540
DB	481	ACCTGTCTCTACAAAAAAATACAAAAATTAGATGGGTGTGCTGGCATGTACTGTGGT	540
QY	541	CCAGCTACTTGGGAGGCTTAAGTGGGGAGATCGCTTCAGCCACAGGAGTGAAGTCTTACA	600
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QY	601	CTGAGCCATCATTTGGATCACTGCATCCAGCCCTGGTACAGACAGCAGACCTGTGTCTCA	660
DB	601	CTGAGCCATCATTTGGATCACTGCATCCAGCCCTGGTACAGACAGCAGACCTGTGTCTCA	660
QY	661	AAAAAAGAAATCAAGAGAAACAAAGAAAGAGGAGAGAGGAGATGACGCGAGGAGG	720
DB	661	AAAAAAGAAATCAAGAGAAACAAAGAAAGAGGAGAGGAGATGACGCGAGGAGG	720
QY	721	GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
DB	721	GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
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DB	781	GATGAACACAGGACAGAAAGACTTTAGCTTAATTCCTCACTATGCTGGTGAAGTTTGA	840
QY	841	CCCAAAACCCAAATTTATTGACCAAGGTTATCTTTGACGAGGAGAGGAGGAGGAGGAGG	900
DB	841	CCCAAAACCCAAATTTATTGACCAAGGTTATCTTTGACGAGGAGAGGAGGAGGAGGAGG	900
QY	901	CTGGGGCTTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATGACATGATTTCTTT	960
DB	901	CTGGGGCTTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATGACATGATTTCTTT	960
QY	961	TATTTTCTTGACCGAGCTCTGCTCTGTCACATCAATGAGATGTGATGATGATGATGATG	1020
DB	961	TATTTTCTTGACCGAGCTCTGCTCTGTCACATCAATGAGATGTGATGATGATGATGATG	1020
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DB	1021	TGCACTCACTGTAACTCTCTGCTCCGGGTTCAGGCAATCTCTGCTCTGCTCTGCTCTG	1080
QY	1081	GATACAGGCGCGCGCCACACATCTGGCTAATTTTCTTATTTTAAAGAGTGTGGTT	1140
DB	1081	GATACAGGCGCGCGCCACACATCTGGCTAATTTTCTTATTTTAAAGAGTGTGGTT	1140
QY	1141	TCATCATGTTGGCAGGTTGGTTTGAATCTGATCTGAGGTGAATGATGATGATGATGATG	1200
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QY	1201	CTCCCAAAGTGTGGGATTACAGGATGAGGACATGAGGTGGGTGAGCTCAGATGATGATG	1260
DB	1201	CTCCCAAAGTGTGGGATTACAGGATGAGGACATGAGGTGGGTGAGCTCAGATGATGATG	1260
QY	1261	CTAAGGCAACAGTCCATGGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1320
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QY	1321	GACTCCAGAAATTCCTTGGCTGTGGGCTCCATGACATGACATGACAGGAGGAGGAGGAGG	1380
DB	1321	GACTCCAGAAATTCCTTGGCTGTGGGCTCCATGACATGACATGACAGGAGGAGGAGGAGG	1380
QY	1381	TCTATCGCTCTGCTCTGAGTGTGATGAACACATGATGATGATGATGATGATGATGATG	1440
DB	1381	TCTATCGCTCTGCTCTGAGTGTGATGAACACATGATGATGATGATGATGATGATGATG	1440
QY	1441	GTGCGCTGGAGATTCCTTCTGACTGTAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1500

[illegible]


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QY 1371 CTTGGGCTCTTCTATCGCTCTGCTCACTGTGATAGAACACACATGATCTAGTACCTG 1430
Db 1381 CTTGGGCTCTTCTATCGGCTCTGCTCACTGTGATAGAACACACATGATCTAGTACCTG 1440
QY 1411 GGCTTGAGCGCTGGCCCTGGAGATCCTGTTGACTGTAGCAAGGAGGGGTCTCTGGAGCTG 1490
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Db 2041 CTAAATACAAATCTCTGTTTATACAGAGAGGCTGATCAATATATGAATATTAAG 2100
QY 2091 GGGGCTGCTCATATGCTGCTGTTTCTTCTTGTGTTGTTGTTGTTGTTTGT 2150
Db 2101 GGGGCTGCTCATATGCTGCTGTTTCTTCTTGTGTTGTTGTTGTTGTTTGT 2160
QY 2151 TTTGTGCTCTCTCTCTCTCAATTTATGAAGAGAGCTAGTAACTGCTCTGCTGCTG 2210
Db 2161 TTTGTGCTCTCTCTCTCTCAATTTATGAAGAGAGCTAGTAACTGCTCTGCTGCTG 2220
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Db 2641 CCTAAGACACCTGCTGTAACCTCCACCCACCCACCCACCCACCCACCCACCCACCCAC 2700
QY 2691 CCTAGATGCTGCTGCGGCGCTGAGCTGCGCCGTTTAAAGGGGCGGCGCGCTCCAG 2750
Db 2701 CCTAGATGCTGCTGCGGCGCTGAGCTGCGCCGTTTAAAGGGGCGGCGCGCTCCAG 2760
QY 2751 TGTCTTCTCTGAGTGAACCTACATAACAGAGCGCGGAGGAGGAGGAGGAGGAGGAGG 2810
Db 2761 TGTCTTCTCTGAGTGAACCTACATAACAGAGCGCGGAGGAGGAGGAGGAGGAGGAGG 2820
QY 2811 GAGAGCAGAGCTTTGACCGATAGTAACCTGCTGCGTCTGCGAGCGCGGAGTCTATAAAG 2870
Db 2821 GAGAGCAGAGCTTTGACCGATAGTAACCTGCTGCGTCTGCGAGCGCGGAGTCTATAAAG 2880
QY 2871 GAACCTAGTCTCCGCAAAACCC 2893
Db 2881 GAACCTAGTCTCCGCAAAACCC 2903

RESULT 27
US-09-770-689A-3
; Sequence 3, Application US/09770689A
; Patent No. US20020115171A1
; GENERAL INFORMATION:
; APPLICANT: VAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01079
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 98865
; TYPE: DNA
; ORGANISM: HUMAN
US-09-770-689A-3

Query Match 1.9% Score 54; DB 10; Length 98865;
Best Local Similarity 100.0%; Pred. No. 2.le-17;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCCACCTTGGCTCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCC 1240
Db 5881 CTGCCCACCTTGGCTCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCC 5934

RESULT 28
US-10-125-540-545/c
; Sequence 545, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: kosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
```


; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 545
; LENGTH: 5351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-540-545

Query Match 1.8%; Score 52; DB 9; Length 5351;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1193 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 989 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 938

RESULT 24
US-09-764-870-545/c

; Sequence 545, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 545
; LENGTH: 5351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-545

Query Match 1.8%; Score 52; DB 10; Length 5351;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1193 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 989 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 938

RESULT 30
US-10-125-540-546/c

; Sequence 546, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 546
; LENGTH: 6461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-540-546

Query Match 1.8%; Score 52; DB 9; Length 6461;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1193 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||

DB 4277 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 4226

RESULT 31

US-09-764-870-546/c
; Sequence 546, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 546
; LENGTH: 6461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-546

Query Match 1.8%; Score 52; DB 10; Length 6461;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1193 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 4277 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 4226

RESULT 32

US-09-764-891-5924
; Sequence 5924, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5924
; LENGTH: 10901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-5924

Query Match 1.8%; Score 52; DB 9; Length 10901;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1189 GCCACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 1240
|||||
DB 3932 GCCACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 3983

RESULT 33

US-10-224-562-3/c
; Sequence 3, Application US/10224562
; Publication No. US2003002229A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3
LENGTH: 53332
TYPE: DNA
ORGANISM: Homo sapiens
US-10-224-562-3

Query Match
Best Local Similarity 100.0%; Score 52; DB 9; Length 5332;
Mismatches 0; Conservative 0; Indels 0; Gaps 0;
QY 1190 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGGCT 1241
|||||
DB 46511 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGGCT 46460

RESULT 34
US-09-801-861-3/C
Sequence 3, Application US/09801861
Patent No. US20020119544A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001098
CURRENT APPLICATION NUMBER: US/09/801,861
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 53332
TYPE: DNA
ORGANISM: Human
US-09-801-861-3

Query Match
Best Local Similarity 100.0%; Score 52; DB 10; Length 5332;
Mismatches 0; Conservative 0; Indels 0; Gaps 0;
QY 1190 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGGCT 1241
|||||
DB 46511 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGGCT 46460

RESULT 35
US-09-764-891-6418/C
Sequence 6418, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6418
LENGTH: 17904
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-6418

Query Match
Best Local Similarity 100.0%; Score 51; DB 9; Length 17904;
Mismatches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1190 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGGCT 1240
|||||
DB 4415 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGGCT 4265

RESULT 36

US-09-764-877-2678/C
Sequence 2678, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2678
LENGTH: 26591
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-2678

Query Match
Best Local Similarity 100.0%; Score 51; DB 10; Length 26591;
Mismatches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGC 1237
|||||
DB 11281 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGC 11231

RESULT 37
US-09-563-728A-36
Sequence 36, Application US/09563728A
Publication No. US20030078216A1
GENERAL INFORMATION:
APPLICANT: MacLeod, Alan R
APPLICANT: Li, Zoumei
TITLE OF INVENTION: Inhibition of Histone Deacetylase
FILE REFERENCE: 106101.229
CURRENT APPLICATION NUMBER: US/09/563,728A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/132,287
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 122186
TYPE: DNA
ORGANISM: Homo sapiens
US-09-563-728A-36

Query Match
Best Local Similarity 100.0%; Score 51; DB 9; Length 122186;
Mismatches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGGCTGGCCAGC 1244
|||||
DB 65150 CTTGGCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGGCTGGCCAGC 65200

RESULT 38
US-09-880-107-3814
Sequence 3814, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, David T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Owe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14

;; PRIOR APPLICATION NUMBER: US 60/237,054
;; PRIOR FILING DATE: 2000-10-02
;; NUMBER OF SEQ ID NOS: 3950
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3814
;; LENGTH: 198285
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. US20020142581A1 X87344
US-09-880-167-3814

Query Match 1.7% Score 51; DB 10; Length 198285;
Best Local Similarity 100.0%; Pred. No. 8,1e-16;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1190 CCACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTGCGG 1240
|||||
DB 3571 CCACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTGCGG 1621

RESULT 39
US-10-091-504-1779
;; Sequence 1779, Application US/10091504
;; Publication No. US2003005908A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC00701
;; CURRENT APPLICATION NUMBER: US/10/091,504
;; CURRENT FILING DATE: 2002-03-07
;; NUMBER OF SEQ ID NOS: 2442
;; Prior Application removed - See File Wrapper of Pat.
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1779
;; LENGTH: 5819
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-091-504-1779

Query Match 1.7% Score 50; DB 9; Length 5819;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1192 CACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTGCGG 1241
|||||
DB 3669 CACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTGCGG 1718

RESULT 40
US-09-764-891-9890
;; Sequence 1779, Application US/09764891
;; Publication No. US20030077808A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC007
;; CURRENT APPLICATION NUMBER: US/09/764,891
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - refer to PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 2442
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1779
;; LENGTH: 5819
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-764-891-9890

Query Match 1.7% Score 50; DB 10; Length 1718;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1192 CACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTGCGG 1718

|||||
DB 3669 CACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTGCGG 3718
RESULT 41
US-09-764-891-9890
;; Sequence 9890, Application US/09764891
;; Publication No. US20030077808A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC006
;; CURRENT APPLICATION NUMBER: US/09/764,891
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 10231
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 9890
;; LENGTH: 11618
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-764-891-9890

Query Match 1.7% Score 50; DB 9; Length 11618;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1187 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTG 1236
|||||
DB 8181 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTG 8243

RESULT 42
US-09-764-891-9810
;; Sequence 7810, Application US/09764891
;; Publication No. US20030077808A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC006
;; CURRENT APPLICATION NUMBER: US/09/764,891
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 10231
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7810
;; LENGTH: 14216
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-764-891-9810

Query Match 1.7% Score 50; DB 9; Length 13216;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1187 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTG 1236
|||||
DB 12177 CTGCCACCTTGGCTCCCAAGTGGTGGATTACAGGCATGACCCACTG 12245

RESULT 43
US-09-764-891-9967
;; Sequence 9967, Application US/09764891
;; Publication No. US20030077808A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC006
;; CURRENT APPLICATION NUMBER: US/09/764,891
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 10241
;; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9967
LENGTH: 19929
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-9967

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1013 AACCTGCTCCCGGTTCAAGCGATTCTCCGATTCGCTCAAGTCTCTGAGA 1482
DB 6669 AACCTGCTCCCGGTTCAAGCGATTCTCCGATTCGCTCAAGTCTCTGAGA 1416

RESULT 44

US-09-764-891-9966
; Sequence 9966, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9966
; LENGTH: 20907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4477)
; OTHER INFORMATION: n equals a.t.g. or c
; NAME/KEY: SITE
; LOCATION: (4480)
; OTHER INFORMATION: n equals a.t.g. or c
; NAME/KEY: SITE
; LOCATION: (4483)
; OTHER INFORMATION: n equals a.t.g. or c
US-09-764-891-9966

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1013 AACCTGCTCCCGGTTCAAGCGATTCTCCGATTCGCTCAAGTCTCTGAGA 1482
DB 6667 AACCTGCTCCCGGTTCAAGCGATTCTCCGATTCGCTCAAGTCTCTGAGA 1416

RESULT 45

US-09-764-891-8807/c
; Sequence 8807, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8807
; LENGTH: 21936
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8807

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAAGTCTCGGATTACAGGCATGAGCCACTG 1236
DB 4160 CTGCCACCTTGGCTCCCAAAGTCTCGGATTACAGGCATGAGCCACTG 4111

RESULT 46

US-09-764-891-9446
; Sequence 9446, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9446
; LENGTH: 21936
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9446

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAAGTCTCGGATTACAGGCATGAGCCACTG 1236
DB 1777 CTGCCACCTTGGCTCCCAAAGTCTCGGATTACAGGCATGAGCCACTG 17826

RESULT 47

US-09-764-891-7809
; Sequence 7809, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7809
; LENGTH: 29163
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7809

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAAGTCTCGGATTACAGGCATGAGCCACTG 1236
DB 12174 CTGCCACCTTGGCTCCCAAAGTCTCGGATTACAGGCATGAGCCACTG 12223

RESULT 48

US-10-067-514-1/c
; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Grellarsdotter, Solveig
; APPLICANT: Jonsdotter, Sit
; APPLICANT: Reynoldsdotter, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE

FILE REFERENCE: 2345.2010-003
CURRENT APPLICATION NUMBER: US/10/067.514
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 09/811/352
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1691139
TYPE: DNA
ORGANISM: Human
US-10-067-514-1

Query Match: 1.7%; Score 50; DB 9; Length 1691139;
Best Local Similarity 100.0%; Pred. No. 6.5e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1198 GGCTCCCAAGTCTGGGATTACAGGATGAGTACGCGGCACTCA 1247
|||||
DB 644059 GGCTCCCAAGTCTGGGATTACAGGATGAGTACGCGGCACTCA 644059

RESULT 49
US-09-918-995-2616/c
Sequence 2616, Application US/99/18995
Publication No. US2003007362A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918.995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/245.076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2616
LENGTH: 448
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(448)
OTHER INFORMATION: n = A,T,C or G
US 09 918 995 2616

Query Match: 1.7%; Score 49; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 6.5e-15;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTCGCTCCCGGTTCAAGCGATTCTCTGCTCAGCTCCTGAG 1081
|||||
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Sequence 11, Application US/09/729835
Patent No. US20010015647A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CURRENT APPLICATION NUMBER: US/09/729.835
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 09/257.179
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 60/056.270
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 60/056.271
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 60/056.247

PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 60/056.073
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patent In Ver. 2.0
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-729-835-11

Query Match: 1.7%; Score 49; DB 10; Length 866;
Best Local Similarity 100.0%; Pred. No. 6.7e-15;
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Search completed: May 10, 2003, 02:58:19
Job time : 3143.36 Secs

GenCore version 5.1.5
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OM nucleic nucleic search, using sw model

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Searched: 2185239 seqs, 1125999159 residues

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5	541	18.7	1643	22	AAF24703	Nucleotide sequenc
6	420	14.5	1197	24	ABL58400	Human large ATP-bi
7	55	1.9	2890	24	ABK34575	Human gene for nov
8	55	1.9	13646	24	AAS20126	Human gene for rec
9	55	1.9	13646	24	AAS20128	Human gene for re

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Human ribosomal S1	1.8	1316	22	AAI64613
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Human polynucleoti	1.8	5351	24	ABQ66790
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Human immune/haema	1.8	8319	22	AAK65197
Human reproductive	1.8	10901	22	AAI03236
Human nervous syst	1.8	29329	22	ABA18026
Human immune/haema	1.8	29329	22	ABA20511
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Human ovarian and	1.8	17904	22	ABA07913
Human reproductive	1.8	17904	22	AAI03730
Human musculoskele	1.8	26591	22	AAI36313
Human DNA for a no	1.8	32186	22	AAS34422
Human thiorodoxin	1.8	66566	22	AAAS3450
Human histone deac	1.8	122186	22	AAAC89560
Retinoblastoma bin	1.8	162450	21	AAZ86967
Human cDNA differe	1.8	198285	24	ABK84699
Gene #3817 used to	1.8	198285	24	ABN97319
Human polynucleoti	1.7	320	22	AAI91676
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Human transcrip	1.7	1989	24	ABK47950
Chromosome 13q31-q	1.7	3001	21	AAH51743
Human cardiovascular	1.7	5819	22	AAS36279
Human nervous syst	1.7	8774	22	ABA21246
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88	50	1.7	21936	22	AAL06115	Human reproductive	c 161	49	1.7	31718	22	AAK90360	Human digestive sy
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99	50	1.7	162450	21	AAK28697	Human fibroblast	c 172	49	1.7	139389	24	ABK84795	Human CDNA differe
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106	49	1.7	761	22	AAK15179	Human neuroblastom	c 179	48	1.7	234	24	AAL169091	Activated T-cell d
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154	49	1.7	31718	22	AAK16416	Human reproductive	c 227	48	1.7	17185	22	AAH16049	Human nervous syst
155	49	1.7	31718	22	AAK74104	Human immune/haema	c 228	48	1.7	17185	22	AAK75628	Human immune/haema

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c 242	48	1.7	24740	21	AAK57743	Human EMP-1 (HLMF-	c 305	47	1.6	4313	22	AAK81673	Human immune/haema
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c 244	48	1.7	33923	22	AAK67071	Human immune/haema	c 307	47	1.6	4432	22	AAK86168	Human immune/haema
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c 246	48	1.7	36651	24	AAK28072	Human kinase gene	c 309	47	1.6	4447	22	AAK36269	Human musculoskele
c 247	48	1.7	43938	22	AAK77216	Human immune/haema	c 310	47	1.6	4622	23	AAK42254	Genomic sequence
c 248	48	1.7	45017	22	AAK77217	Human immune/haema	c 311	47	1.6	5066	22	AAK71166	Human immune/haema
c 249	48	1.7	45993	24	AAK66070	Human liver fluke	c 312	47	1.6	5527	22	AAK42043	Genomic sequence
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c 242	48	1.7	53526	19	AAK94101	Human PKD1 gene	c 315	47	1.6	5527	22	AAK85967	Human immune/haema
c 243	48	1.7	53577	17	AAK18551	Human polyomavirus	c 316	47	1.6	5527	22	AAK85969	Human immune/haema
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c 249	48	1.7	65608	24	AAK167668	Oesophagus cancer	c 322	47	1.6	5529	22	AAK87017	Human immune/haema
c 250	48	1.7	80331	22	AAK49559	Human histone deac	c 323	47	1.6	6159	22	AAK75604	Human immune/haema
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c 252	48	1.7	121724	24	AAK88143	Human osteoblast	c 325	47	1.6	6167	22	AAK75609	Human immune/haema
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c 255	48	1.7	159400	24	AAK88126	Human osteoblast	c 328	47	1.6	6191	22	AAK28643	Genomic sequence
c 256	48	1.7	161425	22	AAK02347	Human AKAP gene	c 329	47	1.6	6315	22	AAK36270	Human musculoskele
c 257	48	1.7	162025	22	AAK02347	Human AKAP gene	c 330	47	1.6	7737	22	AAK490942	Human digestive sy
c 258	48	1.7	162025	24	AAK28713	Human AKAP allele	c 331	47	1.6	7737	22	AAK33977	Human liver associ
c 259	48	1.7	162025	24	AAK28713	Human AKAP allele	c 332	47	1.6	7737	23	AAK43114	Genomic sequence
c 260	48	1.7	174424	24	AAK68122	Human ovarian can	c 333	47	1.6	7737	24	AAK90332	Human liver anti
c 261	48	1.7	178895	24	AAK88146	Human osteoblast	c 334	47	1.6	8056	22	AAK79815	Human immune/haema
c 262	47	1.6	126	22	AAK15943	Human nervous syst	c 335	47	1.6	8537	22	AAK07355	Human pancreatic c
c 263	47	1.6	146	22	AAK82713	Human immune/haema	c 336	47	1.6	8537	22	AAK39827	Genomic sequence
c 264	47	1.6	205	21	AAK12545	Human selected pro	c 337	47	1.6	8537	22	AAK90185	Human digestive sy
c 265	47	1.6	238	24	AAK56485	Human genomic DNA	c 338	47	1.6	8537	22	AAK91086	Human digestive sy
c 266	47	1.6	267	22	AAK162868	Human genomic DNA	c 339	47	1.6	8891	22	AAK26683	Human genomic DNA
c 267	47	1.6	269	24	AAK187463	Human ovarian can	c 340	47	1.6	11132	22	AAK72302	Human immune/haema
c 268	47	1.6	294	23	AAK16918	Human prostate exp	c 341	47	1.6	11132	22	AAK72570	Human immune/haema
c 269	47	1.6	345	22	AAK18881	Human polynucleoti	c 342	47	1.6	12729	22	AAK97873	Nucleotide sequenc
c 270	47	1.6	405	22	AAK03791	Human reproductive	c 343	47	1.6	13158	18	AAK75288	Human neuroblastom
c 271	47	1.6	405	22	AAK03791	Human reproductive	c 344	47	1.6	15177	22	AAK66169	Nucleotide sequenc
c 272	47	1.6	405	22	AAK03791	Human reproductive	c 345	47	1.6	15177	22	AAK66169	Human immune/haema
c 273	47	1.6	405	22	AAK03791	Human reproductive	c 346	47	1.6	15418	21	AAK38595	Human immune/haema
c 274	47	1.6	411	22	AAK19244	Human ovarian relat	c 347	47	1.6	15418	24	AAK38595	Nucleotide sequenc
c 275	47	1.6	418	22	AAK00691	Human polynucleoti	c 348	47	1.6	15418	24	AAK38595	Human TERT promot
c 276	47	1.6	418	22	AAK00691	Human polynucleoti	c 349	47	1.6	15418	24	AAK38595	Human TERT promot
c 277	47	1.6	418	23	AAK23098	Human breast exp	c 350	47	1.6	19659	22	AAK64741	Human atrial fibrill
c 278	47	1.6	418	24	AAK91148	Human DNA replicat	c 351	47	1.6	19659	22	AAK75613	Human immune/haema
c 279	47	1.6	545	22	AAK03742	Human embryonic mus	c 352	47	1.6	19659	22	AAK91504	Human immune/haema
c 280	47	1.6	583	24	AAK03741	Human embryonic mus	c 353	47	1.6	21949	22	AAK15942	Human digestive sy
c 281	47	1.6	608	23	AAK45713	Human prostate relat	c 354	47	1.6	21949	22	AAK15942	Human nervous syst
c 282	47	1.6	700	22	AAK92440	Human prostate relat	c 355	47	1.6	22457	22	AAK82210	Human musculoskele
c 283	47	1.6	729	22	AAK140330	Human polynucleoti	c 356	47	1.6	24457	22	AAK74866	Human immune/haema
c 284	47	1.6	760	23	AAK22463	Human polynucleoti	c 357	47	1.6	24580	22	AAK66230	Human immune/haema
c 285	47	1.6	760	23	AAK22463	Human prostate relat	c 358	47	1.6	24580	22	AAK66230	Human immune/haema
c 286	47	1.6	867	20	AAK30362	Human prostate relat	c 359	47	1.6	24964	24	AAK86595	Human immune/haema
c 287	47	1.6	867	24	AAK84138	Human prostate relat	c 360	47	1.6	27513	22	AAK71186	Human SA (cat hype
c 288	47	1.6	1177	24	AAK16004	Human embryonic mus	c 361	47	1.6	27513	22	AAK19222	Human immune/haema
c 289	47	1.6	1372	24	AAK95183	Human embryonic mus	c 362	47	1.6	27513	22	AAK19222	Human nervous syst
c 290	47	1.6	1856	24	AAK34742	Human cDNA for neu	c 363	47	1.6	28818	22	AAK35901	Human musculoskele
c 291	47	1.6	2159	24	AAK94576	Human protein phos	c 364	47	1.6	32190	22	AAK36709	Human cardiovasecul
c 292	47	1.6	2508	24	AAK154838	Human G-protein s	c 365	47	1.6	32193	22	AAK35782	Human musculoskele
c 293	47	1.6	2744	22	AAK79904	Human immune/haema	c 366	47	1.6	38653	22	AAK72348	Human immune/haema
c 294	47	1.6	2744	22	AAK79904	Human immune/haema	c 367	47	1.6	38653	22	AAK72348	Human immune/haema
c 295	47	1.6	2744	22	AAK79904	Human immune/haema	c 368	47	1.6	49412	21	AAK51594	Human genomic sequ
c 296	47	1.6	2922	22	AAK74866	Human embryonic mus	c 369	47	1.6	51945	22	AAK59607	Human genomic sequ
c 297	47	1.6	3121	22	AAK81181	Human embryonic mus	c 370	47	1.6	51945	22	AAK78883	Human immune/haema
c 298	47	1.6	4164	22	AAK81446	Human embryonic mus	c 371	47	1.6	54607	20	AAK90847	Human PACAP gene
c 299	47	1.6	4285	22	AAK70184	Human embryonic mus	c 372	47	1.6	117574	24	AAK45288	Human KCNR1 gene
c 300	47	1.6	4285	22	AAK70184	Human embryonic mus	c 373	47	1.6	19659	24	AAK84574	Human cDNA differe
c 301	47	1.6	4285	22	AAK70184	Human embryonic mus	c 374	47	1.6	19659	24	AAK84574	Human cDNA differe
c 302	47	1.6	4285	22	AAK70184	Human embryonic mus	c 375	47	1.6	19659	24	AAK84574	Human cDNA differe

375	47	1.6	1503900	22	AAK95240	Human neuroendocrine	c 448	46	1.6	5947	22	AAK86768	Human immune/haema
376	47	1.6	1503900	22	AAK96733	Human neuroendocrine	c 449	46	1.6	6319	24	ABK97631	Human prostate spe
377	46	1.6	132	22	AAK183143	Human polynucleotid	c 450	46	1.6	7417	22	AAK70374	Human immune/haema
378	46	1.6	150	21	AAK12976	Human secreted pro	c 451	46	1.6	7742	22	AAK72501	Human immune/haema
379	46	1.6	150	22	AAK05408	Human secreted pro	c 452	46	1.6	7759	22	AAK72498	Human immune/haema
380	46	1.6	258	22	AAK57746	Human immune/haema	c 453	46	1.6	8047	22	AAK81256	Human immune/haema
381	46	1.6	262	22	AAK89113	Human digestive sy	c 454	46	1.6	8047	22	AAK86767	Human immune/haema
382	46	1.6	262	22	AAK31863	Human liver associ	c 455	46	1.6	8577	22	ABAI17047	Human nervous syst
383	46	1.6	262	24	AAK90218	Human liver outlq	c 456	46	1.6	8577	22	AAI06167	Human reproductive
384	46	1.6	307	22	AAK87671	Human immune/haema	c 457	46	1.6	8577	23	AB198712	Human testicular a
385	46	1.6	315	21	AAK29578	Human secreted pro	c 458	46	1.6	9035	22	AAK75933	Human immune/haema
386	46	1.6	341	24	ABL84368	Human ovarian can	c 459	46	1.6	9035	22	AAK85246	Human immune/haema
387	46	1.6	394	22	ABL82243	Human polynucleot	c 460	46	1.6	10202	22	AAK86002	Human immune/haema
388	46	1.6	394	24	ABL84358	Human ovarian can	c 461	46	1.6	10587	22	AAK82482	Human immune/haema
389	46	1.6	400	24	ABL61718	Human adenocarcino	c 462	46	1.6	10867	22	AAI37605	Human musculoskele
390	46	1.6	400	24	ABL62279	Human adenocarcino	c 463	46	1.6	10867	22	AAK36613	Human cardiovascu
391	46	1.6	418	22	AAK59421	Human encoding nove	c 464	46	1.6	10867	22	AAK66345	Human immune/haema
392	46	1.6	418	22	AAK88273	Human digestive sy	c 465	46	1.6	10894	22	AAK36611	Human cardiovascul
393	46	1.6	438	23	ABV59447	Human prostate exp	c 466	46	1.6	10894	22	AAK66343	Human immune/haema
394	46	1.6	460	24	ABT04066	Human ovary speci	c 467	46	1.6	10907	22	AAI37603	Human musculoskele
395	46	1.6	473	22	AAK359765	Genomic sequence #	c 468	46	1.6	10907	22	AAK36612	Human cardiovascu
396	46	1.6	473	22	AAK90118	Human digestive sy	c 469	46	1.6	10907	22	AAK66344	Human immune/haema
397	46	1.6	505	24	ABN64662	Human cancer relat	c 470	46	1.6	11870	22	AAI07328	Human reproductive
398	46	1.6	518	22	AAK66887	Human immune/haema	c 471	46	1.6	11870	22	AAI07329	Human reproductive
399	46	1.6	520	24	ABO56470	Human colon cancer	c 472	46	1.6	11870	22	AAK82242	Human immune/haema
400	46	1.6	531	22	AAK71044	Human immune/haema	c 473	46	1.6	11870	22	AAK82243	Human immune/haema
401	46	1.6	531	22	AAK71045	Human immune/haema	c 474	46	1.6	11870	22	AAK84792	Human immune/haema
402	46	1.6	535	22	AAH13269	Human cDNA clone (c 475	46	1.6	11870	22	AAK84793	Human immune/haema
403	46	1.6	535	22	AAH12272	Human cDNA clone (c 476	46	1.6	12555	23	AAK78331	Human immune/haema
404	46	1.6	543	24	ABN64981	Human cancer relat	c 477	46	1.6	12555	23	ABK42300	Genomic sequence #
405	46	1.6	552	22	AAK69055	Human immune/haema	c 478	46	1.6	12562	22	AAI36095	Human musculoskele
406	46	1.6	553	24	ABN63320	Human cancer relat	c 479	46	1.6	12562	22	AAK72631	Human immune/haema
407	46	1.6	581	22	AAH13463	Human cDNA clone (c 480	46	1.6	12718	22	AAI37607	Human musculoskele
408	46	1.6	620	24	ABN65477	Human cancer relat	c 481	46	1.6	12718	22	AAK66346	Human immune/haema
409	46	1.6	684	22	AAK90712	Human digestive sy	c 482	46	1.6	13002	22	AAK81377	Human immune/haema
410	46	1.6	695	22	AAI10188	Human breast cancer	c 483	46	1.6	16489	22	AAK27823	DNA encoding novel
411	46	1.6	731	22	AAI19768	Human breast cancer	c 484	46	1.6	16552	22	AAK91416	Human digestive sy
412	46	1.6	762	22	AAI195961	Human neuroblastom	c 485	46	1.6	16552	22	AAK91417	Human digestive sy
413	46	1.6	850	24	ABO89526	Human prostate exp	c 486	46	1.6	16552	22	AAI57784	Human colorectal c
414	46	1.6	903	22	ABAU8242	Human secreted pro	c 487	46	1.6	16552	22	AAI57785	Human colorectal c
415	46	1.6	912	22	AAK08828	Human immune/haema	c 488	46	1.6	17821	22	AAK66003	Human immune/haema
416	46	1.6	917	22	AAK08826	Human immune/haema	c 489	46	1.6	20892	22	ABAI15709	Human nervous syst
417	46	1.6	966	22	AAI188604	Human polynucleot	c 490	46	1.6	27733	22	ABAI19324	Human nervous syst
418	46	1.6	1121	22	AAK82524	Human immune/haema	c 491	46	1.6	29222	24	AB139412	Human electron-tra
419	46	1.6	1124	22	AAK82525	Human immune/haema	c 492	46	1.6	32189	22	AAI04670	Human reproductive
420	46	1.6	1127	22	AAK82521	Human immune/haema	c 493	46	1.6	32189	23	AB197577	Human testicular a
421	46	1.6	1157	22	AAK82522	Human immune/haema	c 494	46	1.6	32221	22	AAK39766	Genomic sequence #
422	46	1.6	1205	24	AAK81823	Human secreted pro	c 495	46	1.6	34514	21	AAK00147	Human digestive sy
423	46	1.6	1389	21	AAK26374	Human secreted pro	c 496	46	1.6	34514	21	AAK00147	Human digestive sy
424	46	1.6	1450	22	AAK82521	Human immune/haema	c 497	46	1.6	34514	21	AAK00147	Human digestive sy
425	46	1.6	1450	22	AAK82521	Human immune/haema	c 498	46	1.6	34514	21	AAK00147	Human digestive sy
426	46	1.6	1733	21	AAK59421	Human cDNA sequenc	c 499	46	1.6	51474	22	AAK97846	Human neuroblastom
427	46	1.6	1954	22	AAH18453	Human cDNA sequenc	c 500	46	1.6	94014	24	ABN96931	Gene #3429 used to
428	46	1.6	1957	22	AAH14756	Human cDNA sequenc	c 501	46	1.6	110096	24	ABN5044	Gene #1542 used to
429	46	1.6	2251	22	AAH17556	Human cDNA sequenc	c 502	46	1.6	138169	21	AAK34791	Human adenosine re
430	46	1.6	2756	22	ABAU06812	Human genomic DNA	c 503	46	1.6	141589	21	AAK20913	Human ELAM-1 polyn
431	46	1.6	2756	22	AAK17552	Human genomic sequenc	c 504	46	1.6	141589	21	AAK21127	Human low adenosin
432	46	1.6	2835	22	AAH14665	Human cDNA sequenc	c 505	46	1.6	141589	21	AAK21152	Human low adenosin
433	46	1.6	2844	22	AAK91523	Human digestive sy	c 506	46	1.6	141589	21	AAK35005	Human adenosine re
434	46	1.6	2844	22	AAK32177	Human liver associ	c 507	46	1.6	141589	21	AAK35030	Human adenosine re
435	46	1.6	2844	24	ABN90512	Human liver outlq	c 508	46	1.6	145831	24	AB182309	Human osteoblast d
436	46	1.6	2844	24	ABU53426	Human zinc finger	c 509	46	1.6	145831	24	AB186806	Human factor relat
437	46	1.6	2876	22	AAK69707	Human immune/haema	c 510	46	1.6	145831	24	AB186806	Human cDNA differe
438	46	1.6	3116	22	AAK39688	Genomic sequence #	c 511	46	1.6	145831	24	AB186806	Human cDNA differe
439	46	1.6	3116	22	AAK90041	Human digestive sy	c 512	46	1.6	145831	21	AAK21442	Human ELAM-1 polyn
440	46	1.6	3185	22	AAK57528	Human pancreas cel	c 513	46	1.6	14708	24	ABQ88154	Human osteoblast d
441	46	1.6	3512	23	ABK43087	Genomic sequence #	c 514	46	1.6	201143	24	ABK83568	Human factor relat
442	46	1.6	3753	22	AAI04946	Human reproductive	c 515	46	1.6	202973	21	AAK21437	Human cDNA differe
443	46	1.6	3753	23	AB197840	Human testicular a	c 516	46	1.6	224930	24	ABK84349	Human musculoskele
444	46	1.6	3917	22	AAH18646	Human cDNA sequenc	c 517	46	1.6	101	22	AAI36545	Human immune/haema
445	46	1.6	4412	22	AAH57372	Human heart cells	c 518	46	1.6	116	22	AAK82023	Human reproductive
446	46	1.6	4727	22	AAK65762	Human immune/haema	c 519	46	1.6	118	22	AAI05885	Human reproductive
447	46	1.6	5032	22	AAK90709	Human digestive sy	c 520	46	1.6	118	22	AAI05886	Human reproductive

c 521	1.6	118	23	ABU98449	Human testicular a	594	45	1.6	1701	20	AAV83945	Bacterial artificial
c 522	1.6	118	23	ABU98450	Human testicular a	595	45	1.6	1837	24	ABA94430	Human Pp1345 prote
c 523	1.6	122	22	AAU16055	Human nervous syst	c 596	45	1.6	1926	24	ABK69884	Human secreted pro
c 524	1.6	137	22	AAU04408	Human reproductive	c 597	45	1.6	2121	24	ABA96972	Human L-3-phospho
c 525	1.6	138	22	AAK76081	Human immune/haema	c 598	45	1.6	2173	23	AAU72272	DNA encoding novel
c 526	1.6	153	17	AAU71589	Probe (BLUR) for	c 599	45	1.6	2566	22	AAH17845	Human cDNA sequenc
c 527	1.6	156	22	AAK76634	Human immune/haema	c 600	45	1.6	2579	22	AAH15692	Human cDNA sequenc
c 528	1.6	166	21	AAU22006	Human secreted pro	c 601	45	1.6	2585	21	AAU64476	Prostate tumour as
c 529	1.6	168	21	AAU06104	Human reproductive	c 602	45	1.6	2648	24	AAK35108	Human cDNA encodin
c 530	1.6	168	23	AAU98669	Human testicular a	c 603	45	1.6	2716	23	ABV22030	Human prostate exp
c 531	1.6	193	21	AAU12609	Human secreted pro	c 604	45	1.6	2716	23	ABV25415	Human prostate exp
c 532	1.6	228	22	AAK76633	Human immune/haema	c 605	45	1.6	2716	23	ABV27864	Human cDNA sequenc
c 533	1.6	234	22	AAK80236	Human immune/haema	c 606	45	1.6	2797	22	AAH18187	Human cDNA sequenc
c 534	1.6	234	22	AAK80241	Human immune/haema	c 607	45	1.6	2843	22	AAU32907	Human genomic DNA
c 535	1.6	264	22	AAU62911	Human genomic DNA	c 608	45	1.6	2863	22	AAU07837	Human secreted pro
c 536	1.6	273	22	AAU20386	Human nervous syst	c 609	45	1.6	2903	24	ABA93808	Human zytot17 CDN
c 537	1.6	282	21	AAU30369	Human secreted pro	c 610	45	1.6	2958	22	AAK81324	Human immune/haema
c 538	1.6	288	22	AAU55522	Human immune/haema	c 611	45	1.6	3011	22	AAU41928	Genomic sequence #
c 539	1.6	295	22	AAK82995	Human immune/haema	c 612	45	1.6	3011	22	AAU35102	DNA #52 encoding h
c 540	1.6	298	21	AAU12082	Human secreted pro	c 613	45	1.6	3091	22	AAU28567	Genomic sequence #
c 541	1.6	298	22	AAU73170	Human immune/haema	c 614	45	1.6	3091	22	AAU28568	Genomic sequence #
c 542	1.6	320	22	AAU85946	Human polynucleoti	c 615	45	1.6	3486	22	AAU52890	Human polynucleoti
c 543	1.6	361	21	AAU45315	Human secreted exp	c 616	45	1.6	3516	22	AAK85421	Human immune/haema
c 544	1.6	372	23	AAU95560	Human prostate exp	c 617	45	1.6	3563	22	AAU14352	Human manganese su
c 545	1.6	414	23	AAU12901	Human prostate exp	c 618	45	1.6	3783	22	AAU71130	Human immune/haema
c 546	1.6	415	22	AAU184146	Human polynucleoti	c 619	45	1.6	3788	22	AAU71131	Human immune/haema
c 547	1.6	425	22	AAU89685	Human polynucleoti	c 620	45	1.6	3844	22	AAU80274	Nucleotide sequenc
c 548	1.6	428	22	AAU85512	Human polynucleoti	c 621	45	1.6	4079	22	AAU2384	Human immune/haema
c 549	1.6	433	23	AAU07432	Human prostate exp	c 622	45	1.6	4502	22	AAU72445	Human immune/haema
c 550	1.6	438	21	AAU23311	Human secreted pro	c 623	45	1.6	5071	22	AAU74516	Human immune/haema
c 551	1.6	443	22	AAU08068	Human secreted pro	c 624	45	1.6	5071	22	AAU69811	Human secreted pro
c 552	1.6	443	23	AAU59216	Human reproductive	c 625	45	1.6	5072	22	AAU74517	Human immune/haema
c 553	1.6	448	23	AAU87410	DNA encoding novel	c 626	45	1.6	5072	24	AAU69833	Human secreted pro
c 554	1.6	449	22	AAU72817	Human immune/haema	c 627	45	1.6	5118	22	AAU59961	Human eukaryotic 1
c 555	1.6	458	23	AAU30873	Human prostate exp	c 628	45	1.6	5581	18	AAU48737	Human leucocyte sp
c 556	1.6	480	23	AAU34077	Human prostate exp	c 629	45	1.6	5581	18	AAU45451	Human LST-1 (leuko
c 557	1.6	480	23	AAU42894	Human prostate exp	c 630	45	1.6	5834	22	AAU40617	DNA encoding human
c 558	1.6	524	23	AAU19795	Human prostate exp	c 631	45	1.6	5834	22	AAU08505	Human reproductive
c 559	1.6	536	24	AAU61361	Human cancer relat	c 632	45	1.6	5834	22	AAU28542	Genomic sequence #
c 560	1.6	542	24	AAU63113	Human cancer relat	c 633	45	1.6	6117	22	AAU68756	Human immune/haema
c 561	1.6	566	22	AAU10559	Human cDNA clone (c 634	45	1.6	6139	19	AAU70354	Coding strand of n
c 562	1.6	574	22	AAU45913	Human musculoskele	c 635	45	1.6	6165	22	AAU75603	Human immune/haema
c 563	1.6	600	23	AAU53773	Human prostate exp	c 636	45	1.6	6195	23	AAU42222	Genomic sequence #
c 564	1.6	607	24	AAU89177	Human prostate exp	c 637	45	1.6	6194	23	AAU42223	Genomic sequence #
c 565	1.6	610	22	AAU77666	Human immune/haema	c 638	45	1.6	6455	22	AAU17328	Human nervous syst
c 566	1.6	612	22	AAU77665	Human immune/haema	c 639	45	1.6	6455	22	AAU34621	Human DNA for a no
c 567	1.6	618	22	AAU18304	Human nervous syst	c 640	45	1.6	6411	16	AAU95493	Human cDNA-2 DNA
c 568	1.6	666	24	AAU04097	Human ovary speci	c 641	45	1.6	6782	22	AAU67165	Human immune/haema
c 569	1.6	695	21	AAU16681	Human arthritis pa	c 642	45	1.6	7573	22	AAU19080	Human excretory re
c 570	1.6	700	22	AAU92573	Human inflammatory	c 643	45	1.6	7573	22	AAU163430	Human kidney relat
c 571	1.6	700	22	AAU92574	Human inflammatory	c 644	45	1.6	7983	22	AAU73139	Human immune/haema
c 572	1.6	709	22	AAU24907	Human breast cancer	c 645	45	1.6	8217	22	AAU07164	Human reproductive
c 573	1.6	739	22	AAU37463	Human musculoskele	c 646	45	1.6	8396	21	AAU59353	Human SRP2 (phenol
c 574	1.6	742	22	AAU72035	Human immune/haema	c 647	45	1.6	8663	22	AAU30133	Human lung antigen
c 575	1.6	767	22	AAU36809	Human musculoskele	c 648	45	1.6	8841	24	AAU84005	Human cDNA differe
c 576	1.6	798	22	AAU1964	Human immune/haema	c 649	45	1.6	8841	24	AAU64081	Breast cancer rela
c 577	1.6	868	22	AAU94388	Human fetal cDNA	c 650	45	1.6	8918	22	AAU26708	Human genomic DNA
c 578	1.6	891	20	AAU40818	Secreted protein E	c 651	45	1.6	8919	22	AAU26709	Human genomic DNA
c 579	1.6	963	22	AAU04364	Human reproductive	c 652	45	1.6	9469	22	AAU79514	Human immune/haema
c 580	1.6	963	22	AAU04365	Human reproductive	c 653	45	1.6	9475	22	AAU72443	Human immune/haema
c 581	1.6	1040	20	AAU79016	Human secreted pro	c 654	45	1.6	9507	22	AAU07097	Human reproductive
c 582	1.6	1089	22	AAU07902	Human secreted pro	c 655	45	1.6	10093	22	AAU07184	Human pancreatic c
c 583	1.6	1383	21	AAU90401	Human polynucleoti	c 656	45	1.6	10093	22	AAU35890	Human cardiovascular
c 584	1.6	1395	21	AAU264955	Methanol-bound pro	c 657	45	1.6	10093	22	AAU89816	Human digestive sy
c 585	1.6	1395	22	AAU92062	Human PR874 cDNA	c 658	45	1.6	10420	22	AAU16598	Human nervous syst
c 586	1.6	1395	22	AAU44103	Human PR874 (JN04	c 659	45	1.6	10885	22	AAU37478	Human musculoskele
c 587	1.6	1395	22	AAU44103	Human PR874 (JN04	c 660	45	1.6	12163	22	AAU14697	Human nervous syst
c 588	1.6	1424	20	AAU89611	Human secreted pro	c 661	45	1.6	12221	22	AAU71585	Human immune/haema
c 589	1.6	1424	20	AAU89611	Human cDNA encodin	c 662	45	1.6	12500	22	AAU77971	Human immune/haema
c 590	1.6	1424	24	AAU90911	Human polynucleoti	c 663	45	1.6	12665	22	AAU71602	Human immune/haema
c 591	1.6	1513	21	AAU18303	Human nervous syst	c 664	45	1.6	12667	22	AAU71604	Human immune/haema
c 592	1.6	1538	21	AAU93347	Human secreted pro	c 665	45	1.6	13058	22	AAU29194	Genomic sequence #
c 593	1.6	1560	21	AAU79746	Human secreted pro	c 666	45	1.6	13058	22	AAU79325	Human immune/haema

667	45	1.6	13255	22	AAK76942	Human immune/haema	c 740	45	1.6	122186	22	AAC89560	Human histone deac
668	45	1.6	13670	24	AAI42369	Human glutathione	c 741	45	1.6	122888	24	ABK83569	Human cDNA differe
669	45	1.6	15061	22	AAI04226	Human reproductive	c 742	45	1.6	129722	24	ABQ88117	Human cDNA differe
670	45	1.6	15061	23	AAK42104	Genomic sequence	c 743	45	1.6	165199	24	ABR83460	Human cDNA differe
671	45	1.6	15651	22	AAK81510	Human immune/haema	744	45	1.6	167343	24	ABL64403	Stomach cancer rel
672	45	1.6	15714	22	AAS36855	Human cardiovascular	745	45	1.6	167343	24	ABL67239	Thyroid cancer rel
673	45	1.6	15870	22	AAI16129	Human nervous syst	746	45	1.6	227968	24	ABK83497	Human cDNA differe
674	45	1.6	16299	22	AAK71100	Human immune/haema	747	45	1.5	51	22	AAI75194	Human silent SNP c
675	45	1.6	17397	22	AAS36645	Human cardiovascular	c 748	44	1.5	130	22	AAI36471	Human musculoskele
676	45	1.6	17462	22	AAI15655	Human nervous syst	749	44	1.5	144	22	AAK81169	Human immune/haema
677	45	1.6	18678	22	AAS32889	Human genomic DNA	c 750	44	1.5	175	22	AAK07200	Human reproductive
678	45	1.6	18678	22	AAK91271	Human digestive sy	c 751	44	1.5	175	22	AAK07200	Human reproductive
679	45	1.6	18692	23	AAK42795	Genomic sequence	c 752	44	1.5	193	22	AAK70913	Human immune/haema
680	45	1.6	19334	22	AAS36443	Human cardiovascular	753	44	1.5	215	21	AAC29849	Human secreted pro
681	45	1.6	19345	22	AAS36444	Human cardiovascular	754	44	1.5	312	24	ABN62536	Human cancer relat
682	45	1.6	19407	22	ABAI5979	Human nervous syst	c 755	44	1.5	343	22	AAI25254	Human breast cance
683	45	1.6	19407	22	AAK81418	Human immune/haema	c 756	44	1.5	348	22	AAI16411	Human breast cance
684	45	1.6	21410	22	AAK81290	Human immune/haema	c 757	44	1.5	355	22	AAI84801	Human polynucleoti
685	45	1.6	21596	22	AAK71582	Human immune/haema	758	44	1.5	383	22	AAI90781	Human polynucleoti
686	45	1.6	21724	22	AAS26629	Human genomic DNA	c 759	44	1.5	389	22	AAK64188	Human immune/haema
687	45	1.6	21724	22	AAK86125	Human immune/haema	c 760	44	1.5	389	22	AAF64283	Novel human polynu
688	45	1.6	21727	22	AAS26630	Human genomic DNA	761	44	1.5	395	22	AAI89981	Human polynucleoti
689	45	1.6	21727	22	AAK86126	Human immune/haema	c 762	44	1.5	399	22	AAI92488	Human polynucleoti
690	45	1.6	22161	23	ABK42133	Genomic sequence	c 763	44	1.5	404	22	AAI85729	Human polynucleoti
691	45	1.6	22467	22	AAS33423	Human encoding human	c 764	44	1.5	407	22	AAK69316	Human immune/haema
692	45	1.6	22467	22	AAS33425	DNA encoding human	c 765	44	1.5	422	22	AAK77117	Human immune/haema
693	45	1.6	22481	17	AAI11658	FEF3 full length s	c 766	44	1.5	425	22	AAK77117	Human immune/haema
694	45	1.6	22484	24	ABQ88196	Human osteoblast 3	c 767	44	1.5	425	24	ABN61884	Human immune/haema
695	45	1.6	22484	24	ABN96844	Genomic sequence	c 768	44	1.5	435	22	AAK60183	Human immune/haema
696	45	1.6	22484	24	AAK96882	Nucleotide sequen	c 769	44	1.5	439	16	AAI22423	Human gene signatu
697	45	1.6	22484	24	AAK05882	Anticoagulant inhib	c 770	44	1.5	462	22	AAK57877	Human immune/haema
698	45	1.6	23855	22	AAI159411	Human excretory re	771	44	1.5	469	22	AAI90079	Human polynucleoti
699	45	1.6	23855	22	AAI63761	Human kidney relat	c 772	44	1.5	506	22	AAK68883	Human immune/haema
700	45	1.6	24983	22	AAK63262	Human reproductive	c 773	44	1.5	522	22	AAK70396	Human immune/haema
701	45	1.6	24983	22	AAK63262	Human reproductive	c 774	44	1.5	522	22	AAK70398	Human immune/haema
702	45	1.6	24983	23	ABL98457	Human reproductive	c 775	44	1.5	522	22	AAK70399	Human immune/haema
703	45	1.6	26995	22	AAS29963	Human lung antiva	776	44	1.5	533	24	ABN63875	Human cancer relat
704	45	1.6	28136	22	AAK69755	Human immune/haema	777	44	1.5	555	22	AAK09876	Human cDNA clone (
705	45	1.6	28180	22	AAK68439	Human immune/haema	778	44	1.5	558	22	AAK68419	Human lung tumour
706	45	1.6	30175	24	AAK32742	Human immune/haema	779	44	1.5	558	24	ABK38530	cDNA encoding elon
707	45	1.6	40515	22	AAK68732	Human immune/haema	780	44	1.5	571	24	ABV58977	Human prostate exp
708	45	1.6	40515	22	AAK85049	Human immune/haema	c 781	44	1.5	576	24	ABN61222	Human cancer relat
709	45	1.6	30515	23	AAK42321	Genomic sequence	c 782	44	1.5	583	22	AAH12473	Human cDNA clone (
710	45	1.6	30803	22	AAK68410	Human immune/haema	c 783	44	1.5	586	23	ABV51058	Human prostate exp
711	45	1.6	30826	22	ABK07345	Human paracrine fac	c 784	44	1.5	634	22	ABK80474	Human immune/haema
712	45	1.6	30826	22	AAS32772	Human genomic DNA	785	44	1.5	671	22	AAK07935	Human cDNA clone (
713	45	1.6	32150	22	AAS32454	Human genomic DNA	c 786	44	1.5	675	21	AAK64573	Nucleotide sequen
714	45	1.6	32176	22	AAS36455	Human cardiovascular	c 787	44	1.5	675	21	AAK64573	Nucleotide sequen
715	45	1.6	32178	22	AAS36454	Human cardiovascular	c 788	44	1.5	675	21	AAK64573	Nucleotide sequen
716	45	1.6	32185	22	AAI76856	Human musculoskele	c 789	44	1.5	675	21	AAK64573	Nucleotide sequen
717	45	1.6	32189	22	AAS40115	Human lung antiva	790	44	1.5	1066	24	AAK52527	Human colon cance
718	45	1.6	32216	22	ABK07741	Human ovarian and	c 791	44	1.5	1094	20	AAV84442	Human secreted pro
719	45	1.6	32216	22	AAI06923	Human reproductive	c 792	44	1.5	1094	22	ABK83425	Human cDNA sequen
720	45	1.6	32217	22	AAS17298	Human immune/haema	c 793	44	1.5	1917	22	AAH16477	Human cDNA sequen
721	45	1.6	32221	22	AAS10113	Human immune/haema	c 794	44	1.5	1917	22	AAH16477	Human cDNA sequen
722	45	1.6	34897	22	AAK84288	Human immune/haema	c 795	44	1.5	1917	22	AAH16477	Human cDNA sequen
723	45	1.6	40023	24	ABL51954	Human secreted pro	c 796	44	1.5	1780	22	AAS32597	Human immune/haema
724	45	1.6	40433	24	ABN96840	Genomic sequence	c 797	44	1.5	1817	22	AAH15104	Human cDNA sequen
725	45	1.6	57296	22	AAK78170	Human immune/haema	798	44	1.5	1832	22	AAH18103	Human cDNA sequen
726	45	1.6	57296	22	AAK78847	Human immune/haema	c 799	44	1.5	1917	22	AAH16477	Human cDNA sequen
727	45	1.6	57296	22	AAK79364	Human immune/haema	c 800	44	1.5	1998	24	ABK50232	cDNA encoding seri
728	45	1.6	57296	22	AAK86799	Human immune/haema	c 801	44	1.5	2056	20	AAK33845	Human HCMV inducib
729	45	1.6	65854	22	AAK86282	Human immune/haema	c 802	44	1.5	2056	24	ABK83487	Human cDNA differe
730	45	1.6	74037	24	ABK94412	Human immune/haema	c 803	44	1.5	2177	22	AAH17283	Human cDNA sequen
731	45	1.6	74962	22	AAK15256	Human protein phosphatase	c 804	44	1.5	2259	22	ABK14782	Human nervous syst
732	45	1.6	75899	24	ABK45261	Human genomic DNA	805	44	1.5	2510	24	ABK35328	Human cDNA encodin
733	45	1.6	81800	24	ABK84756	Human cDNA differe	c 806	44	1.5	2961	22	ABK17151	Human nervous syst
734	45	1.6	81800	24	ABK84756	Human cDNA differe	c 807	44	1.5	3121	20	AAK03037	Human IL-1ra HAC c
735	45	1.6	84495	24	AAS20588	Human reproductive	808	44	1.5	3176	22	AAI60024	Human polynucleoti
736	45	1.6	84539	24	ABK64159	Human secreted pro	809	44	1.5	413	22	AAI14721	Human polynucleoti
737	45	1.6	92638	24	ABK68695	Human osteoblast 3	810	44	1.5	471	22	AAK67524	Human immune/haema
738	45	1.6	94014	24	ABN96941	Genomic sequence	811	44	1.5	472	24	ABK44006	Genomic sequence
739	45	1.6	110000	22	AAK84799	Nucleotide sequen	c 812	44	1.5	491	22	AAK68488	Human immune/haema

813	44	1.5	3945	22	AAK83730	Human immune/haema	886	44	1.5	31168	22	AAK89940	Human digestive sy
814	44	1.5	3977	22	AAH18230	Human cDNA sequence	887	44	1.5	31169	22	AAK41761	Genomic sequence
815	44	1.5	4372	22	AAH18649	Human cDNA sequence	888	44	1.5	31169	22	AAK75191	Human immune/haema
816	44	1.5	4900	24	ALA44026	Human P2X7 gene 5'	889	44	1.5	31169	23	ABK44029	Genomic DNA endodi
817	44	1.5	5041	22	ALA17153	Human nervous syst	890	44	1.5	31304	22	ABA08089	Human ovarian and
818	44	1.5	5841	22	ABA20175	Human nervous syst	891	44	1.5	31304	22	AAI06868	Human reproductive
819	44	1.5	5845	22	ABA20477	Human nervous syst	892	44	1.5	32134	22	ABA15354	Human nervous syst
820	44	1.5	6045	22	AAH18244	Human cDNA sequence	893	44	1.5	32134	22	ABA15813	Human nervous syst
821	44	1.5	6107	22	AAH05182	Human reproductive	894	44	1.5	32134	22	AAI04075	Human reproductive
822	44	1.5	6107	23	AAH98246	Human testicular a	895	44	1.5	32184	22	AAI18001	Human nervous syst
823	44	1.5	6286	22	AAH27503	Human testicular a	896	44	1.5	32184	22	AAI04612	Human reproductive
824	44	1.5	6286	22	AAH64759	Human immune/haema	897	44	1.5	32188	23	ABL97535	Human testicular a
825	44	1.5	6737	22	AAH58438	Human polynucleoti	898	44	1.5	32205	22	AAH28365	Genomic sequence
826	44	1.5	6737	21	AAH94062	Human hydrocortiso	899	44	1.5	32205	22	AAH29831	Human cytoskeletal
827	44	1.5	7588	22	AAI07036	Human reproductive	900	44	1.5	32205	22	AAH33426	Human complete genom
828	44	1.5	7588	22	AAI16274	Human breast of ov	901	44	1.5	35651	22	AAH75795	Human immune/haema
829	44	1.5	7703	22	AAH90404	Human digestive sy	902	44	1.5	37449	22	AAH66874	Human immune/haema
830	44	1.5	7703	22	AAH90445	Human digestive sy	903	44	1.5	39969	22	AAH5853	Human immune/haema
831	44	1.5	7703	22	AAH31439	Human liver associ	904	44	1.5	46107	22	AAH71730	Human immune/haema
832	44	1.5	10634	22	AAH31460	Human liver associ	905	44	1.5	50000	24	AAH98944	Human asthma-assoc
833	44	1.5	7703	24	AAH90294	Human liver antiq	906	44	1.5	56804	22	AAH87050	Human transporter
834	44	1.5	7703	24	AAH90345	Human liver antiq	907	44	1.5	75384	22	AAH85590	Human immune/haema
835	44	1.5	9181	22	AAH70944	Human immune/haema	908	44	1.5	84539	24	ABL64158	Stomach cancer rel
836	44	1.5	9211	22	AAH70941	Human immune/haema	909	44	1.5	90220	24	AAH83576	Human cDNA differe
837	44	1.5	10503	22	AAH89097	Human digestive sy	910	44	1.5	103747	24	AAH88139	Human osteoblast d
838	44	1.5	10634	22	AAH05488	Human reproductive	911	44	1.5	121724	24	AAH88143	Human osteoblast d
839	44	1.5	10634	23	AAH58431	Human testicular a	912	44	1.5	125439	24	AAH88177	Human osteoblast d
840	44	1.5	11566	22	AAH14380	Human nervous syst	913	44	1.5	149480	24	ABL61947	Colon adenocarcino
841	44	1.5	11942	22	AAH15442	Human CHRNA2 gene	914	44	1.5	149480	24	ABL61948	Colon adenocarcino
842	44	1.5	12931	22	AAH80322	Human immune/haema	915	44	1.5	149480	24	ABL68365	Kidney cancer rela
843	44	1.5	15266	22	AAH37432	Human musculoskele	916	44	1.5	149671	24	AAH84797	Human cDNA differe
844	44	1.5	15266	22	AAH73549	Human immune/haema	917	44	1.5	227968	24	AAH83497	Genomic sequence
845	44	1.5	15271	22	AAH37433	Human musculoskele	918	43	1.5	105	22	AAH28262	Genomic sequence
846	44	1.5	15271	22	AAH73550	Human immune/haema	919	43	1.5	105	22	AAH31529	Human DNA for a no
847	44	1.5	17216	22	AAH18237	Human nervous syst	920	43	1.5	105	24	AAH66853	Human polynucleoti
848	44	1.5	17216	22	AAH37200	Human musculoskele	921	43	1.5	109	22	AAH70222	Human immune/haema
849	44	1.5	17217	22	AAH18249	Human nervous syst	922	43	1.5	129	22	AAH73560	Human immune/haema
850	44	1.5	17217	22	AAH37301	Human musculoskele	923	44	1.5	133	22	AAH67352	Human immune/haema
851	44	1.5	17450	22	AAH05453	Human reproductive	924	43	1.5	233	22	AAH67364	Human immune/haema
852	44	1.5	17450	22	AAH70834	Human immune/haema	925	43	1.5	266	22	AAH77717	Human immune/haema
853	44	1.5	17450	23	AAH98517	Human testicular a	926	43	1.5	280	14	AAH61255	Human brain expres
854	44	1.5	17679	22	AAH167271	Human PK556-Eindin	927	43	1.5	299	22	AAH42942	Human cDNA 3'-end
855	44	1.5	17679	22	AAH167272	Human PK556-Eindin	928	43	1.5	300	20	AAH214872	Human gene express
856	44	1.5	17906	22	AAH20616	Human nervous syst	929	43	1.5	300	21	AAH00232	Human colon cancer
857	44	1.5	17909	22	AAH20606	Human nervous syst	930	43	1.5	302	22	AAH83454	Human immune/haema
858	44	1.5	18010	22	AAH67807	Human immune/haema	931	43	1.5	304	24	AAH77791	Human ovarian can
859	44	1.5	18047	22	AAH80292	Human immune/haema	932	43	1.5	309	23	AAH42588	Genomic sequence
860	44	1.5	18132	22	AAH67073	Human immune/haema	933	43	1.5	309	23	AAH42589	Genomic sequence
861	44	1.5	18132	22	AAH70622	Human immune/haema	934	43	1.5	324	22	AAH04245	Human reproductive
862	44	1.5	19851	22	AAH85652	Human immune/haema	935	43	1.5	324	22	AAH04247	Human reproductive
863	44	1.5	20512	24	AAH38449	Human cDNA endodi	936	43	1.5	324	22	AAH04249	Human immune/haema
864	44	1.5	20869	22	AAH16245	Human cardiovascular	937	43	1.5	337	22	AAH76181	Human immune/haema
865	44	1.5	20869	22	AAH36927	Human cardiovascular	938	43	1.5	337	22	AAH76182	Human immune/haema
866	44	1.5	20869	22	AAH85501	Human immune/haema	939	43	1.5	348	22	AAH88781	Human polynucleoti
867	44	1.5	20966	21	AAH00552	Human AP1 (Adipos	940	43	1.5	361	24	AAH83474	Human ovarian can
868	44	1.5	20966	22	AAH01074	Human AP2 gene	941	43	1.5	370	24	AAH64074	Human cancer relat
869	44	1.5	20966	24	AAH96121	Human nucleic acid	942	43	1.5	371	14	AAH60868	Human brain expres
870	44	1.5	20966	24	AAH69243	Human AP1 DNA	943	43	1.5	383	22	AAH183636	Human polynucleoti
871	44	1.5	21423	22	AAH36470	Human musculoskele	944	43	1.5	391	24	ABL84923	Human ovarian can
872	44	1.5	21777	22	AAH74596	Human immune/haema	945	43	1.5	395	22	AAH89318	Human polynucleoti
873	44	1.5	23130	22	AAH77045	Human immune/haema	946	43	1.5	402	23	AAH12344	Human prostate exp
874	44	1.5	24132	22	AAH28227	Human immune/haema	947	43	1.5	407	24	AAH61166	Human cancer relat
875	44	1.5	24132	22	AAH68729	Human cDNA differe	948	43	1.5	417	23	AAH03175	Human prostate exp
876	44	1.5	24843	24	AAH17764	Human immune/haema	949	43	1.5	420	22	AAH10569	Human cDNA clone
877	44	1.5	25837	22	AAH85952	Human immune/haema	950	43	1.5	422	21	AAH22862	Human secreted pro
878	44	1.5	26059	22	AAH69104	Human immune/haema	951	43	1.5	433	23	AAH50990	Human prostate exp
879	44	1.5	28068	21	AAH59650	Human modified adenovira	952	43	1.5	435	22	AAH64271	Human immune/haema
880	44	1.5	28772	24	AAH83355	Human cDNA differe	953	43	1.5	443	23	AAH33488	Human prostate exp
881	44	1.5	30393	22	AAH67239	Human immune/haema	954	43	1.5	443	23	AAH42411	Human prostate exp
882	44	1.5	31168	22	AAH07245	Human factoratio	955	43	1.5	459	22	AAH17152	Human breast cance
883	44	1.5	31168	22	AAH42115	Genomic sequence	956	43	1.5	471	22	AAH89210	Human polynucleoti
884	44	1.5	31168	22	AAH22864	Human encoding factor	957	43	1.5	479	24	AAH62597	Human cancer relat
885	44	1.5	31168	22	AAH64760	Human immune/haema	958	44	1.5	483	23	AAH49071	Human prostate exp

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C 959      43      1.5      484      22      AAL09263      Human breast cancer
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C 961      43      1.5      491      23      ABV48603      Human prostate exp
C 962      43      1.5      504      24      ABN64112      Human cancer relat
C 963      43      1.5      505      23      ABV39239      Human prostate exp
C 964      43      1.5      506      23      ABV50106      Human prostate exp
C 965      43      1.5      508      24      AAK65485      Human cancer relat
C 966      43      1.5      551      22      AAK58126      Human immune/haema
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C 969      43      1.5      635      22      AAK80472      Human immune/haema
C 970      43      1.5      646      22      AAK36382      Human card.ovascu
C 971      43      1.5      669      23      ABV19297      Human prostate exp
C 972      43      1.5      670      22      AAL06366      Human reproductive
C 973      43      1.5      721      22      AAK04257      Human cDNA clone (
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C 978      43      1.5      780      23      ABV28166      Human prostate exp
C 979      43      1.5      975      22      AAK98367      Human ESR-derived
C 980      43      1.5      1001      21      AAK51346      Human GGT5 related
C 981      43      1.5      1043      20      AAZ24882      Human secreted pro
C 982      43      1.5      1100      22      AAF82458      Human survivin pro
C 983      43      1.5      1115      24      ABA96904      Human peroxisome f
C 984      43      1.5      1141      21      AAK59410      Human secreted pro
C 985      43      1.5      1173      22      AAK94575      Human foetal cDNA
C 986      43      1.5      1248      24      AAD33244      Human secreted pro
C 987      43      1.5      1383      20      AAZ10651      cDNA encoding a hu
C 988      43      1.5      1504      21      AAK59926      Human cDNA sequenc
C 989      43      1.5      1574      22      AAK16957      cDNA sequence #292
C 990      43      1.5      1635      24      AAK62505      Human cDNA encodin
C 991      43      1.5      1778      24      ABK28648      Human nervous syst
C 992      43      1.5      1813      22      ABA20204      Human cDNA sequenc
C 993      43      1.5      1925      22      AAK17259      Human cDNA sequenc
C 994      43      1.5      2266      22      AAK16444      Human cDNA sequenc
C 995      43      1.5      2305      24      ABA05055      Human phosphoster
C 996      43      1.5      2310      12      AAK14851      cGene p1u1283 enco
C 997      43      1.5      2400      22      AAK16542      Human cDNA sequenc
C 998      43      1.5      2453      23      AAS90977      cDNA encoding novel
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1000      43      1.5      2761      22      AAS22438      Human cDNA encodin

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ALIGNMENTS

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ID      AAD37267 standard; DNA; 2910 bp.
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XX      21-AUG-2002 (first entry)
XX
XX      Human ABC1 transcription regulatory DNA #3.
DE
XX      Human; A1P-binding cassette 1; ABC1 gene regulation; atherosclerosis;
KW      cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.
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XX      Homo sapiens.
XX
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XX      /bound_moiety= "LMO2/COM/MYOD"
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XX      /tag      c
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FT	protein_bind	/*tag- ae	FT	protein_bind	/bound_moiety- "MZF1"
FT	protein_bind	/bound_moiety- "SRY"	FT	protein_bind	2634..2648
FT	protein_bind	1840..1850	FT	protein_bind	/*tag- bd
FT	protein_bind	/*tag- af	FT	protein_bind	/bound_moiety- "LMO2COM/MYOD/E47"
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FT	protein_bind	1942..1956	FT	protein_bind	/*tag- be
FT	protein_bind	/*tag- ag	FT	protein_bind	/bound_moiety- "RREB1"
FT	protein_bind	/bound_moiety- "HNF3beta"	FT	protein_bind	2680..2698
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FT	protein_bind	/*tag- ak	FT	protein_bind	/bound_moiety- "NFE2A1"
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Gaps	0;						
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DB	1	ACAGGGCATGGTGGCAGGTGGCTGTAATCTCAGTTACTCGGAGGTGAGGTTCGAATGA	60				
QY	61	GCCAGATCGGACCATTCGACCTCCAGCCTGGGCAACAAAGGTGAACTCCATCTCAATT	120				
DB	61	GCCAGATCGGACCATTCGACCTCCAGCCTGGGCAACAAAGGTGAACTCCATCTCAATT	120				
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DB	121	AAAAAANAAGATGATTTTGGTGGCTGACTCAATAGGTAGGAGAGAGAGAGAGG	180				
QY	181	AGATGGAGGTCAGGAGATCTAATTAATCTCTAAAATCATGCTAGGAAAGATAACACCT	240				
DB	181	AGATGGAGGTCAGGAGATCTAATTAATCTCTAAAATCATGCTAGGAAAGATAACACCT	240				
QY	241	TTTAATAACACTCTCTGCTTTTATAACATCATCTGCCAAGAGCTCAAGGTTTCACA	300				
DB	241	TTTAATAACACTCTCTGCTTTTATAACATCATCTGCCAAGAGCTCAAGGTTTCACA	300				
QY	301	AAGTTCACTTTCAGAAACCCCTTTGAGGAGACAGATATACATCTTCTCTCCATTTTA	360				
DB	301	AAGTTCACTTTCAGAAACCCCTTTGAGGAGACAGATATACATCTTCTCTCCATTTTA	360				
QY	361	AGATGAGAAACAGGTCGGGACAAATGGCTAATGCCCTGATCCAGCCTTTGGGAGG	420				
DB	361	AGATGAGAAACAGGTCGGGACAAATGGCTAATGCCCTGATCCAGCCTTTGGGAGG	420				
QY	421	CTGAGGCCAGAGATCGCTTGAGCTCCAGAGTTTGAGACACAGCTGGGATACATCGGAA	480				
DB	421	CTGAGGCCAGAGATCGCTTGAGCTCCAGAGTTTGAGACACAGCTGGGATACATCGGAA	480				
QY	481	ACCTGTCTCTACAAAAAATACAAAAATAGATGGGTGGTGGGATGCACCTGTGGT	540				
DB	481	ACCTGTCTCTACAAAAAATACAAAAATAGATGGGTGGTGGGATGCACCTGTGGT	540				
QY	541	CCAGCTACTTGGAGGCTAAGTGGGAGGATCGCTTGAGCCCGGAGTCAAGCTACAC	600				
DB	541	CCAGCTACTTGGAGGCTAAGTGGGAGGATCGCTTGAGCCCGGAGTCAAGCTACAC	600				

CC with cholesterol transport. The genes and proteins are also useful for
CC. CC are also useful as diagnostic indicators of cardiovascular disease and
CC. CC are other disorders associated with hypercholesterolemia.
XX
SQ Sequence 1643 BP: 370 A: 413 C: 457 G: 403 T: 0 others:

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Query Match      18.7%; Score 541; DB 22; Length 1643;
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[illegible]

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RESULT 5
AAF24703
10 AAF24703 standard; DNA: 1643 bp.
XX
XX AAF24703;
XX
XX 20-APR 2001 (first entry)

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Nucleotide sequence of the 5' flanking region of the human ANGII gene

KW human; adenosine triphosphate binding cassette protein-1; ANG1;
XX angiotensinogenase
KW angiotensinogenase; cholesterol; lipid; enzyme;
XX chromosome q22-q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss

XX
XX
XX Homo sapiens.
XX
XX W250C78971-A2.
XX
XX
XX 28 DEC 2000.
XX
XX 15 JUN 2000: 2000WC-US16591.
XX OF

XX 18-JUN-1999; 99US-0140264.
 XX PR 14-SEP-1999; 99US-0153872.
 XX PR 19-NOV-1999; 99US-0166573.
 XX
 XX (CVTH-) CV THERAPEUTICS INC.
 XX (UNIW) UNIV WASHINGTON.
 XX PA
 XX PA
 XX PA
 XX PI Lawn RM, Wade D, Oram JF, Garvin M;
 XX WPI; 2001-137811/14.
 XX
 XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
 XX PT polynucleotides and polypeptides, useful for treatment of heart disease
 XX PT and other disorders associated with hypercholesterolemia and
 XX PT atherosclerosis -
 XX
 XX Disclosure: Page 138-149; 211pp; English.
 XX PS

The present sequence represents the 5' flanking region of the human adenosine triphosphatase (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for other disorders associated with hypercholesterolemia.

Sequence 1643 BP: 370 A; 413 C; 457 G; 403 T; 0 other;

Query Match	18.7%	Score 541	DB 22	Length 1643
Best Local Similarity	100.0%	pred. No. 1.7e+236		
Matches 541	Conservative 0	Mismatches 0	Indels 0	Gaps 0

[illegible]

QY 2190 GTAAGATGTTCTCTCTCGGGTCCCTCTGAGCGACCTGGGAGCTTGGTAAATCTTAA 4241

[illegible]

DR WPI:

DR WPI: 2002-179323/23.

XX The invention relates to the human ribosomal S11 protein 12 with
CC cytosolic, virucidal, immunomodulatory, antiinflammatory and
CC haemostatic activity. The protein and encoding polynucleotide are used
CC in diagnosis and treatment of malignant tumour, haemophy, human
CC immunodeficiency virus (HIV) infection, immunological diseases and
CC various inflammations. The polynucleotide is useful in gene therapy.

SQ Sequence 1416 BP; 338 A; 306 C; 297 G; 375 T; 0 other;

Query Match 1.88; Score 52; EB 22; Length 1376
Best Local Similarity 100.0%; Pred. No. 20-13; Mismatches 0 Gaps 0
Matches 52; Conservative 0;

Qy 1193 ACCTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACATGGGCAAT 1244
|||||
Db 977 ACCTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACATGGGCAAT 1028
|||||

RESULT 14

AAS31466/c

ID AAS31466 standard; DNA; 5351 BP.

XX AAS31466;

XX 04-DEC-2001 (first entry)

DE Human DNA for a novel extracellular matrix protein. Seq ID No 545.

XX Human; secreted extracellular matrix protein; ds; immunomodulatory;
KW Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiac; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
KW antihelmets; immune/autoimmune disease; HIV infection; anaemia;
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
KW cancers; hyperproliferative disorder; breast neoplasm; melanoma;
KW Searcy syndrome; Gaucher's disease; neurological diseases;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW cardiac arrest; tachycardia; angina; infection; corneal infections;
KW wound healing; immunogen; gene therapy; antisense; food additive.

OS Home sapiens.

PN W0200155468-A1.

XX 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01348.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 12-SEP-2000; 2000US-0231968.
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PR 14-SEP-2000; 2000US-0232400.
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PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-465572/50.

Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers

Claim 1: SEQ ID NO 545; 577pp; English.

The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SEPs), the polypeptides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SEPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SEPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SEPs may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SEPs. The anti-SEP antibodies and antagonists may also be used to down regulate expression and activity of SEPs and as diagnostic agents for detecting the presence of SEPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections), other uses

CC Include wound healing, maintenance of organs before transplantation,
CC support of cell culture of primary tissues, modulation of for example

Query Match 1.8%; Score 52; DB 22; Length 5351;
Best Local Similarity 100.0%; Pred No. 1.9e-13;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1193 ACCITGGCTCCCAAGTGTGGATTACAGGATGAGCCACTGCCGCCAGC 1244
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DB 989 ACCITGGCTCCCAAGTGTGGATTACAGGATGAGCCACTGCCGCCAGC 938

RESULT 15

AHQ66790/c

ID AHQ66790 standard; DNA: 5351 BP.

XX AC ABQ66790;

XX DT 23-AUG-2002 (first entry)

DE Human polynucleotide SEQ ID NO 545.

XX Human; nontropic; neuroprotective; cytostatic; dermatological; viricide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antistickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antitungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

OS Homo sapiens.

XX US2002042386-A1.

XX PD 11-APR-2002.

XX PE 17-JAN-2001; 2001US-0764870.

XX PR 31-JAN-2000; 2000US-179065P.

PR 04-FEB-2000; 2000US-180628P.

PR 28-JUN-2000; 2000US-214886P.

PR 07-JUL-2000; 2000US-216647P.

PR 07-JUL-2000; 2000US-216680P.

PR 11-JUL-2000; 2000US-217487P.

PR 11-JUL-2000; 2000US-217495P.

PR 26-JUL-2000; 2000US-220963P.

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PR 14-AUG-2000; 2000US-224518P.

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PR 14-AUG-2000; 2000US-225268P.

PR 14-AUG-2000; 2000US-225270P.

PR 14-AUG-2000; 2000US-225447P.

PR 14-AUG-2000; 2000US-225757P.

PR 22-AUG-2000; 2000US-225758P.

PR 30-AUG-2000; 2000US-226468P.

PR 01-SEP-2000; 2000US-229287P.

PR 01-SEP-2000; 2000US-229343P.

PR 01-SEP-2000; 2000US-229344P.

PR 01-SEP-2000; 2000US-229445P.

PR 05-SEP-2000; 2000US-229509P.

PR 05-SEP-2000; 2000US-229513P.

PR 08-SEP-2000; 2000US-231413P.

PR 21-SEP-2000; 2000US-234223P.

PR 21-SEP-2000; 2000US-234274P.

PR 25-SEP-2000; 2000US-234997P.

PR 27-SEP-2000; 2000US-235834P.

PR 29-SEP-2000; 2000US-236327P.

PR 29-SEP-2000; 2000US-236367P.

PR 29-SEP-2000; 2000US-236368P.

PR 29-SEP-2000; 2000US-236369P.


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PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
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PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
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PR 29-SEP-2000; 2000US-0236367.
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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237038.
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PR 08-NOV-2000; 2000US-0246476.
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PR 08-NOV-2000; 2000US-0246523.
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PR 17-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
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PR 17-NOV-2000; 2000US-0249224.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMAN) HUMAN GENOME SCI INC.
XX
PI Kosen CA, Harash SC, Ruben SM:
XX
DR WP1: 2001-465572/50.
XX
PT Nucleic acid molecules encoding human secreted extracellular matrix
PT proteins, used in preventing, treating or ameliorating a disorder, e.g.
PT Alzheimer's and Parkinson's diseases and cancers -
XX
PS Claim 1: SEQ ID No 546; 577pp; English.
XX
CC The invention relates to isolated nucleic acid molecules encoding
CC novel human secreted extracellular matrix proteins (SPs). The
CC polynucleotides and proteins are used to prevent, treat a medical
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
CC chickens or sheep. For example, disorders associated with decreased
CC expression of SPs. The SP polynucleotide or a vector expressing them may
CC be administered to treat diseases by gene therapy. Antisense molecules
CC may be administered to down regulate expression of SPs by binding with
CC the cells own genes and preventing their expression. The polynucleotides
CC may also be used as DNA probes in diagnostic assays. The SPs may also be
CC used as antigens to produce antibodies and to identify modulators
CC (agonists and antagonists) of the SPs. The anti-SP antibodies and
CC antagonists may also be used to down regulate expression and activity of
CC SP and as diagnostic agents for detecting the presence of SPs in samples.
CC The disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
CC Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac
CC arrest, tachycardia and angina), infections caused by bacteria, viruses
CC and fungi and ocular disorders (e.g. corneal infections). Other uses
CC include wound healing, maintenance of organs before transplantation,
CC support of cell culture of primary tissues, modulation of for example
CC
Query Match 1.8%; Score 52; DB 22; Length 6461.
Best Local Similarity 100.0%; Pred. No. 1.9e-13; Mismatches 0; Gaps 0;
Matches 52; Conservative 0; Indels 0;
QY 1193 ACCTTGCTGTCACAAAGTGTGGATTCAGGCATGACGACCTGCGCCGACG 1244
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ID 4277 ACCTTGCTGTCACAAAGTGTGGATTCAGGCATGACGACCTGCGCCGACG 4266
RESULT 17
ABQ66791/C
ID ABQ66791 standard; DNA: 6461 BP.
XX
AC ABQ66791;
XX
XX 23-AUG-2002 (first entry)
DE Human polynucleotide SEQ ID NO 546.
XX
KW human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antiskinning; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
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PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
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PR 08-SEP-2000; 2000US-0231242.
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PR 02-OCT-2000; 2000US-0237037.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
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PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis.
PS Disclosure: SEQ ID NO 20009; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 8319 BP; 2521 A; 1610 C; 1560 G; 2628 T; 0 other;

PR 08-NOV-2000: 2000US-0246613.
PR 17-NOV-2000: 2000US-0249207.
PR 17-NOV-2000: 2000US-0249208.
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PR 17-NOV-2000: 2000US-0249300.
PR 01-DEC-2000: 2000US-0250160.
PR 01-DEC-2000: 2000US-0250391.
PR 05-DEC-2000: 2000US-0251030.
PR 05-DEC-2000: 2000US-0251988.
PR 05-DEC-2000: 2000US-0256719.
PR 05-DEC-2000: 2000US-0251479.
PR 08-DEC-2000: 2000US-0251856.
PR 08-DEC-2000: 2000US-0251868.
PR 08-DEC-2000: 2000US-0251869.
PR 08-DEC-2000: 2000US-0251989.
PR 08-DEC-2000: 2000US-0251990.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-483426/52.

Nucleic acids encoding human immune/haematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure: SEQ ID NO 25603; 307lpp + Sequence Listing: English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have catalytic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or (I) supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK64702 and AAK82169 represent sequences used in the exemplification of the present invention.

Sequence 29329 BP: 6864 A: 6756 C: 7225 G: 8484 T: 0 other:

Query Match 1.8%; Score 52; BB 22; Length 29329;
Best local Similarity 100.0%; Pred. No. 1-5e 13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CIGCCACCTTGGGCTCCCAAGTGGGATACAGGATAGAGGACACTG 1248
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DB 22210 CIGCCACCTTGGGCTCCCAAGTGGGATACAGGATAGAGGACACTG 22159

RESULT 23

AAK78512/C

1D AAK78512 standard; DNA; 29329 BP.

XX

AC AAK78512;

XX 07-NOV-2001 (first entry)

DT Human immune/haematopoietic antigen genomic sequence SEQ ID NO:13124.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

XX WO200157182-A2.

PN 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

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PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

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PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

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PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233085.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 26-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.

PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMAN) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI: 2001-483426/52.
DR
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis.
PT
XX
PS Disclosure: SEQ ID NO 33324; 3071pp + Sequence Listing: English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 29329 BP: 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
Query Match 1.8%; Score 52; DB 22; Length 29329;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1187 CTGCCACCTTAACTTCCAAAGTCTGGATTACAGGCATGAGCCACTGG 1238
|||||
DB 22210 CTGCCACCTTGGCTCCAAAGTCTGGATTACAGGCATGAGCCACTGG 22159
RESULT 24
AAC25949/c
ID AAC25949 standard; cDNA: 149 BP.
XX
AC AAC25949:
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 30024.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX Homo sapiens.
OS
XX
PN EF1033401-A2.
XX
PD 06-SEP-2000.

CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (4) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 381 BP; 81 A; 103 C; 86 G; 111 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 396;
Best Local Similarity 100.0%; Prod. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CTTGGGCTCCCAAGTCTGGGATTACAGGCAATGAGCACTGGGCTAG 1244
|||||
DB 217 CTTGGGCTCCCAAGTCTGGGATTACAGGCAATGAGCACTGGGCTAG 267
|||||

RESULT 29
AA181653/C
ID AA181653 standard; cDNA; 396 BP.
XX
AC AA181653;
XX
DT 06-MAY-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1713;
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens;
XX
PN W0200164835-A2.
XX
PD 07-SEP-2001.
XX
TF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577459.
XX
XX (HYSEQ) HYSEQ INC.
XX
PI Tang YL, Liu C, Drmanac RT;
XX
DR WPI: 2001 514838/56.
DR P PSDB: AA001722.
XX
PI Isolated nucleic acids and polypeptides, useful for preventing
PI diagnosing and treating e.g. leukaemia, inflammation and immune
PI disorders.
XX
PS Claim 1: SEQ ID NO 1713; 1399pp. Sequence tested. Federal.
XX
XX The invention relates to human polynucleotides (AA179943-AA194847) and
CC the encoded proteins (AA000010-AA021816) that exhibit activity related to
CC cytokine, cell proliferation or cell differentiation of which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful to generate vaccines or
CC peptide therapy. The polypeptides have various cytokine like activities,
CC e.g. stem cell growth factor activity, haematopoiesis-inducing
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO
CC at http://wipo.int/pub/published_pot_sequences.

SQ Sequence 396 BP; 124 A; 75 C; 87 G; 110 T; 0 other;

Query Match 1.8%; Score 51; DB 22; Length 396;
Best Local Similarity 100.0%; Prod. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGGCTCCCAAGTCTGGGATTACAGGCAATGAGCACTGC 1237
|||||
DB 378 CTGCCACCTTGGGCTCCCAAGTCTGGGATTACAGGCAATGAGCACTGC 328
|||||

RESULT 30
ABV34857
ID ABV34857 standard; cDNA; 406 BP.
XX
AC ABV34857;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 34848.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200150860-A2.
XX
PD 23-AUG-2001.
XX
PR 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US 183119P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219607P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX
PI Novel isolated nucleic acid molecule associated with cancerous state of
PI prostate cells and correlating with presence of prostate cancer, useful
PI for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1: Page 1246-7291; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (i) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV02213) of the
CC specification or its complement, (ii) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 406 BP; 86 A; 108 C; 93 G; 117 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 406;
Best Local Similarity 100.0%; Prod. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244
|||||
DB 242 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 292

RESULT 3:

ID ABV34074
XX
AC ABV34074;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 34064.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200160860 A2.
XX
PD 24-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
XX
PR 16-MAR-2000; 2000US-189862P.
XX
PR 25-MAY-2000; 2000US-207454P.
XX
PR 09-JUN-2000; 2000US-211314P.
XX
PR 18-JUL-2000; 2000US-219007P.
XX
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX

PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

PS Claim 1: Page 7178; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 412 BP: 98 A; 88 C; 89 G; 137 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 412;
Best Local Similarity 100.0%; Pred. No. 5, 6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244

|||||

DB 158 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 268

RESULT 12

ABV42939
ID ABV42939 standard; cDNA: 412 BP.
XX
AC ABV42939;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 42930.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200160860 A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
XX
PR 16-MAR-2000; 2000US-189862P.
XX
PR 25-MAY-2000; 2000US-207454P.
XX
PR 09-JUN-2000; 2000US-211314P.
XX
PR 18-JUL-2000; 2000US-219007P.
XX
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX

PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

PS Claim 1: Page 8579; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 412 BP: 98 A; 88 C; 89 G; 137 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 412;
Best Local Similarity 100.0%; Pred. No. 5, 6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244

|||||

DB 158 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 208

RESULT 33

AA187958/c
ID AA187958 standard; cDNA: 425 BP.
XX
AC AA187958;
XX
DT 06-NOV-2001 (first entry)


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PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1: Page 799; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (1) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (1) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenetic marker.
XX
XX Sequence 446 BP: 108 A; 112 C; 96 G; 127 T; 3 other;
XX
XX Query Match 1.8%; Score 51; DB 23; Length 446;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-13;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1194 CTTGGCTGCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCGCAAT 244
XX |||||
XX 212 CTTGGCTGCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCGCAAT 262
XX
XX RESULT 46
XX ABV02959
XX ID ABV02959 standard: cDNA; 459 BP.
XX
XX AC ABV02959;
XX
XX DT 14-SEP-2002 (first entry)
XX
XX DE Human prostate expression marker cDNA 2959.
XX
XX KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenetic marker; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200160860-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 20-FEB-2001; 2001WO-US05171.
XX
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX
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XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1: Page 549; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (1) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (1) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenetic marker.
XX
XX Sequence 459 BP: 106 A; 118 C; 100 G; 135 T; 0 other;
XX
XX Query Match 1.8%; Score 51; DB 23; Length 459;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-13;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1194 CTTGGCTGCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCGCAGC 1244
XX |||||
XX 210 CTTGGCTGCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCGCAGC 260
XX
XX RESULT 37
XX ABV34901
XX ID ABV34901 standard: cDNA; 512 BP.
XX
XX AC ABV34901;
XX
XX DT 16-SEP-2002 (first entry)
XX
XX DE Human prostate expression marker cDNA 34892.
XX
XX KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenetic marker; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200160860-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 20-FEB-2001; 2001WO-US05171.
XX
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI: 2001-662795/76.
XX
```

XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer;
 XX Claim 1: Page 7297-7298; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification of its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 512 BP; 118 A; 136 C; 114 G; 144 T; 0 other;

Query Match 1.8%; Score 51; DB 24; Length 512;
 Best Local Similarity 100.0%; Pred. No. 5.6e-13;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTTGGCTCCCAAGTCTCGGATTACAGGATGAGCCACTGCGCCAGC 1244
 |||||||
 DB 250 CTTTGGCTCCCAAGTCTCGGATTACAGGATGAGCCACTGCGCCAGC 300

RESULT 38

ABV33273
 ID ABV33273 standard; cDNA; 515 BP.
 AC ABV33273;
 XX
 XX
 XX 16-SEP-2002 (first entry)
 XX Human prostate expression marker cDNA 33264.
 DE
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 KW
 OS Homo sapiens.
 OS
 XX WO200160860-A2.
 PN
 XX 23-AUG-2001.
 XX
 XX 20-FEB-2001; 2001WO-US05171.
 XX
 XX 17-FEB-2000; 2000US-183319P.
 PR
 PR 16-MAR-2000; 2000US-189862P.
 PR
 PR 25-MAY-2000; 2000US-207454P.
 PR
 PR 09-JUN-2000; 2000US-211314P.
 PR
 PR 18-JUL-2000; 2000US-219007P.
 PR
 PR 13-DEC-2000; 2000US-255281P.
 XX
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA
 XX Schlegel R, Endege WO, Monahan JE;
 P1
 XX WPI: 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer;
 XX Claim 1: Page 7053; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification of its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) determining whether prostate cancer has metastasized in a patient;
 CC (g) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 515 BP; 118 A; 135 C; 115 G; 146 T; 1 other;

Query Match 1.8%; Score 51; DB 23; Length 515;
 Best Local Similarity 100.0%; Pred. No. 5.6e-13;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTTGGCTCCCAAGTCTCGGATTACAGGATGAGCCACTGCGCCAGC 1244
 |||||||
 DB 255 CTTTGGCTCCCAAGTCTCGGATTACAGGATGAGCCACTGCGCCAGC 305

RESULT 39

ABV43707
 ID ABV43707 standard; cDNA; 515 BP.
 AC ABV43707;
 XX
 XX
 XX 16-SEP-2002 (first entry)
 XX Human prostate expression marker cDNA 43698.
 DE
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 KW
 OS Homo sapiens.
 OS
 XX WO200160860-A2.
 PN
 XX 23-AUG-2001.
 XX
 XX 20-FEB-2001; 2001WO-US05171.
 XX
 XX 17-FEB-2000; 2000US-183319P.
 PR
 PR 16-MAR-2000; 2000US-189862P.
 PR
 PR 25-MAY-2000; 2000US-207454P.
 PR
 PR 09-JUN-2000; 2000US-211314P.
 PR
 PR 18-JUL-2000; 2000US-219007P.
 PR
 PR 13-DEC-2000; 2000US-255281P.
 XX
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA
 XX Schlegel R, Endege WO, Monahan JE;
 P1
 XX WPI: 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer;
 XX Claim 1: Page 8698; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification of its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 515 BP: 118 A; 135 C; 115 G; 146 T; 1 other;
SQ

Query Match 1.8%; Score 51; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 255 CTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCCAGC 305
|||||

RESULT 4C
ABV32646
ID ABV32646 standard; cDNA: 521 BP.
XX
AC ABV32646;
XX
UT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 32637.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 15-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

Claim 1: Page 6956; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
(i) is also useful as a pharmacodynamic or pharmacogenomic marker.

CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 521 BP: 119 A; 138 C; 118 G; 146 T; 0 other;
SQ

Query Match 1.8%; Score 51; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 255 CTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCCAGC 300
|||||

RESULT 41
ABV41571
ID ABV41571 standard; cDNA: 521 BP.
XX
AC ABV41571;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 41562.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

Claim 1: Page 8451; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
(i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 521 BP: 119 A; 138 C; 118 G; 146 T; 0 other;
SQ

Query Match 1.8%; Score 51; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244
|||||
DB 250 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 300
|||||

RESULT 42
ABV42196
ID ABV42196 standard; cDNA: 521 BP.
XX AC ABV42196;
XX CT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 42187.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN W0200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI: 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer;
XX Claim 1: Page 8456; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-4 (ABV0010-ABV0213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 521 BP; 119 A; 138 C; 118 G; 146 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244
|||||

Db 250 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 300
|||||

RESULT 43
ABV43750
ID ABV43750 standard; cDNA: 521 BP.
XX AC ABV43750;
XX CT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 43741.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN W0200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI: 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer;
XX Claim 1: Page 8705-8706; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 521 BP; 119 A; 138 C; 118 G; 146 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244
|||||

Db 250 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 300
|||||

RESULT 44
ABV21487


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XX FN W0200160860-A2.
XX PN 23-AUG-2001.
XX PP 20-FEB-2001; 2001W0-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE.
XX PP WPI: 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX PS Claim 1; Page 3919-3920; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (1) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (1) is useful for:
XX CC (a) assessing whether a patient is afflicted with prostate cancer;
XX CC (b) monitoring the progression of prostate cancer in a patient;
XX CC (c) assessing the efficacy of a test compound to inhibit prostate
XX CC cancer in a patient;
XX CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX CC in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound;
XX CC (g) determining whether prostate cancer has metastasized in a patient;
XX CC (h) assessing the aggressiveness or indolence of prostate cancer in a
XX CC patient;
XX CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX SQ Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other.

Query Match 1.8%; Score 51; DB 23; Length 670;
Best Local Similarity 100.0%; Pred. No. 5,6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CTTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAGC 1244
      |||||
DB 198 CTTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAGC 248

RESULT 48
ABV27305
LQ ABV27305 standard; cDNA; 670 BP.
XX AC ABV27305;
XX DI 13-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 22943.
XX KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX CS Homo sapiens.
XX PN W0200160860-A2.
XX PP 23-AUG-2001.
XX PR 20-FEB-2001; 2001W0-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.

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XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE.
XX PP WPI: 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX PS Claim 1; Page 4073; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (1) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (1) is useful for:
XX CC (a) assessing whether a patient is afflicted with prostate cancer;
XX CC (b) monitoring the progression of prostate cancer in a patient;
XX CC (c) assessing the efficacy of a test compound to inhibit prostate
XX CC cancer in a patient;
XX CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX CC in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound;
XX CC (g) determining whether prostate cancer has metastasized in a patient;
XX CC (h) assessing the aggressiveness or indolence of prostate cancer in a
XX CC patient;
XX CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX SQ Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other.

Query Match 1.8%; Score 51; DB 23; Length 670;
Best Local Similarity 100.0%; Pred. No. 5,6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CTTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAGC 1244
      |||||
DB 198 CTTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAGC 248

RESULT 48
ABV27305
LQ ABV27305 standard; cDNA; 670 BP.
XX AC ABV27305;
XX DI 13-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 27296.
XX KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX CS Homo sapiens.
XX PN W0200160860-A2.
XX PP 23-AUG-2001.
XX PR 20-FEB-2001; 2001W0-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.

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PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
PS WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PI prostate cells and correlating with presence of prostate cancer, useful
PI for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1: Page 5550; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other:

Query Match 1.8%; Score 51; DB 23; Length 670;
Best Local Similarity 100.0%; Pred. No. 5,6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAC 1244
|||||
DB 198 CTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAC 248
|||||

RESULT 49
ABV27742
ID ABV27742 standard; cDNA; 670 BP.
XX
AC ABV27742;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 27742.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200160460-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
PS WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PI prostate cells and correlating with presence of prostate cancer, useful
PI for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1: Page 5550; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other:

Query Match 1.8%; Score 51; DB 23; Length 670;
Best Local Similarity 100.0%; Pred. No. 5,6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAC 1244
|||||
DB 198 CTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAC 248
|||||

RESULT 49
ABV27742
ID ABV27742 standard; cDNA; 670 BP.
XX
AC ABV27742;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 27742.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200160460-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
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PS Claim 1: Page 5888: 11750pp: English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in tables 1-9 (ABV00010-ABV0213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacokinetic marker.
XX
SQ Sequence 670 BP: 164 A; 167 C; 146 G; 190 T; 4 other:

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Query Match 1.88; Score 51; LH 28; Length 200;
Host Local Similarity 100.08; Pred No. 5,6e 13;
Matches 5: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1164 CTTGGGCTCCCAAGTCTGGGATTACAGCAATGAGCACTGCTCTAGT 1244
    |||||
DB 198 CTTGGGCTCCCAAGTCTGGGATTACAGCAATGAGCACTGCTCTAGT 248

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Search completed: May 9, 2003, 19:01:43
Job Time : 1790.62 secs

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QM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 16:20:31 : Search time 4448.15 seconds
(without alignment)
10533.268 Million cell updates/sec

Title: US-09-846-456-3

Perfect score: 2893

Sequence: 1 acaggcatggtgacagggtg.....ctagtcacgaacaaacccc 2693

Scoring Table: Origo, NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 30

Total number of hits satisfying chosen parameters: 42756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:

1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: qb_estli.*
10: qb_est2.*
11: qb_hic.*
12: qb_est3.*
13: qb_est4.*
14: qb_est5.*
15: em_estfun.*
16: em_estom.*
17: qb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
C	1	126	4.4	289	10	AW748338	AW748338 RC5-BT025
C	2	111	3.8	467	9	AA527406	AA527406 Bq37c02.S
C	3	58	2.0	617	10	BE178833	BE178833 PWC-H1060
C	4	57	2.0	219	17	AO538994	AO538994 K233-11-3
C	5	57	2.0	424	9	AA652813	AA652813 ON74C05.S
C	6	57	2.0	674	17	AO67644	AO67644 Pac trogl

7	56	1.9	569	13	BI059823	BI059823 IL3-UT011
8	56	1.9	600	13	BI015195	BI015195 M84-ET014
9	56	1.9	1054	12	BG745912	BG745912 602724092
10	55	1.9	384	12	BG014649	BG014649 IL5-GN023
11	55	1.9	387	12	BG007260	BG007260 IL5-GN023
12	55	1.9	444	17	AQ056873	AQ056873 CIT-HSP-2
13	54	1.9	325	9	AA010265	AA010265 nab50H08
14	54	1.9	405	12	BF431825	BF431825 nab50H08
15	54	1.9	468	10	AW104031	AW104031 X64405.X
16	54	1.9	814	12	BG576148	BG576148 602597119
17	53	1.8	453	17	AO663862	AO663862 HS-2151-B
18	53	1.8	658	9	A1610507	A1610507 tp19q09.X
19	52	1.8	233	13	BI062371	BI062371 IL3-UT011
20	52	1.8	249	13	BI710918	BI710918 i394q04.Y
21	52	1.8	348	13	BI711369	BI711369 i394q04.X
22	52	1.8	391	9	A1264119	A1264119 q108h11.X
23	52	1.8	392	14	BM730147	BM730147 1353f05.Y
24	52	1.8	414	9	AA481408	AA481408 zv02q09.S
25	52	1.8	416	9	A1679442	A1679442 tu63h07.X
26	52	1.8	417	9	A1337065	A1337065 qx82g11.X
27	52	1.8	417	9	A1679952	A1679952 tu67h07.X
28	52	1.8	450	13	BI062368	BI062368 IL3-UT011
29	52	1.8	455	9	A1089524	A1089524 OZ22a01.X
30	52	1.8	484	9	A1002969	A1002969 an23g03.S
31	52	1.8	493	14	BO007739	BO007739 UI-H-E10-
32	52	1.8	501	17	AO489571	AO489571 RPECI-11-2
33	52	1.8	530	10	AW971724	AW971724 EST383813
34	52	1.8	545	17	AO623696	AO623696 HS-5319-A
35	52	1.8	583	9	A1084593	A1084593 ox63f01.S
36	52	1.8	717	17	AO589333	AO589333 CITBI-E1-
37	52	1.8	753	10	AV718287	AV718287 AV718287
38	51	1.8	171	17	AQ198714	AQ198714 RPECI-11-59
39	51	1.8	232	9	AA662976	AA662976 ac52b01.S
40	51	1.8	360	14	H90008	H90008 yu83d03.S1
41	51	1.8	369	9	AA486970	AA486970 ab17f12.R
42	51	1.8	375	12	BF924753	BF924753 CM1-WT020
43	51	1.8	379	17	AQ280600	AQ280600 CITBI-E1-
44	51	1.8	394	17	AQ178114	AQ178114 HS-2217-B
45	51	1.8	448	14	H58672	H58672 yr20d05.S1
46	51	1.8	476	17	AO503896	AO503896 RPECI-11-2
47	51	1.8	479	17	AO334511	AO334511 HS-5011-A
48	51	1.8	498	17	AQ342716	AQ342716 RPECI-11-11
49	51	1.8	531	9	A1912862	A1912862 t220b03.X
50	51	1.8	539	17	AQ395413	AQ395413 CITBI-E1-
51	51	1.8	554	17	AQ260373	AQ260373 CITBI-E1-
52	51	1.8	591	17	AO586921	AO586921 RPECI-11-4
53	51	1.8	598	10	BF062160	BF062160 RCI-BT025
54	51	1.8	601	9	AL707228	AL707228 DKF2p686J
55	51	1.8	609	9	AA004719	AA004719 zh95b06.S
56	51	1.8	612	17	AO937500	AO937500 NB6-1040R
57	51	1.8	678	17	AG176924	AG176924 Pan trogl
58	51	1.8	686	17	AG083391	AG083391 Pan trogl
59	51	1.8	712	17	AG184007	AG184007 Pan trogl
60	51	1.8	925	14	BO800055	BO800055 AGENCECOURT
61	51	1.8	15970	17	AO839852	AO839852 260L13-C5
62	50	1.7	390	14	R48131	R48131 yj66a12.r1
63	50	1.7	468	17	AQ296069	AQ296069 HS-3080-A
64	50	1.7	488	14	HL6875	HL6875 ym33f04.r1
65	50	1.7	501	12	BE972845	BE972845 60152083
66	50	1.7	525	11	BC015976	BC015976 Homo sapi
67	50	1.7	572	14	BM722770	BM722770 UI-E-E00-
68	50	1.7	665	17	AG059141	AG059141 Pan trogl
69	50	1.7	672	17	AQ394009	AQ394009 CITBI-E1-
70	50	1.7	696	17	AG053850	AG053850 Pac trogl
71	50	1.7	700	13	BI259846	BI259846 60291503
72	50	1.7	747	12	BO385823	BO385823 602454059
73	50	1.7	763	12	BF674499	BF674499 602137277
74	50	1.7	890	14	BQ926504	BQ926504 AGENCECOURT
75	50	1.7	933	12	BF526040	BF526040 602071145
76	50	1.7	993	9	AL537956	AL537956 AL537956
77	49	1.7	134	14	H64265	H64265 y770d11.r1
78	49	1.7	218	17	AQ490631	AQ490631 RPECI-11-2
79	49	1.7	253	9	A1926104	A1926104 wo42d11.X

80 49 1.7 254 9 AA338542
81 49 1.7 259 9 A1278111
82 49 1.7 260 9 A1283112
83 49 1.7 261 9 BF029774
84 49 1.7 270 12 A153772
85 49 1.7 271 10 BE168893
86 49 1.7 280 12 BF962210
87 49 1.7 306 17 AQ311377
88 49 1.7 328 14 H86301
89 49 1.7 330 17 AQ310071
90 49 1.7 336 10 AW194192
91 49 1.7 366 14 H85616
92 49 1.7 372 9 A1445088
93 49 1.7 377 17 AQ148696
94 49 1.7 379 9 AA715387
95 49 1.7 380 9 AA613624
96 49 1.7 386 17 AQ048958
97 49 1.7 388 17 AQ216195
98 49 1.7 388 17 AQ123840
99 49 1.7 389 17 AQ050505
100 49 1.7 390 17 B79179
101 49 1.7 394 12 BF857377
102 49 1.7 401 9 A1635819
103 49 1.7 403 17 AQ059217
104 49 1.7 404 10 BE153364
105 49 1.7 405 17 AQ017686
106 49 1.7 411 10 AV764334
107 49 1.7 413 12 BF808898
108 49 1.7 414 17 B65097
109 49 1.7 417 9 A1348435
110 49 1.7 418 12 BF888339
111 49 1.7 425 9 A1150131
112 49 1.7 427 14 B0376641
113 49 1.7 430 14 B0540547
114 49 1.7 431 10 BE153393
115 49 1.7 435 17 AQ337020
116 49 1.7 436 9 A1860424
117 49 1.7 438 9 A1253371
118 49 1.7 438 17 AQ588742
119 49 1.7 449 17 AQ062661
120 49 1.7 449 17 AQ602891
121 49 1.7 457 10 AW816516
122 49 1.7 461 9 AF246229
123 49 1.7 466 17 AQ389944
124 49 1.7 470 12 BF739086
125 49 1.7 472 14 T60200
126 49 1.7 475 17 AQ061657
127 49 1.7 484 17 B85314
128 49 1.7 487 17 AQ542550
129 49 1.7 494 10 AW814772
130 49 1.7 497 17 AQ785185
131 49 1.7 500 12 BF853383
132 49 1.7 502 17 AQ145517
133 49 1.7 510 17 AQ480286
134 49 1.7 513 13 BM271936
135 49 1.7 525 17 AQ536736
136 49 1.7 527 17 AQ439778
137 49 1.7 541 17 AQ610275
138 49 1.7 563 17 AQ144334
139 49 1.7 564 17 AQ390407
140 49 1.7 571 13 B1600892
141 49 1.7 573 17 AQ317848
142 49 1.7 586 17 B54949
143 49 1.7 660 17 AG137693
144 49 1.7 666 17 AQ156950
145 49 1.7 675 12 BE895666
146 49 1.7 676 17 AQ179333
147 49 1.7 686 10 AV764051
148 49 1.7 706 9 A1866487
149 49 1.7 724 17 AG012710
150 49 1.7 735 9 AG170263
151 49 1.7 748 9 A0125936
152 49 1.7 750 17 AG184338
AA548542 EST43572
A1278111 qm53601.x
A1283112 qm51411.x
BF029774 fm1556665
A153772 fm29411.x
BE168893 fm11051
BF962210 fm5 NN156
AQ311377 fm11116
H86301 fm54412.S1
AQ310071 fm11116
AW194192 fm07408.x
H85616 fm1111.S1
A1445088 fm1944.x
AQ148696 fm5073.A
AA715387 fm52612.S1
AA613624 fm11934.S
AQ048958 fm11.HSP-2
AQ216195 fm52.B
AQ123840 fm5073.B
AQ050505 fm11-2
B79179 fm19788.S1
BF857377 fm311020
A1635819 fm281112.x
AQ059217 fm1.HSP-2
BE153364 fm1.H03
AQ017686 fm1.HSP-2
AV764334 fm76334
BF808898 fm41015
B65097 fm1.HSP-203
A1348435 fm24131.x
BF888339 fm155059
A1150131 fm44112.x
B0376641 fm4.TN020
B0540547 fm29410.Y
BE153393 fm5.H03
AQ337020 fm513.A
A1860424 fm11408.x
A1253371 fm5511.x
AQ588742 fm52065.B
AQ062661 fm1.HSP-2
AQ602891 fm229.A
AW816516 fm0.ST023
AF246229 fm246229
AQ389944 fm1111-5
BF739086 fm556395
T60200 fm22634.T
AQ061657 fm1637.CIT-HSP-2
B85314 fm5414.RPC111-16A2
AQ542550 fm111-3
AW814772 fm31.ST015
AQ785185 fm5159.A
BF853383 fm31.EN008
AQ145517 fm52179.A
AQ480286 fm11-2
BM271936 fm37864.Y
AQ536736 fm111-3
AQ439778 fm5376.B
AQ610275 fm5093.A
AQ144334 fm4080.A
AQ390407 fm11.E1
B1600892 fm3249223
AQ317848 fm111-96
B54949 fm1.HSP-385
AG137693 fm1.L041
AQ156950 fm1.L041
BE895666 fm432672
AQ179333 fm1.L041
AV764051 fm764051
A1866487 fm249e2.x
AG012710 fm030.S02
AG170263 fm22586M
A0125936 fm125936
A184338 fm1.L041

C 226	48	1.7	494	10	BE148337	AG187206	17	726	17	AG187206	AG187206	Pan trogl
C 227	48	1.7	499	14	H73306	H73306	17	746	17	AG104781	AG104781	Pan trogl
C 228	48	1.7	500	17	AQ215816	AQ215816	17	741	17	BH021064	BH021064	HS 00332
C 229	48	1.7	501	17	AQ040260	AQ040260	17	745	17	AG029705	AG029705	Pan trogl
C 230	48	1.7	507	9	AL073903	AL073903	17	777	12	BG565021	BG565021	AGENCOURT
C 231	48	1.7	510	9	AL073903	AL073903	17	784	14	BQ429000	BQ429000	AGENCOURT
C 232	48	1.7	513	10	AW174443	AW174443	17	797	12	BG743440	BG743440	HS 2634956
C 233	48	1.7	515	14	N20867	N20867	17	802	10	HE300400	HE300400	AG0944523
C 234	48	1.7	516	17	AQ616105	AQ616105	17	805	12	BG776292	BG776292	AG0944523
C 235	48	1.7	518	9	AW765173	AW765173	17	817	17	AG0942973	AG0942973	HS_31000_B
C 236	48	1.7	518	10	AW719687	AW719687	17	819	12	BF541930	BF541930	AG0942973
C 237	48	1.7	519	10	AW902110	AW902110	17	822	12	BG105498	BG105498	AG0942973
C 238	48	1.7	523	12	BF724819	BF724819	17	832	17	AQ743503	AQ743503	HS 5482_B
C 239	48	1.7	525	17	AQ0505403	AQ0505403	17	848	14	BG881909	BG881909	AGENCOURT
C 240	48	1.7	529	17	AQ212840	AQ212840	17	854	12	BG697926	BG697926	AG0942973
C 241	48	1.7	530	10	BE180767	BE180767	17	894	10	BE548613	BE548613	AG0942973
C 242	48	1.7	532	10	BE019370	BE019370	17	914	10	BE564637	BE564637	AG0942973
C 243	48	1.7	532	17	AG031058	AG031058	17	916	12	HE742399	HE742399	AG0942973
C 244	48	1.7	534	17	AQ636175	AQ636175	17	922	12	BG755473	BG755473	AG0942973
C 245	48	1.7	535	17	AQ118105	AQ118105	17	938	12	BG828741	BG828741	AG0942973
C 246	48	1.7	538	17	AQ675788	AQ675788	17	940	12	BF304788	BF304788	AG0942973
C 247	48	1.7	541	10	BE245107	BE245107	17	954	12	AG387907	AG387907	AG0942973
C 248	48	1.7	543	17	AQ415818	AQ415818	17	955	9	AL518143	AL518143	AG0942973
C 249	48	1.7	548	9	AL711524	AL711524	17	957	12	BE742779	BE742779	AG0942973
C 250	48	1.7	549	10	AW577917	AW577917	17	983	10	BE300452	BE300452	AG0942973
C 251	48	1.7	549	17	AQ529507	AQ529507	17	984	12	BG679183	BG679183	AG0942973
C 252	48	1.7	552	9	AI669485	AI669485	17	991	12	BF304111	BF304111	AG0942973
C 253	48	1.7	555	17	AQ384299	AQ384299	17	1045	13	BM905988	BM905988	AGENCOURT
C 254	48	1.7	555	17	AQ485647	AQ485647	17	1049	14	BM905988	BM905988	AGENCOURT
C 255	48	1.7	561	9	AI076609	AI076609	17	1072	14	BM905516	BM905516	AGENCOURT
C 256	48	1.7	564	10	AW379447	AW379447	17	1072	14	BM905516	BM905516	AGENCOURT
C 257	48	1.7	573	17	AQ676078	AQ676078	17	1097	13	BM480344	BM480344	AGENCOURT
C 258	48	1.7	574	17	AQ530304	AQ530304	17	1129	13	BM475425	BM475425	AGENCOURT
C 259	48	1.7	575	14	BM979245	BM979245	17	108	17	BQ473479	BQ473479	AGENCOURT
C 260	48	1.7	576	10	BE142940	BE142940	17	143	17	AQ471444	AQ471444	AGENCOURT
C 261	48	1.7	583	10	AW577913	AW577913	17	203	14	N83807	N83807	AGENCOURT
C 262	48	1.7	592	10	AV718792	AV718792	17	205	13	BM510118	BM510118	AGENCOURT
C 263	48	1.7	601	12	AG193326	AG193326	17	241	9	AA372590	AA372590	AGENCOURT
C 264	48	1.7	601	12	AG193326	AG193326	17	246	9	AA078384	AA078384	AGENCOURT
C 265	48	1.7	604	10	AV720014	AV720014	17	247	13	BG960713	BG960713	AGENCOURT
C 266	48	1.7	613	10	AV720842	AV720842	17	259	9	AA287502	AA287502	AGENCOURT
C 267	48	1.7	613	13	BE1194113	BE1194113	17	259	9	AA287502	AA287502	AGENCOURT
C 268	48	1.7	622	12	BF724818	BF724818	17	269	9	AI648558	AI648558	AGENCOURT
C 269	48	1.7	630	17	AG088067	AG088067	17	269	9	AI648558	AI648558	AGENCOURT
C 270	48	1.7	631	17	AQ423832	AQ423832	17	281	13	B1019636	B1019636	AGENCOURT
C 271	48	1.7	634	17	AQ414084	AQ414084	17	281	13	B1019636	B1019636	AGENCOURT
C 272	48	1.7	639	17	AG093412	AG093412	17	288	9	AI493828	AI493828	AGENCOURT
C 273	48	1.7	642	12	BG365387	BG365387	17	295	14	N84136	N84136	AGENCOURT
C 274	48	1.7	648	17	AG065044	AG065044	17	299	17	AQ057900	AQ057900	AGENCOURT
C 275	48	1.7	650	17	AQ385940	AQ385940	17	305	9	AA488004	AA488004	AGENCOURT
C 276	48	1.7	659	17	AG149814	AG149814	17	314	10	AW804477	AW804477	AGENCOURT
C 277	48	1.7	660	12	BG568118	BG568118	17	315	10	AW591754	AW591754	AGENCOURT
C 278	48	1.7	661	9	AL710488	AL710488	17	326	9	AL134332	AL134332	AGENCOURT
C 279	48	1.7	661	17	AG167520	AG167520	17	326	9	AL134332	AL134332	AGENCOURT
C 280	48	1.7	663	17	AG119366	AG119366	17	329	14	T06284	T06284	AGENCOURT
C 281	48	1.7	666	17	AG091887	AG091887	17	335	17	AQ072807	AQ072807	AGENCOURT
C 282	48	1.7	670	10	AV705697	AV705697	17	337	13	B1052645	B1052645	AGENCOURT
C 283	48	1.7	671	10	BE254911	BE254911	17	340	12	BE694479	BE694479	AGENCOURT
C 284	48	1.7	677	17	AG104958	AG104958	17	342	10	AW089016	AW089016	AGENCOURT
C 285	48	1.7	678	17	AQ318835	AQ318835	17	352	10	AW089016	AW089016	AGENCOURT
C 286	48	1.7	678	17	AQ388600	AQ388600	17	359	17	AQ123162	AQ123162	AGENCOURT
C 287	48	1.7	681	17	AQ081594	AQ081594	17	361	10	AV762442	AV762442	AGENCOURT
C 288	48	1.7	681	17	AQ081594	AQ081594	17	361	10	AV762442	AV762442	AGENCOURT
C 289	48	1.7	688	10	AV706016	AV706016	17	369	9	AA507632	AA507632	AGENCOURT
C 290	48	1.7	688	17	AG128463	AG128463	17	376	12	BF820446	BF820446	AGENCOURT
C 291	48	1.7	689	17	AG105457	AG105457	17	381	17	AG0410	AG0410	AGENCOURT
C 292	48	1.7	690	10	BE315308	BE315308	17	382	17	AQ773460	AQ773460	AGENCOURT
C 293	48	1.7	700	17	AG014845	AG014845	17	383	17	AQ232555	AQ232555	AGENCOURT
C 294	48	1.7	701	17	AG065119	AG065119	17	389	17	AQ715520	AQ715520	AGENCOURT
C 295	48	1.7	703	14	BM997575	BM997575	17	392	9	AI493546	AI493546	AGENCOURT
C 296	48	1.7	704	12	BG827248	BG827248	17	392	17	AQ715468	AQ715468	AGENCOURT
C 297	48	1.7	712	13	BF860732	BF860732	17	397	9	AA507632	AA507632	AGENCOURT
C 298	48	1.7	714	14	BQ000785	BQ000785	17	398	9	AA507632	AA507632	AGENCOURT

C 372	47	1.6	406	10	AW440424	AW440424 hb90c11.x	C 445	47	1.6	679	17	AG049015	*AG049015 Pan trogl
C 373	47	1.6	407	17	AQ047364	AQ047364 CIT-HSP-2	C 446	47	1.6	683	17	AG112753	AG112753 Pan trogl
C 374	47	1.6	409	10	AW770153	AW770153 hb36f03.x	C 447	47	1.6	688	14	BM988443	BM988443 UI-H-DHO-
C 375	47	1.6	410	9	AA568314	AA568314 nfi5c01.s	C 448	47	1.6	691	17	AG001893	AG001893 Homo sapi
C 376	47	1.6	413	10	AW827418	AW827418 hm30h09.x	C 449	47	1.6	694	12	BG28213	BG28213 602763617
C 377	47	1.6	417	14	R06632	R06632 yf10a0b.r1	C 450	47	1.6	709	17	AG001891	AG001891 Homo sapi
C 378	47	1.6	421	9	A1521901	A1521901 t18u0d03.x	C 451	47	1.6	712	17	AG001892	AG001892 Homo sapi
C 379	47	1.6	421	9	AA211881	AA211881 q984f07.r	C 452	47	1.6	713	12	BE796673	BE796673 601592078
C 380	47	1.6	423	9	AA133556	AA133556 z014a02.s	C 453	47	1.6	722	12	HG617782	HG617782 602645311
C 381	47	1.6	423	9	A1610321	A1610321 tp40c09.x	C 454	47	1.6	732	13	B1091782	B1091782 602688834
C 382	47	1.6	424	9	AA147102	AA147102 z032h02.s	C 455	47	1.6	760	12	HG207240	HG207240 RST26709
C 383	47	1.6	426	9	A1219747	A1219747 q988d07.x	C 456	47	1.6	760	13	BG914229	BG914229 602808455
C 384	47	1.6	426	17	AG533345	AG533345 RPT-11-4	C 457	47	1.6	769	17	AG185105	AG185105 Pan trogl
C 385	47	1.6	434	10	AV760945	AV760945 AV760945	C 458	47	1.6	783	12	HE974022	HE974022 601680351
C 386	47	1.6	434	14	W38468	W38468 z021b01.r1	C 459	47	1.6	796	14	BQ051998	BQ051998 AGENCOURT
C 387	47	1.6	438	17	AG033761	AG033761 RPT-11-4	C 460	47	1.6	838	12	HG571201	HG571201 602592138
C 388	47	1.6	443	17	AG034649	AG034649 HS-5086-B	C 461	47	1.6	857	12	BF983604	BF983604 602304714
C 389	47	1.6	447	9	AA463831	AA463831 z057e05.r	C 462	47	1.6	868	17	AQ747663	AQ747663 HS-5533-A
C 390	47	1.6	454	17	AG061236	AG061236 HS-2093-A	C 463	47	1.6	891	12	BF678918	BF678918 602153543
C 391	47	1.6	455	17	AQ146946	AQ146946 HS-2248-A	C 464	47	1.6	923	14	BM915281	BM915281 AGENCOURT
C 392	47	1.6	457	17	AQ197732	AQ197732 CIT-HSP-2	C 465	47	1.6	1038	13	BM551072	BM551072 AGENCOURT
C 393	47	1.6	459	12	BF805746	BF805746 QV1-C1017	C 466	47	1.6	1058	12	BG036337	BG036337 602326634
C 394	47	1.6	460	12	BF805744	BF805744 QV1-C1017	C 467	47	1.6	1086	11	BC015672	BC015672 Homo sapi
C 395	47	1.6	468	17	AQ571846	AQ571846 HS-2094-A	C 468	47	1.6	1223	13	BM451554	BM451554 AGENCOURT
C 396	47	1.6	469	17	AG677080	AG677080 HS-5527-A	C 469	47	1.6	1334	10	AV759784	AV759784 AV759784
C 397	47	1.6	471	17	AG317069	AG317069 CIT-HSP-2	C 470	47	1.6	1808	11	AF130050	AF130050 Homo sapi
C 398	47	1.6	473	12	BF514867	BF514867 UI-H-BW1-	C 471	47	1.6	4125	11	BC028413	BC028413 Homo sapi
C 399	47	1.6	477	17	AG053694	AG053694 RPT-11-3	C 472	47	1.6	152	17	AQ585086	AQ585086 RPT-11-4
C 400	47	1.6	489	10	BE178244	BE178244 KC3-H-060	C 473	46	1.6	168	17	AQ018519	AQ018519 CIT-HSP-2
C 401	47	1.6	491	10	AA193512	AA193512 xm17b12.x	C 474	46	1.6	172	10	AW072994	AW072994 x433908.x
C 402	47	1.6	493	9	AA551170	AA551170 nk75d09.s	C 475	46	1.6	190	17	AQ051043	AQ051043 RPT-11-4
C 403	47	1.6	493	17	AQ417229	AQ417229 RPT-11-1	C 476	46	1.6	196	17	AQ051012	AQ051012 RPT-11-4
C 404	47	1.6	494	10	BA971073	BA971073 EST183159	C 477	46	1.6	214	17	B83900	B83900 RPT-11-21B1
C 405	47	1.6	494	10	BE148723	BE148723 CM1-H-024	C 478	46	1.6	215	9	A1753878	A1753878 cr15d12.x
C 406	47	1.6	501	9	AA599749	AA599749 ag11q08.s	C 479	46	1.6	233	14	F34605	F34605 HSP029880.H
C 407	47	1.6	501	17	AG971097	AG971097 EST383184	C 480	46	1.6	278	17	BH861012	BH861012 UP 419-15
C 408	47	1.6	503	10	BE154973	BE154973 PM3-H-034	C 481	46	1.6	279	9	AA605266	AA605266 no81c03.s
C 409	47	1.6	509	17	AQ155570	AQ155570 HS-3107-B	C 482	46	1.6	287	10	AW836658	AW836658 PM3-LT003
C 410	47	1.6	517	10	BE166690	BE166690 QV0-HT049	C 483	46	1.6	292	9	AA362009	AA362009 EST71352
C 411	47	1.6	530	9	A1683742	A1683742 t053d11.x	C 484	46	1.6	303	10	AW513905	AW513905 x090b12.x
C 412	47	1.6	531	10	BE157319	BE157319 KC3-H1047	C 485	46	1.6	317	10	BE045105	BE045105 hm28e08.x
C 413	47	1.6	531	17	AQ286075	AQ286075 RPT111-90	C 486	46	1.6	326	17	AQ081931	AQ081931 UP 474-24
C 414	47	1.6	537	17	AG513307	AG513307 HS-5115-B	C 487	46	1.6	331	14	Z30049	Z30049 HFEA21C ALR
C 415	47	1.6	540	12	BF828758	BF828758 MR2-HM003	C 488	46	1.6	333	10	AW189434	AW189434 x106e04.x
C 416	47	1.6	554	17	AQ516291	AQ516291 RPT-11-3	C 489	46	1.6	341	9	AA828145	AA828145 od13c10.s
C 417	47	1.6	560	10	HK674880	HK674880 t096f10.x	C 490	46	1.6	341	9	AA820095	AA820095 EST22413
C 418	47	1.6	562	17	AQ715971	AQ715971 HS-543-H	C 491	46	1.6	349	14	H95587	H95587 yv16e08.s1
C 419	47	1.6	566	10	AV720827	AV720827 AV720827	C 492	46	1.6	349	9	AA744175	AA744175 ny50h10.s
C 420	47	1.6	566	17	AQ549290	AQ549290 RPT-11-4	C 493	46	1.6	349	9	AA468957	AA468957 nc79a10.r
C 421	47	1.6	567	12	BF678893	BF678893 602153514	C 494	46	1.6	352	17	AQ307070	AQ307070 HS-2008-A
C 422	47	1.6	571	10	BE544872	BE544872 601678879	C 495	46	1.6	354	14	BQ331932	BQ331932 PM1-ET026
C 423	47	1.6	580	10	AV658841	AV658841 AV658841	C 496	46	1.6	366	9	AA584756	AA584756 no04c01.s
C 424	47	1.6	584	17	AG000686	AG000686 Homo sapi	C 497	46	1.6	366	9	AA632994	AA632994 nq11h10.s
C 425	47	1.6	585	17	AQ549426	AQ549426 RPT-11-4	C 498	46	1.6	369	10	AW023511	AW023511 df55h11.y
C 426	47	1.6	590	13	BM091350	BM091350 j021i04.x	C 499	46	1.6	373	17	AQ062553	AQ062553 CITBI-E1-
C 427	47	1.6	593	17	AQ420289	AQ420289 RPT-11-1	C 500	46	1.6	377	10	AV708727	AV708727 AV708727
C 428	47	1.6	595	17	AQ267692	AQ267692 RPT111-71	C 501	46	1.6	380	9	AA654968	AA654968 nt61e05.s
C 429	47	1.6	606	17	AQ042325	AQ042325 CIT-HSP-2	C 502	46	1.6	384	9	AA180214	AA180214 zp35901.s
C 430	47	1.6	608	17	AQ196470	AQ196470 CIT-HSP-2	C 503	46	1.6	386	9	AA565105	AA565105 nk48a02.s
C 431	47	1.6	615	9	AL603163	AL603163 DKF2p686g	C 504	46	1.6	387	10	AW438551	AW438551 x0336901.x
C 432	47	1.6	627	17	AG000685	AG000685 Homo sapi	C 505	46	1.6	387	17	AQ056769	AQ056769 HS-2118-B
C 433	47	1.6	632	10	BE171849	BE171849 MR0-HT055	C 506	46	1.6	388	9	A1570906	A1570906 tr58g03.x
C 434	47	1.6	635	13	B1916602	B1916602 603178533	C 507	46	1.6	394	9	AA827978	AA827978 od70d06.s
C 435	47	1.6	638	17	AG129313	AG129313 Pan trogl	C 508	46	1.6	396	10	AW502078	AW502078 UI-H-BRO
C 436	47	1.6	643	10	AV706522	AV706522 AV706522	C 509	46	1.6	396	14	H68120	H68120 yu68b06.s1
C 437	47	1.6	647	12	BF996071	BF996071 MR1-GN017	C 510	46	1.6	398	9	A1587400	A1587400 tr50b03.x
C 438	47	1.6	649	17	AG075635	AG075635 Pan trogl	C 511	46	1.6	398	12	HF878243	HF878243 CM3-ET009
C 439	47	1.6	651	14	BM677523	BM677523 UI-E-B01-	C 512	46	1.6	399	14	W45434	W45434 zc83c03.s1
C 440	47	1.6	651	17	AG177756	AG177756 Pan trogl	C 513	46	1.6	400	9	AA449991	AA449991 zx38e12.s
C 441	47	1.6	653	10	BE562953	BE562953 601346394	C 514	46	1.6	400	10	AW169531	AW169531 x127b07.x
C 442	47	1.6	657	14	BM998859	BM998859 UI-H-B10-	C 515	46	1.6	404	9	AA551575	AA551575 nk73b02.s
C 443	47	1.6	669	17	AG176227	AG176227 Pan trogl	C 516	46	1.6	407	17	AQ241984	AQ241984 CITBI-E1-
C 444	47	1.6	672	14	BM975543	BM975543 UI-E-BN1	C 517	46	1.6	408	17	AQ213205	AQ213205 HS-3243-A

C 519	46	1.6	408	17	B53103	AG161080 Pan trogl
C 520	46	1.6	410	9	AL603409	BH609895 Hiv24H01
C 521	46	1.6	411	9	AA086405	A1587389 tr50a01.x
C 522	46	1.6	413	9	A1753267	BM565530 1426408.x
C 523	46	1.6	414	9	A1733748	BG753048 16273217
C 524	46	1.6	415	17	B86947	AW993436 RC2-BN003
C 525	46	1.6	416	17	AQ936318	AS27989 RUC1-11.3
C 526	46	1.6	417	17	AQ089819	AQ593243 RC2-BN003
C 527	46	1.6	420	9	AA302960	AL698581 DKF2p686G
C 528	46	1.6	422	17	B48182	AW992953 RC2-BN003
C 529	46	1.6	423	9	AA704684	AW993233 RC2-BN003
C 530	46	1.6	423	10	AV760046	B79772 CIT-HSP-205
C 531	46	1.6	427	9	A1636341	AG109077 Pan trogl
C 532	46	1.6	427	14	B69258	AW992880 R.2-BN003
C 533	46	1.6	428	9	AA197155	AW993295 RC2-BN003
C 534	46	1.6	432	10	AV718694	AG055742 Pan trogl
C 535	46	1.6	432	13	B1053122	AG078319 Pan trogl
C 536	46	1.6	436	17	AQ024286	AW992942 RC2-BN003
C 537	46	1.6	436	10	AW873417	AG061030 Pan trogl
C 538	46	1.6	438	17	AQ262458	BM760792 K-EST0041
C 539	46	1.6	439	10	AW502079	AW993235 RC2-BN003
C 540	46	1.6	444	14	W60523	AG150441 Pan trogl
C 541	46	1.6	449	9	AA812058	AG118635 Pan trogl
C 542	46	1.6	461	17	B17342	AW991232 RC2-BN003
C 543	46	1.6	462	17	AQ370589	AQ282877 RUC11-90
C 544	46	1.6	465	9	AA644545	AL040521 DKF2p434G
C 545	46	1.6	466	9	A1809818	HG111026 602284705
C 546	46	1.6	466	9	AL600388	BG913368 60207669
C 547	46	1.6	466	9	AA304344	AG063648 HS.3072.B
C 548	46	1.6	474	17	AQ801651	B1913527 603179160
C 549	46	1.6	478	9	A1554807	B1913527 603179160
C 550	46	1.6	479	14	B16880	B1913527 603179160
C 551	46	1.6	484	17	AQ485411	BQ242238 AGENCOURT
C 552	46	1.6	486	9	A1732430	BQ959144 AGENCOURT
C 553	46	1.6	495	9	A1494587	PQ060984 AGENCOURT
C 554	46	1.6	496	14	BQ676318	C05051 C05051 Huma
C 555	46	1.6	496	14	BQ682181	BE158801 IL2-HT039
C 556	46	1.6	496	17	AQ493194	BE158756 IL2-HT039
C 557	46	1.6	503	17	AQ269264	BE157799 IL2-HT039
C 558	46	1.6	509	17	AQ476515	BE158802 IL2-HT039
C 559	46	1.6	514	12	BQ082388	AA906629 OK-9602.S
C 560	46	1.6	516	17	AQ080833	BE158690 CMQ-HT039
C 561	46	1.6	516	17	AQ496870	BM844518 K-EST0122
C 562	46	1.6	517	13	B1027907	AM818067 CMQ-ST027
C 563	46	1.6	524	9	A1791156	AA526856 n192e12.S
C 564	46	1.6	529	14	BM843663	A1678368 t083C09.x
C 565	46	1.6	529	17	AQ320695	A1657559 t083C09.x
C 566	46	1.6	530	12	BQ725304	A1657559 t083C09.x
C 567	46	1.6	531	9	AQ158549	AA826079 ce24b04.S
C 568	46	1.6	535	9	AQ155619	A1926296 W044B09.x
C 569	46	1.6	540	10	AW993009	BI024997 CMQ-HT028
C 570	46	1.6	543	12	BE840964	AA366716 EST77705
C 571	46	1.6	545	17	B69657	AA366716 EST77705
C 572	46	1.6	547	14	BQ710429	AA564565 n191a01.S
C 573	46	1.6	548	10	AW993493	A1805187 tx14b05.x
C 574	46	1.6	549	10	AW966315	A1805187 tx14b05.x
C 575	46	1.6	558	10	AW992995	A1805187 tx14b05.x
C 576	46	1.6	562	17	AQ551078	A1805187 tx14b05.x
C 577	46	1.6	563	10	AW979004	A1805187 tx14b05.x
C 578	46	1.6	565	17	B59827	A1805187 tx14b05.x
C 579	46	1.6	566	9	AA26763	A1805187 tx14b05.x
C 580	46	1.6	568	9	AL596800	A1805187 tx14b05.x
C 581	46	1.6	570	17	AQ567234	A1805187 tx14b05.x
C 582	46	1.6	573	17	AQ537592	A1805187 tx14b05.x
C 583	46	1.6	579	17	B596476	A1805187 tx14b05.x
C 584	46	1.6	581	9	AQ159341	A1805187 tx14b05.x
C 585	46	1.6	586	9	AA126811	A1805187 tx14b05.x
C 586	46	1.6	594	9	AA159603	A1805187 tx14b05.x
C 587	46	1.6	607	14	BQ271419	A1805187 tx14b05.x
C 588	46	1.6	610	10	BE154115	A1805187 tx14b05.x
C 589	46	1.6	627	17	AQ019248	A1805187 tx14b05.x
C 590	46	1.6	629	13	B5956588	A1805187 tx14b05.x
C 591	46	1.6	640	17	AG161080	AG161080 Pan trogl
C 592	46	1.6	645	17	BH609895	BH609895 Hiv24H01
C 593	46	1.6	651	9	A1587389	A1587389 tr50a01.x
C 594	46	1.6	653	13	BM565530	BM565530 1426408.x
C 595	46	1.6	655	12	BG753048	BG753048 16273217
C 596	46	1.6	663	17	AW993436	AW993436 RC2-BN003
C 597	46	1.6	663	17	AQ936318	AS27989 RUC1-11.3
C 598	46	1.6	664	10	AW993243	AQ593243 RC2-BN003
C 599	46	1.6	670	9	AA302960	AL698581 DKF2p686G
C 600	46	1.6	673	10	AW992953	AW992953 RC2-BN003
C 601	46	1.6	675	10	AW993233	AW993233 RC2-BN003
C 602	46	1.6	675	17	B79772	B79772 CIT-HSP-205
C 603	46	1.6	677	17	AG109077	AG109077 Pan trogl
C 604	46	1.6	683	10	AW992880	AW992880 R.2-BN003
C 605	46	1.6	683	10	AW993295	AW993295 RC2-BN003
C 606	46	1.6	683	17	AG055742	AG055742 Pan trogl
C 607	46	1.6	692	17	AG078319	AG078319 Pan trogl
C 608	46	1.6	693	10	AW992942	AW992942 RC2-BN003
C 609	46	1.6	694	17	AG061030	AG061030 Pan trogl
C 610	46	1.6	705	14	BM760792	BM760792 K-EST0041
C 611	46	1.6	710	10	AW993235	AW993235 RC2-BN003
C 612	46	1.6	713	17	AG150441	AG150441 Pan trogl
C 613	46	1.6	717	17	AG118635	AG118635 Pan trogl
C 614	46	1.6	733	10	AW991232	AW991232 RC2-BN003
C 615	46	1.6	740	17	AQ282877	AQ282877 RUC11-90
C 616	46	1.6	757	9	AL040521	AL040521 DKF2p434G
C 617	46	1.6	772	12	HG111026	HG111026 602284705
C 618	46	1.6	786	13	BG913368	BG913368 60207669
C 619	46	1.6	836	17	AG063648	AG063648 HS.3072.B
C 620	46	1.6	842	13	B1913527	B1913527 603179160
C 621	46	1.6	875	12	B1688183	B1913527 603179160
C 622	46	1.6	879	14	BQ242238	BQ242238 AGENCOURT
C 623	46	1.6	933	14	BQ959144	BQ959144 AGENCOURT
C 624	46	1.6	979	14	PQ060984	PQ060984 AGENCOURT
C 625	45	1.6	104	14	C05051	C05051 C05051 Huma
C 626	45	1.6	128	10	BE158801	BE158801 IL2-HT039
C 627	45	1.6	143	10	BE158756	BE158756 IL2-HT039
C 628	45	1.6	143	10	BE158799	BE157799 IL2-HT039
C 629	45	1.6	143	10	BE158802	BE158802 IL2-HT039
C 630	45	1.6	154	9	AA906629	AA906629 OK-9602.S
C 631	45	1.6	174	10	BE158690	BE158690 CMQ-HT039
C 632	45	1.6	176	14	BM844518	BM844518 K-EST0122
C 633	45	1.6	184	10	AM818067	AM818067 CMQ-ST027
C 634	45	1.6	188	9	AA526856	AA526856 n192e12.S
C 635	45	1.6	189	9	A1678368	A1678368 t083C09.x
C 636	45	1.6	208	12	HC271598	A1657559 t083C09.x
C 637	45	1.6	209	9	A1054911	A1657559 t083C09.x
C 638	45	1.6	214	14	FO0818	AA826079 ce24b04.S
C 639	45	1.6	222	10	AW419209	A1926296 W044B09.x
C 640	45	1.6	223	9	AA634750	BI024997 CMQ-HT028
C 641	45	1.6	228	9	AA526856	AA366716 EST77705
C 642	45	1.6	229	9	A1678368	AA366716 EST77705
C 643	45	1.6	229	9	A1665759	AA564565 n191a01.S
C 644	45	1.6	231	9	AA826079	A1805187 tx14b05.x
C 645	45	1.6	231	9	A1926296	A1805187 tx14b05.x
C 646	45	1.6	234	13	BI024997	A1805187 tx14b05.x
C 647	45	1.6	242	9	AA366716	A1805187 tx14b05.x
C 648	45	1.6	243	12	BF8672053	A1805187 tx14b05.x
C 649	45	1.6	255	3	AA564865	A1805187 tx14b05.x
C 650	45	1.6	256	9	A1805487	A1805187 tx14b05.x
C 651	45	1.6	268	9	AA807845	A1805187 tx14b05.x
C 652	45	1.6	273	14	F17142	A1805187 tx14b05.x
C 653	45	1.6	276	9	AA557883	A1805187 tx14b05.x
C 654	45	1.6	276	12	HC013793	A1805187 tx14b05.x
C 655	45	1.6	276	13	BI850333	A1805187 tx14b05.x
C 656	45	1.6	277	9	AA327667	A1805187 tx14b05.x
C 657	45	1.6	278	9	AA339692	A1805187 tx14b05.x
C 658	45	1.6	279	12	BF744621	A1805187 tx14b05.x
C 659	45	1.6	280	9	AA570441	A1805187 tx14b05.x
C 660	45	1.6	283	12	BF680898	A1805187 tx14b05.x
C 661	45	1.6	283	10	AW197926	A1805187 tx14b05.x
C 662	45	1.6	285	14	FO6449	A1805187 tx14b05.x
C 663	45	1.6	285	14	FO6449	A1805187 tx14b05.x
C 664	45	1.6	285	14	FO6449	A1805187 tx14b05.x
C 665	45	1.6	285	14	FO6449	A1805187 tx14b05.x

C 664 45 1.6 290 17 AQ485309 RPT1-11-2 737 45 1.6 431 9 AA635135
C 665 45 1.6 292 17 AQ352122 738 45 1.6 431 9 AT801540
C 666 45 1.6 297 14 F31654 RPT1-11-2 739 45 1.6 431 9 AA593828
C 667 45 1.6 308 10 AA339622 740 45 1.6 431 9 AA601125
C 668 45 1.6 303 9 AA328844 741 45 1.6 432 17 AQ486252
C 669 45 1.6 307 9 AA224434 742 45 1.6 433 17 AQ024319
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1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS (bases 1 to 424)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Bethesda, M.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Genoa, London, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINC at:
www.bio.lnlnl.gov/bbrp/image/image.html
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histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the HD5 cloning
method (Life technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
BASE COUNT 89 a 102 c 104 g 129 t
ORIGIN

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RESULT 6
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SOURCE
ORGANISM
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 674)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpesqsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the K&D process and may have higher chance of
clone tracking errors.
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LIBRARY
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R.Site 1 : SacI
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/clone="PTB-057L02.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 152 a 162 c 179 g 179 t
ORIGIN
Query Match      2.0%; Score 57; DB 17; Length 674;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 CTCACGTGAACCTGCTCCGCGGTTCAGCGATTCTCTGCTCAGCTCTGAG 108;
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DB 219 CTCACGTGAACCTGCTCCGCGGTTCAGCGATTCTCTGCTCAGCTCTGAG 163

RESULT 7
BI059823 569 bp mRNA linear EST 15-JUN-2001
LOCUS IL3-UT015-C80101-378-H06 UT015 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BI059823
VERSION BI059823.1 GI:14467350
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 569)
Dias Neto, F., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brustein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

```

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 4491-4496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=11&tbl2=113 01115-C&tbl3=178-H06&tbl4=3-2001-01-08&tbl5=1)
Seq primer: puc 18 forward
High quality sequence stop: 568.
Location/Qualifiers
1..569
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0115"
/dev_stage="Adult"
/note="Organ: uterus_tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES source
BASE COUNT 175 a 114 c 119 g 151 t
ORIGIN
Query Match 1.9%; Score 56; DB 13; Length 669;
Best local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCACCTTGGCTCCCAAGTCTGGGATTACAGGCAATGAGCCACTGCGCCACCT 1245
|||||
DB 120 CCACCTTGGCTCCCAAGTCTGGGATTACAGGCAATGAGCCACTGCGCCACCT 175
|||||

RESULT 8
B1015195/c
LOCUS MR4-ET0140-190201-006 e12 ET0140 Homo sapiens cDNA clone IMAGE:4850375 3'
ACCESSION B1015195
VERSION B1015195.1 GI:14419266
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
NIH-MGC http://imgc.ncbi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: rstraus@imgc.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1691 row: h column: 24
High quality sequence stop: 841.
Location/Qualifiers
1..1054
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH-MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGT-ACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 4491-4496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=11&tbl2=113 01115-C&tbl3=178-H06&tbl4=3-2001-02-19&tbl5=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 72.
Location/Qualifiers
1..600
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0140"
/dev_stage="Adult"
/note="Organ: lung_tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES source
BASE COUNT 208 a 102 c 130 g 160 t
ORIGIN
Query Match 1.9%; Score 56; DB 13; Length 600;
Best local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGCAATGAGCCACTGCGCCAC 1244
|||||
DB 451 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGCAATGAGCCACTGCGCCAC 396
|||||

RESULT 9
BG745912
LOCUS 602724092T1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4850375 3'
DEFINITION mRNA sequence.
ACCESSION BG745912
VERSION BG745912.1 GI:14056565
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1054)
NIH-MGC http://imgc.ncbi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: rstraus@imgc.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1691 row: h column: 24
High quality sequence stop: 841.
Location/Qualifiers
1..1054
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH-MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGT-ACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a

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BASE COUNT      265 a   270 c   231 g   288 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 56; DB 12; Length 1054;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GGCACCTTGGCTCCCAAGTGTGGGATTACAGGCAAGGCACTGGCGTACG 1244
|||||
Db 188 GGCACCTTGGCTCCCAAGTGTGGGATTACAGGCAAGGCACTGGCGTACG 243

RESULT 10
LOCUS      BG014649
DEFINITION 115-GN0239-211200-342-g07 GN0239 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG014649
VERSION     BG014649.1 GI:12466063
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=115&st2=115-GN0239-
211200-342-g07&st3=2000-12-21&st4=1)
Seq primer: puc 18 forward
High quality sequence stop: 360.
Location/Qualifiers
1..384
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0239"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT      86 a   110 c   87 g   100 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 55; DB 12; Length 484;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGGATTACAGGCAAGGCACTGGCGTACG 1244
|||||
Db 115 GGCACCTTGGCTCCCAAGTGTGGGATTACAGGCAAGGCACTGGCGTACG 169
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RESULT 11
LOCUS      BG007260
DEFINITION 115-GN0239-271100-281-e06 GN0239 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG007260
VERSION     BG007260.1 GI:12451267
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=115&st2=115-GN0239-
271100-281-e06&st3=2000-11-27&st4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 371.
Location/Qualifiers
1..387
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0239"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT      86 a   113 c   87 g   99 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 55; DB 12; Length 387;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGGATTACAGGCAAGGCACTGGCGCCAGC 1244
|||||
Db 129 CCCACCTTGGCTCCCAAGTGTGGGATTACAGGCAAGGCACTGGCGCCAGC 183

RESULT 12
LOCUS      AQ056873/c
DEFINITION CIT-HSP-2339H7.TF CIT-HSP Homo sapiens genomic clone 2339H7, DNA
sequence.
ACCESSION  AQ056873
VERSION     AQ056873.1 GI:3454479
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
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```

Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9749-9754 (1999)
99380589
JOURNAL
MEDLINE
COMMENT
Contract: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.hsc.washington.edu
Plate: 2151 row: N column: 19
Seq primer: T7
Class: BAC ends
High quality sequence stop: 455.
FEATURES
SOURCE
1..453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate-2151 Col-19 Row-N"
/clone_lib="CIT Approved Human Genomic Stem Library II"
/sex="male"
/note="Organ: sperm; Vector: pBluepAC11; BAC clones in
E-Coli DH10B"
BASE COUNT 108 a 114 c 82 g 149 t
ORIGIN
Query Match 1.88; Score 53; DB 17; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1189 GCCACCTTGCCCTCCCAAGTGTGGATTACAGGATGAGCCACTGGCCGC 1241
|||||
DB 142 GCCACCTTGCCCTCCCAAGTGTGGATTACAGGATGAGCCACTGGCCGC 194
|||||
A1610607 658 bp mRNA linear EST 19-MAY-1999
tp19409.x1 NCI-CGAP-Gas4 Homo sapiens cDNA clone IMAGE:2188288
Similar to TR099634.099634 RIG-3.111 contains A1610607
elementL; mRNA sequence.
A1610607
A1610607.1 GI:4619774
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 658)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@email.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael K.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Leighton, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium (http://
www.bio.lnl.gov/bbrp/image/image.html)
Insert length: 2270 Std Error: 6.00
Seq primer: -400P from Gibco
High quality sequence stop: 372
POLYA-No.
Location/Qualifiers
1..658

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2188288"
/clone_lib="NCI-CGAP-Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site: 1; Salt;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
21549-011"
BASE COUNT 110 a 196 c 144 g 187 t 1 others
ORIGIN
Query Match 1.88; Score 53; DB 9; Length 658;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1189 GCCACCTTGCCCTCCCAAGTGTGGATTACAGGATGAGCCACTGGCCGC 1241
|||||
DB 243 GCCACCTTGCCCTCCCAAGTGTGGATTACAGGATGAGCCACTGGCCGC 295
|||||
RESULT 19
B1062371
LOCUS
DEFINITION B1062371 233 bp mRNA linear EST 15-JUN-2001
sequence.
ACCESSION B1062371
VERSION B1062371.1 GI:14469898
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 233)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordini, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bal, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, J.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202665
JOURNAL
MEDLINE
COMMENT
Contact: Simpson, A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3st2-IL3-UT0117-
160301-502-E10.1st3-2001-03-16st4-1)
Seq primer: puc 18 forward
High quality sequence stop: 233.
FEATURES
Location/Qualifiers
1..233
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0117"
/dev_stage="Adult"
/note="Organ: uterus_tumor; Vector: puc18; Site: 1; SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from GRESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

BASE COUNT 53 a 65 c 53 g 62 t
ORIGIN

Query Match 1.8%; Score 52; DB 13; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 1240
|||||
DB 137 GCCCACTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 188
|||||

RESULT 20

BI710918/c 249 bp mRNA linear EST 11-MAR-2002
LOCUS 1094904.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5023662
DEFINITION 5' similar to SW:AL07_HUMAN P39194 ALU SUBFAMILY SQ SEQUENCE
CONTAMINATION WARNING ENTRY. [1] ; mRNA sequence.

ACCESSION BI710918
VERSION
KEYWORDS
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 249)
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,
M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, H., Williams, T.,
Jackson, Y., and Bowers, Y.

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute,
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

TEL: 617-495-1812
FAX: 617-495-8557
EMAIL: dmelton@biohp.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)

Seq primer: -40BP from Gibco
High quality sequence stop: 140

FEATURES
SOURCE
1..249
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5023662"
/tissue_type="Insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1;
XhoI; Site: 2; EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 69 a 59 c 57 g 64 t
ORIGIN

Query Match 1.8%; Score 52; DB 14; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 21

BI711369 348 bp mRNA linear EST 11-MAR-2002
LOCUS 1094904.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:5023662
DEFINITION 3' similar to SW:AL07_HUMAN P39194 ALU SUBFAMILY SQ SEQUENCE
CONTAMINATION WARNING ENTRY. [1] ; mRNA sequence.

ACCESSION BI711369
VERSION
KEYWORDS
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 348)
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,
M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, H., Williams, T.,
Jackson, Y., and Bowers, Y.

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute,
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

TEL: 617-495-1812
FAX: 617-495-8557
EMAIL: dmelton@biohp.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)

Seq primer: -40BP from Gibco
High quality sequence stop: 316

FEATURES
SOURCE
1..348
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5023662"
/tissue_type="Insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1;
XhoI; Site: 2; EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 80 a 89 c 79 g 100 t
ORIGIN

Query Match 1.8%; Score 52; DB 13; Length 348;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCCACTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 1240
|||||
DB 246 GCCCACTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 297
|||||

```

RESULT 22
A1264119/c
LOCUS      A1264119      391 bp      mRNA      linear      EST 27-JAN-1999
DEFINITION q108h11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1855941
            3' similar to contains Alu repetitive element; mRNA sequence.
ACCESSION  A1264119
VERSION    A1264119.1 GI:3872322
KEYWORDS   EST
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 391)
REFERENCE  1
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-r@mail.nih.gov
            This clone is available royalty-free through LLN: contact the
            IMAGE Consortium (info@image.lln.gov) for further information.
            Insert length: 1507 Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES   Location/Qualifiers
            1..391
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:1855941"
            /clone_lib="Soares_NHMPu_S1"
            /tissue_type="Pooled human melanocyte, fetal heart, and
            pregnant uterus"
            /lab_host="DH10B"
            /note="Organ: mixed (see below); Vector: pTZ19-Pac
            (Pharmacia) with a modified polylinker; Site 1: Not 1;
            Site 2: Eco RI; Equal amounts of plasmid DNA from three
            normalized libraries (melanocyte 2N8M, pregnant uterus
            NHMPu, and fetal heart NBH19W) were mixed, and ss circles
            were made in vitro. Following RAP purification, this DNA
            was used as tracer in a subtractive hybridization
            reaction. The driver was PCR-amplified cDNAs from pools of
            5,000 clones made from the same 3 libraries. The pools
            consisted of T.M.A.G.E. clones 262242-265224,
            340488-345479, and 484488-485479."
            BASE COUNT  115 a  94 c  100 g  82 t
            ORIGIN
            Query Match      1.8%; Score 52; DB 14; Length 392;
            Best local Similarity 100.0%; Pred. No. 4.5e-09;
            Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  119  ACCCTGGCTCCCAAGTGGGATTACAGCATGACATGCTGGGACTGTCGGGACT 1244
            |||||||
DB   347  ACCCTGGCTCCCAAGTGGGATTACAGCATGACATGCTGGGACTGTCGGGACT 296
            |||||||

BASE COUNT  115 a  94 c  100 g  82 t
ORIGIN
            Query Match      1.8%; Score 52; DB 14; Length 392;
            Best local Similarity 100.0%; Pred. No. 4.5e-09;
            Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  119  ACCCTGGCTCCCAAGTGGGATTACAGCATGACATGCTGGGACTGTCGGGACT 1240
            |||||||
DB   120  GCCACCTTGGCTCCCAAGTGGGATTACAGCATGACATGACATGACATGAC 69
            |||||||

RESULT 23
BM730147/c
LOCUS      BM730147      392 bp      mRNA      linear      EST 01-MAR-2002
DEFINITION BM730147.1 Human insulinoma Homo sapiens cDNA clone IMAGE:5644585
            5' mRNA sequence.
ACCESSION  BM730147
VERSION    BM730147.1 GI:19051480
KEYWORDS   EST
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 392)
REFERENCE  1
AUTHORS   Hillier, L., Marra, M., Pape, D., Wyllie, T., Matten, L., Blaisdell, A.,
            Lemishka, I., Seearce, M., Brestelli, J., Gradwohl, J., Clifton, S.,
            Hillier, L., Marra, M., Pape, D., Wyllie, T., Matten, L., Blaisdell, A.,

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Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
, Jackson, Y. and Bowers, Y.
Endocrine pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco.
FEATURES   Location/Qualifiers
            1..392
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:5634585"
            /clone_lib="Human insulinoma"
            /tissue_type="Insulinoma"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
            XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
            (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue following the Washington
            University protocol
            (http://genome.wustl.edu/est/lambda_protocol.shtml).
            Please contact Hiroshi Inoue, MD/PhD for further
            information on this library (Metabolism Division, Permutt
            Laboratory, Washington University School of Medicine, Box
            8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
            is a Washington University Pancreas EST project library."
            BASE COUNT  115 a  91 c  102 g  84 t
            ORIGIN
            Query Match      1.8%; Score 52; DB 14; Length 392;
            Best local Similarity 100.0%; Pred. No. 4.5e-09;
            Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1189  GCCCAGCTTGGCTCCCAAGTGGGATTACAGCATGACGACCTGGGCC 1240
            |||||||
DB   120  GCCCAGCTTGGCTCCCAAGTGGGATTACAGCATGACGACCTGGGCC 69
            |||||||

RESULT 24
AA481408
LOCUS      AA481408      414 bp      mRNA      linear      EST 14-AUG-1997
DEFINITION zV02909.s1 NCI-CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746368 3'
            similar to contains Alu repetitive element; mRNA sequence.
ACCESSION  AA481408
VERSION    AA481408.1 GI:2210960
KEYWORDS   EST
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 414)
REFERENCE  1
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.

```

DNA Sequencing by: Washington University Genome Sequencing Center:
 Clone distribution: NCI-CGAP clone distribution: information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -41m13 fwd. RT from Amersham
 High quality sequence stop: 400.
 Location/Qualifiers

FEATURES

SOURCE

1..414

/organism="Homo sapiens"
 /db_xref="GDB:5945900"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:746368"
 /clone_lib="NCI-CGAP_GCH1"
 /tissue_type="germinal center: B cell"
 /lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (G2020+, IgD+),
 provided by Dr. Louis M. Staudt (NCI). ... David Allman
 (NCI) and Dr. Gerald Marti (CHER). cDNA synthesis was
 primed with a Not I oligo(dT) primer
 [5'-TGTTCAATCTCAAGTCGAGCGCGCGCTCATTTTITTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaído."

BASE COUNT

106 a

112 c

86 g

110 t

Query Match

1.8% Score 52; DB 9; Length 414;

Best Local Similarity 100.0%; Pred. No. 4.3e-09;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190

CCACCTTGGCTCCCAAGTCTGGGATTACAGCAGCCACTGCGCC 1241

DB 180

CCACCTTGGCTCCCAAGTCTGGGATTACAGCAGCCACTGCGCC 231

RESULT 25

A1679442

LOCUS

DEFINITION

tub3h07.x1 NCI-CGAP_Gas4 416 bp mRNA linear EST 15-DEC-1999
 similar to contains Alu repetitive element; contains element TAR1
 repetitive element ;, mRNA sequence.

ACCESSION

A1679442

VERSION

A1679442.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;

1 (bases 1 to 416)

NCI-CGAP

http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer

Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution: information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1074

Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 400.

Location/Qualifiers

1..416

FEATURES

SOURCE

1..416

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:2255773"

/clone_lib="NCI-CGAP_Gas4"

/tissue_type="poorly differentiated adenocarcinoma with

signet ring cell features"

/lab_host="JHI10B"

/note="Organ: stomach; Vector: pCHV-SPORT6, Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.69 kb. Life Technologies catalog #:

11549-011"

BASE COUNT

83 a

106 c

102 g

125 t

ORIGIN

1.8% Score 52; DB 9; Length 416;

Best Local Similarity 100.0%; Pred. No. 4.3e-09;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190

CCACCTTGGCTCCCAAGTCTGGGATTACAGCAGCCACTGCGCC 1241

DB 210

CCACCTTGGCTCCCAAGTCTGGGATTACAGCAGCCACTGCGCC 261

RESULT 26

A1337065

LOCUS

DEFINITION

417 bp mRNA linear EST 15-FEB-1999

qx82q11.x1 NCI-CGAP_G06 Homo sapiens cDNA clone IMAGE:2009050 3'

similar to contains Alu repetitive element; mRNA sequence.

ACCESSION

A1337065

VERSION

A1337065.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;

1 (bases 1 to 417)

NCI-CGAP

http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer

Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaído, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution: information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 528

Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 400.

Location/Qualifiers

1..417

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:2009060"

/clone_lib="NCI-CGAP_G06"

/tissue_type="pooled germ cell tumors"

/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA

from the normalized library NCI-CGAP_G04 was prepared, and

ss circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (cloneIDs

1257096-1258631, 1469064-1470983, and 1475592-1476743).

Subtraction by Bento Soares and M. Fatima Bonaído."

BASE COUNT

101 a

97 c

94 g

125 t

ORIGIN

101 a

97 c

94 g

125 t

FEATURES

SOURCE

1..417

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:2009060"

/clone_lib="NCI-CGAP_G06"

/tissue_type="pooled germ cell tumors"

/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA

from the normalized library NCI-CGAP_G04 was prepared, and

ss circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (cloneIDs

1257096-1258631, 1469064-1470983, and 1475592-1476743).

Subtraction by Bento Soares and M. Fatima Bonaído."

IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 761 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 444.
 Location/Qualifiers
 1. 455
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:1676040"
 /clone_lib="Soares_total_fetus_ND2HFR_9w"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /note="Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not 1 - oligo(dT) primer (5'-TGTTCAATCTGAATGGGAGCGCGGCAATTTTITTTTITTTT 4'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not 1 and cloned into the Not 1 and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Ronaldo."

BASE COUNT 136 a 105 c 111 g 103 t
 ORIGIN
 Query Match 1.8% Score 52: DB 9: Length 484:
 Best local Similarity 100.0%; Pred. No. 4: 10-09;
 Matches 52: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 ACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGGACGATGAGGACG 1244
 |||||||
 DB 359 ACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGGACGATGAGGACG 308

RESULT 30
 A1002969
 LOCUS
 DEFINITION
 A1002969 484 bp mRNA linear: EST 06-JUN-1998
 IMAGE:1699540 3' similar to contains Alu repetitive element
 ; contains element MER22 repetitive element 3' mRNA sequence.

ACCESSION A1002969
 VERSION A1002969.1 GI:3203383
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
 1 (bases 1 to 484)
 Hillier, L., Allen, M., Bowles, L., Dubouque, T., Gelsner, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, M.,
 Moore, B., Schellenberg, K., Stepien, M., Tan, E., Theisohn, R.,
 White, Y., Wyllie, J., Waterston, R., and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)
 Contact: Willson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8401, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu.
 This clone is available royalty free through LNCX. Contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 448.
 Location/Qualifiers
 1. 484
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1699540"
 /clone_lib="Gessler Wilms tumor"
 /sex="pooled (6)"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; RNA

was prepared from a pool of 6 anonymous Wilms' tumor RNAs. RNA was prepared by acid-phenol, followed by one round of oligo dT selection. cDNA library preparation was with the BRL/Life Tech. Superscript Plasmid system. An oligo-dT NotI primer for first strand synthesis generated gggccacccc(t)n at the 3' end of the clones. A 5' SalI adaptor was used with sequence 5'-gtgaccacgcgcg-3'. Resulting cDNAs were size selected (average size 2 kb), NotI digested, and ligated into NotI/SalI-cut pSPORT1. Library was constructed by Dr. Manfred Gessler."

BASE COUNT 126 a 131 c 103 g 124 t
 ORIGIN
 Query Match 1.8% Score 52: DB 9: Length 484:
 Best local Similarity 100.0%; Pred. No. 3: 9e-09;
 Matches 52: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGGACGATGAGGACG 1241
 |||||||
 DB 227 CCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGGACGATGAGGACG 278

RESULT 31
 BQ007739/c
 LOCUS
 DEFINITION
 BQ007739 493 bp mRNA linear: EST 26-MAR-2002
 IMAGE:5838861 3' mRNA sequence.
 BQ007739.1 GI:19732639
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
 1 (bases 1 to 493)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 310-440, >ALU
 Seq primer: M13 FORWARD
 POLYA+Yes.
 Location/Qualifiers
 1. 493
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5838861"
 /clone_lib="NCI-CGAP-E10"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: left pelvis; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI-CGAP-E10 is a cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Ronaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACTTGAC.

```

TAG-UI-H-E10
TAG-TISSUE=chondrosarcoma
TAG-SEQ=ACACTTCACAC
BASE COUNT      152 a   116 c   116 g   109 t
ORIGIN

Query Match      1.8%  Score 52:  DB 14:  Length 144:
Best Local Similarity 100.0%:  Pred. No. 3.9e-09:
Matches 52:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY  1193 ACCTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAGG 1244
      |||||
DB   362 ACCTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAGG 31:

RESULT 32
AQ489571
LOCUS      RPCL11-230P5-TV RPCL11 Homo sapiens genomic clone RPCL11-230P5,
DEFINITION DNA sequence.
ACCESSION  AQ489571
VERSION    AQ489571.1  GI:4675445
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
            1 (bases 1 to 501)
            Zhao, S., Adams, M.D., Niernman, W., Malek, J., de la Chapelle, and Vogel
            J.C.
            Use of BAC End Sequences from Library RPCL11 for Sequence Ready
            Map Building (1997)
            Unpublished (1997)
            Other_GSSs: RPCL11-230P5-TV
            Contact: Shaying Zhao, William Niernman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCL11. For BAC
            library availability, please contact Peter de Jong
            (peter@dejong.med.buffalo.edu). Clones may be purchased from
            BAC/RAC Resources (http://bacpac.med.buffalo.edu/~edering) or from
            Research Genetics (http://resgen.com). BAC end search page:
            http://www.tigr.org/tdb/human/human_end_search/human_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source           1..501
     organism="Homo sapiens"
     db_xref="GDB:7588109"
     db_xref="taxon:9606"
     clone="RPCL11-230P5"
     clone_lib="RPCL11"
     sex="Male"
     cell_type="Lymphocytes"
     note="Vector: pBACel61; Site 1: BACel61; Site 2: BACel61"
BASE COUNT      196 a   123 c   107 g   165 t
ORIGIN

Query Match      1.8%  Score 52:  DB 17:  Length 144:
Best Local Similarity 100.0%:  Pred. No. 7.9e-09:
Matches 52:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY  119 ACCTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAGG 1244
      |||||
DB   495 ACCTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAGG 44:

RESULT 34
AQ623696
LOCUS      RS-5319 A2.11.17A RPCL11 Human Male BAC library Homo sapiens
DEFINITION genomic clone Plate 895 Col-20 Row-E, DNA sequence.
ACCESSION  AQ623696
VERSION    AQ623696.1  GI:5086011
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
            1 (bases 1 to 545)
            Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, I.,
            Keller, A., Staker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and
            Hood, L.
            Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
            Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
            99380589
            Contact: Mahairas G.G., Wallace J.C., Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Green Acme Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3687
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCL11. For BAC
            library availability, please contact Peter de Jong
            (peter@dejong.med.buffalo.edu). Clones may be purchased from

```

```

AW971724
LOCUS      AW971724
DEFINITION EST384813 MAGE resequences, MAGL Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW971724
VERSION    AW971724.1  GI:8161570
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
            1 (bases 1 to 530)
            Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt
            J.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J., and
            Quackenbush, J.
            Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
            Unpublished (2000)
            Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 294
            Seq primer: Forward
            Location/Qualifiers
     source           1..530
     organism="Homo sapiens"
     db_xref="taxon:9606"
     clone_lib="MAGE resequences, MAGL"
     note="Vector: pBluescriptSKm"
BASE COUNT      135 a   139 c   111 g   145 t
ORIGIN

Query Match      1.8%  Score 52:  DB 10:  Length 530:
Best Local Similarity 100.0%:  Pred. No. 3.7e-09:
Matches 52:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY  1190 CCCACCTTGGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGC 1242
      |||||
DB   227 CCCACCTTGGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGC 278

RESULT 34
AQ623696
LOCUS      RS-5319 A2.11.17A RPCL11 Human Male BAC library Homo sapiens
DEFINITION genomic clone Plate 895 Col-20 Row-E, DNA sequence.
ACCESSION  AQ623696
VERSION    AQ623696.1  GI:5086011
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
            1 (bases 1 to 545)
            Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, I.,
            Keller, A., Staker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and
            Hood, L.
            Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
            Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
            99380589
            Contact: Mahairas G.G., Wallace J.C., Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Green Acme Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3687
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCL11. For BAC
            library availability, please contact Peter de Jong
            (peter@dejong.med.buffalo.edu). Clones may be purchased from

```

BACPAC Resources (http://bacpac.med.buffalo.edu/submiting_bac.htm)
or from Research Genetics (info@resgen.com) BAC End Web Server:
<http://www.htsc.washington.edu>
Plate: 895 row: E column: 20
Seq primer: 17
Class: BAC ends
High quality sequence stop: 545.

Location/Qualifiers
1, 545
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-895 Col-20 Row-E"
/clone_lib="RPC1-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6, Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

BASE COUNT 117 a 139 c 139 g 144 t 5 others
ORIGIN

Query Match 1.8%, Score 52; DB 17; Length 545;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGCATGAGCCACTGCGCCAGC 1245
|||||
Db 349 CCTTGGCTCCCAAGTCTGGGATTACAGCATGAGCCACTGCGCCAGC 402

RESULT 35
A1084593/c
LOCUS
DEFINITION
ox63f01.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE166107
3' similar to contains Alu repetitive element; mRNA sequence.
A1084593
VERSION
KEYWORDS
SOURCE
EST.
A1084593.1 GI:3423016
human.
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
1 (bases 1 to 583)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap/>
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available to all scientists through LNCX; contact the
IMAGE Consortium (<http://image.llnl.gov>) for further information.
Insert Length: 470 Std Error: 0.00
Seq primer: -40m13 fwd. E1 from Aresnaue
High quality sequence stop: 411.

Location/Qualifiers
1, 583
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:166107"
/clone_lib="Soares_NIHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH108"
/note="Organ: mixed (see below); Vector: pTZ19 Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NHM, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR amplified cDNAs from pools of
5,000 clones made from the same 4 libraries. The pools

FEATURES
Source

consisted of 1 M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479.
BASE COUNT 165 a 138 c 139 g 140 t 1 others
ORIGIN

Query Match 1.8%, Score 52; DB 9; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 ACCTTGGCTCCCAAGTCTGGGATTACAGCATGAGCCACTGCGCCAGC 1244
|||||
Db 346 ACCTTGGCTCCCAAGTCTGGGATTACAGCATGAGCCACTGCGCCAGC 295

RESULT 36
A0589333/c
LOCUS
DEFINITION
C17B1-EL-2645K6.TF C17B1-EL Homo sapiens genomic clone 2645K6, DNA
sequence.
A0589333
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
1 (bases 1 to 717)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hue@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M14-21
Class: BAC ends.

Location/Qualifiers
1, 717
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2645K6"
/clone_lib="C17B1-EL"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 222 a 175 c 140 g 180 t
ORIGIN

Query Match 1.8%, Score 52; DB 17; Length 717;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 CTCACGTGAATCTGCTCGCGGTTCAAGCGATTCTCTCGCTCAGCCCTC 1076
|||||
Db 464 CTCACGTGAATCTGCTCGCGGTTCAAGCGATTCTCTCTCGCTCAGCCCTC 413

RESULT 37
AV718287/c
LOCUS
DEFINITION
AV718287 FHTB Homo sapiens cDNA clone FHTB2 5', mRNA sequence.
AV718287
ACCESSION
VERSION
KEYWORDS
EST.
AV718287 1 GI:10815449


```

Source
ORGANISM human
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo;
Xiao, H., Peng, Y., Song, H., Gu, Y., Yang, Y., Gao, B., Xu, X., Li, S.,
Qian, B., Liu, F., Ou, J., Gao, X., Cheng, Z., Xu, Z., Peng, J., Xi, S., Gao,
W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Li, J., Chen, Z., and Han,
Z.
TITLE Homo sapiens cDNA FHTB clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zequang Han
Chinese National Human Genome Centre at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzq@cgsc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..753
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FHTB"
/clone_lib="FHTB"
/tissue_type="hypothalamus"
/dev_stage="Fetal"
/lab_host="BM25.8"
/Note="Vector: pTripletX2; Site_1: str1A; Site_2: str1B"
BASE COUNT 214 a 186 c 182 g 171 t
ORIGIN

Query Match 1.8%; Score 52; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCGACCTGGCTCCCAAGTCTGGGATTACAGCCATGACGACCTGCTG 1238
|||||
DB 52 CTGCGACCTGGCTCCCAAGTCTGGGATTACAGCCATGACGACCTGCTG 1238

RESULT 48
AC198714/c 171 bp DNA linear JSS 26 APR-1999
LOCUS RGC11-59J23.T3 RGC1-11 Homo sapiens genomic clone RGC1-11-59J23.
DEFINITION DNA sequence.
ACCESSION AC198714
VERSION AC198714.1 GI:3610913
KEYWORDS GSS
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo;
1 (bases 1 to 171)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Lurie, K., Geloen, K.,
Berry, K., Granger, D., Sub, E., Wilford, J., de Jong, J., and Vertel, J.C.
Use of human BAC End Sequences for Sequence Ready Map Building
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@igrr.org
Clones are derived from the human BAC library shc1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/bac\_ordering) or from
Research Genetics (http://www.resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html
Class: BAC ends.
Location/Qualifiers

Source
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo;
1 (bases 1 to 232)
Hillier, L., Allen, M., Bowles, L., Dubouque, T., Geisel, G., Jost, S.,
Krieman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schefflenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wyllie, T., Waterston, R., and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Willson, R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (infosimade.linl.gov) for further information.
Seq primer: -40m3 fwd. Et from Amersham
High quality sequence stop: 216.
Location/Qualifiers
1..232
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:B66185"
/clone_lib="Stratagene fetal retina 937202"
/sex="mixed"
/lab_host="SOLR (kanamycin resistant)"
/Note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled
retinal tissue Average insert size: 1.0 kb; Uni-ZAP XR
Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTITTTTITTT 3'"
BASE COUNT 48 a 51 c 55 g 78 t
ORIGIN

Query Match 1.8%; Score 51; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1031 GTAAAGCTCTGCGCTTCTGGGATTACAGGATTCCTGCTGCTGCTGCTGAG 1081

```

```

Source
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo;
1 (bases 1 to 232)
Hillier, L., Allen, M., Bowles, L., Dubouque, T., Geisel, G., Jost, S.,
Krieman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schefflenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wyllie, T., Waterston, R., and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Willson, R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (infosimade.linl.gov) for further information.
Seq primer: -40m3 fwd. Et from Amersham
High quality sequence stop: 216.
Location/Qualifiers
1..232
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:B66185"
/clone_lib="Stratagene fetal retina 937202"
/sex="mixed"
/lab_host="SOLR (kanamycin resistant)"
/Note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled
retinal tissue Average insert size: 1.0 kb; Uni-ZAP XR
Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTITTTTITTT 3'"
BASE COUNT 48 a 51 c 55 g 78 t
ORIGIN

Query Match 1.8%; Score 51; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1031 GTAAAGCTCTGCGCTTCTGGGATTACAGGATTCCTGCTGCTGCTGCTGAG 1081

```


JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000).
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-900, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/CICOR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?L:CM1812-031:NT0209-231100-609-cl08t3-2000-11-28&t4-1>)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 374.

FEATURES
SOURCE

1..375
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0209"
/dev_stage="Adult"

/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from OPSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
99 a 94 c 113 g 69 t

BASE COUNT
ORIGIN

Query Match 1.8%; Score 51; DB 12; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTGGCTCCCAAGTGTGGATTACAGCATGAGCCACTGGCCG 1240
|||||
Db 165 CCCACCTGGCTCCCAAGTGTGGATTACAGCATGAGCCACTGGCCG 115

RESULT 43
LOCUS

AQ280600 375 bp DNA linear GSS 22-Nov-1998
DEFINITION CITR1-EL-2516H22.Hr CITR1 EL Homo sapiens genomic clone 2516H22.
DNA sequence.

ACCESSION
VERSION
A0280600.1 GI:3906419
KEYWORDS
GSS.

SOURCE
ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 375)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linnard, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Witte, G., Shizuya, B., Simon, M. and
Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building

JOURNAL
COMMENT

Unpublished (1998)
Other GSSs: CITR1-EL-2516H22.FF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (int-resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/ls_and_search.htm.
Seq primer: M13 Reverse

FEATURES
SOURCE

Class: BAC ends.
Location/Qualifiers
1..379
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="2516H22"
/clone_lib="CITR1-EL"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
85 a 98 c 111 q 85 t

BASE COUNT
ORIGIN

Query Match 1.8%; Score 51; DB 17; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTGTGGATTACAGCATGAGCCACTGGCCCGC 1244
|||||
Db 174 CCTTGGCTCCCAAGTGTGGATTACAGCATGAGCCACTGGCCCGC 224

RESULT 44
LOCUS

AQ178114 394 bp DNA linear GSS 17-OCT-1998
DEFINITION HS-2217-B2_F01_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate-2217 Col-2 Row-L. DNA sequence.

ACCESSION
VERSION
A0178114
KEYWORDS
GSS.

AQ178114.1 GI:3575481
SOURCE
human.

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 394)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas G.G., Wallace J.C., Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-4887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2217 row: 1 column: 2
Class: BAC ends
High quality sequence stop: 394.
Location/Qualifiers
1..394
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_plate="2217 Col-2 Row-L"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
F-Coli DH10B"

FEATURES
SOURCE

71 a 104 c 78 g 137 t 4 others
Location/Qualifiers
1..394
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_plate="2217 Col-2 Row-L"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
F-Coli DH10B"

BASE COUNT
ORIGIN

Query Match 1.8%; Score 51; DB 17; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTGTGGATTACAGCATGAGCCACTGGCCCGC 1244
|||||
Db 252 CCTTGGCTCCCAAGTGTGGATTACAGCATGAGCCACTGGCCCGC 302

RESULT 45
#58672
LOCUS

DEFINITION
Y120405.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:205833 3' similar to contains Alu repetitive element; contains
1HR repetitive element ; mRNA sequence.

ACCESSION
#58672
VERSION
#58672.1 GI:1011504

KEYWORDS
EST.
SOURCE
human.

ORGANISM

Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Haxkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Leeman, G., Mathe, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tach, F., Treva, S., E., Waterston,
R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 353
Source: IMAGE Consortium, INL
This clone is available royalty-free through ENL. Contact the
IMAGE Consortium (info@image.lnln.gov) for further information.
Seq primer: Promega -2lm13
High quality sequence stop: 354.

JOURNAL

COMMENT

FEATURES
Location/Qualifiers
1..448

/organism="Homo sapiens"
/db_xref="GDB:3774964"
/db_xref="taxon:9606"
/clone="IMAGE:205833"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pTZ19 (Pharmacia)
with a modified polylinker. Site 1: Par 1; Site 2: Pco R1;
1st strand cDNA was primed with 4 Par 1 oligo(dT) primer
[5'-ACGCGAAGATTAACAAA-3']; 2nd strand cDNA was primed with
double-stranded cDNA was ligated to EcoRI adapters
(Pharmacia), digested with Par 1 and cloned into the Par 1
and Eco RI sites of the modified pTZ19 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Patricia Ronaldo."

BASE COUNT 98 a 131 c 103 g 114 t
ORIGIN

Query Match 1.8%; Score 51; DB 14; Length 448;
Best Local Similarity 100.0%; Pred. No. 9.7e 09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CTTGGCTCCCAAGTGGGATTACAGGATGAGACATGAGTGGCCAGC 1244
|||||
DB 215 CTTGGCTCCCAAGTGGGATTACAGGATGAGACATGAGTGGCCAGC 265

RESULT 46
AQ503896

LOCUS
DEFINITION
RPC1-11-280G12-TJ RPC1-11 Homo sapiens genomic clone RPC1-11-280G12
DNA sequence.

ACCESSION
AQ503896

VERSION
AQ503896.1 GI:4708643

KEYWORDS
GSS.

SOURCE
ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 476)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
J.C.
Use of PAC End Sequences from Library RPC1-11 for Sequence-Ready
Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeatigr.org

REFERENCE
AUTHORS

TITLE

JOURNAL

COMMENT

Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..476
/organism="Homo sapiens"
/db_xref="GDB:7607291"
/db_xref="taxon:9606"
/clone="RPC1-11-280G12"
/clone_lib="RPC1-11"
/sex="male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: PcoRI;
RPC111 Human Male BAC Library"

BASE COUNT 120 a 98 c 104 g 154 t
ORIGIN

Query Match 1.8%; Score 51; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 9.4e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACTTGGCTGCCAAAGTGGGATTACAGGATGAGCCACTGC 1237
|||||
DB 159 CTGCCACTTGGCTGCCAAAGTGGGATTACAGGATGAGCCACTGC 209

RESULT 47
AQ334511/c

LOCUS

DEFINITION
HS-5011-AL-F08-I7 RPC111 Human Male BAC Library Homo sapiens
genomic clone Plate-587 Col-15 Row-I, DNA sequence.

ACCESSION
AQ334511

VERSION
AQ334511.1 GI:4129372

KEYWORDS
GSS.

SOURCE
human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618

Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>.
Plate: 587 row: 1 column: 15
Seq primer: T7
Class: BAC ends
High quality sequence stop: 479.

FEATURES

Source
Location/Qualifiers
1..479
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-587 Col-15 Row-1"
/clone_lib="RPC111 Human Male BAC Library"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; RPC111 Human Male BAC Library"

BASE COUNT 149 a 99 c 113 g 117 t 1 others

Query Match 1.8%; Score 51; DB 17; Length 479;
Best Local Similarity 100.0%; Pred. No. 9.4e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGACCACTGGCTCCCAAGTCTGGGATTACAGGATGAGGACTG 1237

DB 342 CTGCCACTTGGCTCCCAAGTCTGGGATTACAGGATGAGGACTG 292

RESULT 48

AQ342716/C

LOCUS AQ342716 498 bp DNA linear GSS 06-MAY-1999
DEFINITION RPC111-113P19.TJ RPC111 Homo sapiens genomic clone RPC111-113P19,
DNA sequence.

ACCESSION AQ342716

VERSION AQ342716.1 GI:4167612

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
1 (bases 1 to 498)

REFERENCE Zhao,S., Adams,M.D., Nierman,W., Matek,J., de Jesus,P., and Venter
J.C.

AUTHORS Use of BAC End Sequences from Library RPC111-113P19 Sequence Ready

TITLE Map Building

JOURNAL Unpublished (1997)

COMMENT Other_GSSs: RPC111-113P19.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeettig@org

Clones are derived from the human BAC library RPC111. For BAC
library availability, please contact Dieter de Jager
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/bacpac/>) or from
Research Genetics (<http://info@resgen.com>). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.htm

seq primer: SP6

Class: BAC ends.

FEATURES

Source
Location/Qualifiers
1..498
/organism="Homo sapiens"
/db_xref="GDB:7543386"
/db_xref="taxon:9606"
/clone="RPC111-113P19"
/clone_lib="RPC111-113P19"
/cell_type="Lymphocytes"
/sex="Male"
/note="Vector: pBACe3.6; Site_1: EORI1; Site_2: EORI2"

BASE COUNT 146 a 114 c 122 g 115 t 1 others

Query Match 1.8%; Score 51; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 9.1e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCGACCTGGCTCCCAAGTCTGGGATTACAGGATGAGGACTGCGCC 1240
DB 210 CCGACCTGGCTCCCAAGTCTGGGATTACAGGATGAGGACTGCGCC 159

RESULT 49

A1912862

LOCUS A1912862

DEFINITION

531 bp mRNA linear EST 16-DEC-1999
t220b03.x1 NCI-CGAP Ut2 Homo sapiens cDNA clone IMAGE:2289101 3'
similar to contains Alu repetitive element; contains L1.13 L1
repetitive element 1; mRNA sequence.

ACCESSION A1912862

VERSION A1912862.1 GI:5632717

KEYWORDS EST.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
1 (bases 1 to 531)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cybpb@remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1410 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 415.

FEATURES

Source

Location/Qualifiers

1..531

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2289101"

/clone_lib="NCI-CGAP Ut2"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma; 3 pooled tumors"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.85 kb. Life Technologies catalog #:

11539-012"

BASE COUNT 152 a 141 c 106 g 131 t 1 others

Query Match 1.8%; Score 51; DB 9; Length 531;

Best Local Similarity 100.0%; Pred. No. 8.8e-09;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGATGAGGACTGCGCCGAGC 1244

DB 230 CCTTGGCTCCCAAGTCTGGGATTACAGGATGAGGACTGCGCCGAGC 280

RESULT 50

AQ395413

LOCUS AQ395413

DEFINITION

539 bp DNA linear GSS 06-MAR-1999

CITB1 E1-2546N10.1R CITB1-E1 Homo sapiens genomic clone 2546N10,

```

DNA sequence..
ACCESSION      AQ395411
VERSION        GI:4366439
KEYWORDS       GSS,
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae;
Homo;
Zhao,S., Adams,M.D., Nierman,W., Malek,J.J., Shizuya,H., Simon,M. and
Venter,J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSS: CITBI-EI-2546N10.IF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel.: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are available from Research Genetics (http://resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES             Location/Qualifiers
     source            1..539
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2546N10"
                     /clone_lib="CITBI-EI"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                        Caltech Human BAC Library J"
BASE COUNT          114 a   131 c   149 g   145 t
ORIGIN
Query Match               18%; Score 51; DB 17; Length 549;
Read local Similarity    100.0% ; Prod. No. 8,7e+09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1194 CTTGGCTGTCCAAAGTGTGGATTATCAAGAATGAAATAATCGTAATCCGAAT...244
|||||
|||
bb 175 GTTGTCCTCCCCAAGTGTGTGGATTATCAAGAATGAAATAATCGTAATCCGAAT...222

```

Search completed: May 10, 2003, 01:55:16
Job time : 4470.15 secs